



BACTERIOLOGICAL PROFILES OF SKIN FLORA ON EARLY CADAVER

By

CHONG CHI KWAN

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia in
Fulfilment of the Requirements for the Degree of Master of Science**

January 2022

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January 2022

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Post-mortem microbiology (PMM) has gained significant importance in the forensic department nowadays to determine the actual cause of death of adults and infants, especially for deaths caused by infection. PMM is of utmost importance when the cadaver does not show any apparent signs of infection. An infective that leads to death is usually suspected in sudden death. Therefore, the determination of infective cause can help in further management of pathogenic transmission and is thus able to prevent the occurrence of outbreaks. However, the current challenge in PMM is the difficulty in interpreting culture results, for example, differentiating the true pathogen from the contaminants, especially when there is a mixed growth in the samples. Mixed growth or contamination from skin flora may induce false positive results, leading to uncertainty and failure in identifying true pathogen. Therefore, information on post-mortem skin flora can be helpful in providing references for interpreting microbiological investigations in post-mortem cases. Early cadavers ($n=39$), which have an estimated post-mortem (ePMI) of less than 24 hours, under sudden unexpected death cases, were included in this study. Two body sites, namely the neck and femoral, of each cadaver were chosen as the sites to obtain skin samples. Blood samples from these two sites were routinely obtained for post-mortem microbiological culture. Cotton swabs were moistened with normal saline and were then rubbed vigorously and rotated to ensure that homogeneity in the skin areas were achieved by each swab. The swabs were then kept in 200 μ l of phosphate-buffered saline (PBS) for storage and transportation. DNA was extracted from each skin swab and high-throughput 16S rRNA sequencing was performed on the extracted DNA using the Illumina Miseq system to assess bacterial diversity and abundance. The sequence outputs were analysed by using the LotuS pipeline while the α -diversity and β -diversity were analysed by using the Quantitative Insights into Microbial Ecology (QIIME) software. The samples were mostly predominated by phylum *Proteobacteria* (61.20%), followed by *Firmicutes* (28.10%), *Actinobacteria* (10.00%) and *Bacteroidetes* (0.60%). In addition, the top 10 dominant genera from the samples were *Ochrobactrum* (24.70%), *Staphylococcus* (20.60%), other members of *Enterobacteriaceae* (17.70%), *Corynebacterium* (6.00%), *Enhydrobacter* (5.30%), *Acinetobacter* (4.30%), *Klebsiella* (3.40%), *Pseudomonas* (2.70%),

Stenotrophomonas (2.10%) and *Phycoccus* (2.00%) accordingly. Moreover, there were no statistical difference between the bacterial communities of the neck and femoral sites, except for genus *Corynebacterium* which showed significant difference in abundance between both body sites. Nevertheless, the results showed significant difference between the abundance of some bacterial genera found on the cadavers with ePMI less than 5 hours (ePMI<5H) and the cadavers with ePMI more than 5 hours (ePMI>5H). The findings of this study provides data on the known skin flora that presents on early cadavers, thus may help in determining the actual cause of death due to pathogenic infections.

Key words: Post-mortem microbiology; contamination; skin flora; post-mortem interval



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PROFIL BAKTERIOLOGI FLORA KULIT KE ATAS KADAVAR AWAL

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Ujian mikrobiologi bagi spesimen post-mortem atau dikenali sebagai post-mortem microbiology (PMM) telah mendapat perhatian oleh jabatan forensik bagi menentukan sebab sebenar kematian dalam kalangan orang dewasa dan bayi, terutama bagi kematian yang disebabkan oleh jangkitan. PMM adalah paling penting ketika kadaver tidak menunjukkan sebarang tanda jangkitan yang ketara. Jangkitan yang membawa kepada kematian biasanya disyaki dalam kes kematian tiba-tiba. Oleh itu, penentuan penyebab jangkitan membantu dalam pengurusan dan kawalan jangkitan dan berupaya mengelak berlakunya wabak. Walau bagaimanapun, cabaran PMM adalah kesukaran dalam menginterpretasi keputusan kultur dan membezakan patogen sebenar daripada kontaminan, terutama ketika terdapatnya pertumbuhan campuran dalam sampel. Pertumbuhan campuran atau kontaminasi dari flora kulit boleh menyebabkan keputusan positif palsu, seterusnya membawa kepada ketidakpastian dan kegagalan dalam mengenalpasti patogen sebenar. Oleh yang demikian, maklumat mengenai flora kulit dari ujian post-mortem dapat membantu dalam memberikan rujukan bagi menginterpretasi investigasi mikrobiologi dalam kes post-mortem. Kajian ini melibatkan kadaver awal (n=39) daripada kes kematian tiba-tiba, dengan anggaran selang post-mortem (ePMI) kurang daripada 24 jam. Dua bahagian tubuh, iaitu leher dan femoral, daripada setiap kadaver telah dipilih sebagai tempat bagi mendapatkan sampel kulit. Manakala, sampel darah daripada kedua-dua tempat tersebut secara rutin telah diperolehi bagi kultur mikrobiologi post-mortem. Swab kapas telah dibasahkan dengan salin normal dan kemudian digosokkan dengan kuat dan diputar bagi memastikan bahawa homogeniti pada kawasan kulit tercapai bagi setiap swab. Swab tersebut kemudiannya di simpan dalam 200µl salin fosfat tertimbang (PBS) bagi penyimpanan dan pemindahan. DNA telah diekstrak daripada setiap swab kulit dan penjujukan 16S rRNA celusan tinggi telah dijalankan ke atas DNA yang diekstrak menggunakan sistem Illumina Miseq bagi menilai kepelbagaian bakteria dan kelimpahan. Urutan output telah dianalisis menggunakan talian paip LotuS manakala α -diversiti dan β -diversiti telah dianalisis menggunakan Insight Kuantitatif ke dalam perisian Ekologi Mikrobial (QIIME). Sampel kebanyakannya didominasi oleh filum Proteobacteria (61.20%), diikuti oleh Firmicutes (28.10%), Actinobacteria (10.00%) dan Bacteroidetes (0.60%). Di samping itu, 10 genus

dominan daripada sampel ialah *Ochrobactrum* (24.70%), *Staphylococcus* (20.60%), penghuni lain *Enterobacteriaceae* (17.70%), *Corynebacterium* (6.00%), *Enhydrobacter* (5.30%), *Acinetobacter* (4.30%), *Klebsiella* (3.40%), *Pseudomonas* (2.70%), *Stenotrophomonas* (2.10%) dan *Phycococcus* (2.00%) mengikut urutan. Di samping itu, tidak terdapat perbezaan secara statistik antara komuniti bakteria bagi bahagian leher dan femoral, kecuali bagi genus *Corynebacterium* yang menunjukkan perbezaan yang signifikan dari segi kelimpahan antara kedua-dua lokasi tubuh. Walau bagaimanapun, hasil kajian menunjukkan perbezaan yang signifikan antara kelimpahan beberapa genus bakteria yang didapati pada kadaver dengan ePMI kurang daripada 5 jam (ePMI<5H) dan kadaver dengan ePMI lebih daripada 5 jam (ePMI>5H). Hasil kajian ini memberikan maklumat mengenai flora kulit yang wujud pada kadaver awal. Oleh itu, maklumat ini dapat membantu dalam menentukan sebab sebenar kematian yang diakibatkan oleh jangkitan patogen.

Kata Kunci: Mikrobiologi post-mortem; kontaminasi; flora kulit; selang post-mortem

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LIST OF ABBREVIATIONS

PMM	Post-mortem Microbiology
PMI	Post-mortem Interval
RNA	Ribonucleic acid
DNA	Deoxyribonucleic acid
PCR	Polymerase chain reaction
ATCC	American Type Culture Collection
QIIME	Quantitative Insights Into Microbial Ecology
SPSS	Statistical package for the social science
PCoA	Principal coordinate analysis
UPM	Universiti Putra Malaysia
HKL	Hospital Kuala Lumpur
PBS	Phosphate-buffered saline
TBE	Tris Borate EDTA
RTA	Real-time Analysis
SAV	Sequencing Analysis Viewer
OTU	Operational taxonomic units
RDP	Ribosomal Database Project
TTD	Time to detection

CHAPTER 1

INTRODUCTION

1.1 Background

Post-mortem microbiology (PMM) is becoming a trend in the field of forensic pathology. It is useful for investigating the possible cause of death, especially in cases of sudden death in adults and infants. PMM is important for determining the pathogenic agents that could contribute to deaths caused by infection. Identification of unknown pathogenic agents or biological warfare agents that can harm human life is one of the roles of PMM in preventing outbreaks. The 2001 anthrax letter attacks incident in the United States has highlighted the importance of PMM in preventing the occurrence of bioterrorism.

PMM examination is useful for evaluating ante-mortem clinical laboratory reports, as it can compare ante-mortem laboratory findings and post-mortem culture results. The results from a post-mortem culture can be used to confirm an ante-mortem diagnosis. The results can also be used to evaluate the efficacy of ante-mortem antimicrobial therapy (Riedel, 2014). Moreover, drug resistance can also be evaluated through PMM examination (Fernández-Rodríguez et al., 2015). Furthermore, the bacterial community changes as the time since death, the post-mortem interval (PMI), increases, as reported by Pechal et al. (2014). The bacterial community showed significant differences in the taxon richness and relative abundance at both phylum and family levels as the decomposition process proceeded (Pechal et al., 2014). Hence, PMM can be used to estimate the PMI. Determination of the PMI is crucial in forensic science, especially in criminal cases; it can be used as a clue to track down a criminal.

The results of PMM can be categorised into (a) genuine positive, (b) agonal spread, (c) bacterial translocation and (d) contamination (Riedel, 2014). Genuine positive can be referred to as true infection, which means the pathogenic agent that causes the death has been successfully isolated, and the microorganism isolated is usually a single isolate. The result is significant for confirming an infection. On the other hand, false positive results can include situations such as agonal spread, bacterial translocation and contamination. False positive results of post-mortem microbiological cultures may have mixed growth results, which means there are more than two microorganisms isolated (Spagnolo et al., 2019). Both agonal spread and bacterial translocation can represent the result of bacterial invasion of the bloodstream. Agonal spread occurs during the agonal period when systemic circulation is weakening, whereas bacterial translocation occurs when the circulation has ceased and the bacteria invade the bloodstream from the mucosal surface. Although the concept of agonal spread has been proposed, the definition of the concept is not literally verified. The occurrence of agonal spread is rare, and there are only a few historic studies explaining it (Riedel, 2014). Compared to agonal spread, bacterial translocation has been proven by researchers for decades. Bacterial translocation has been proven by substantial evidence, and usually occurs when the body is not being stored at a low temperature (Riedel, 2014). The microorganisms involved in bacterial

translocation are usually gastrointestinal tract commensals. Bacterial translocation can be avoided by storing the body at a low temperature (4°C), at which the PMM culture results will not be affected (Palmiere et al., 2016; Spagnolo et al., 2019).

Contrary to the concepts of agonal spread and bacterial translocation, contamination is the main problem in the field of forensic science in identifying true pathogenic agents. Standards issued by the American Society of Microbiology state that the rate of blood culture contamination should not exceed 3%. However, in practice, most hospital contamination rates are greater than that, with some of them reaching 7% of the contamination rate (Miller et al., 2018; Nannan Panday et al., 2019). Contamination generally happens during sampling. Bacteria are introduced into samples while the samples are being collected and therefore cause false positive results. Improper sampling techniques, the use of unsuitable transport media, anatomical sites for sampling and transient or resident bacterial colonisation of skin prior to death can be the reasons for contamination. Differentiation between true infection and contamination remains a major challenge in PMM examinations. Blood from heart, spleen cultures or peripheral venous sites is commonly obtained for PMM cultures. The positive rate has been reported as between 7% and 69% (Riedel, 2014). The contaminants can be normal skin flora, since bacteria may be introduced into samples while obtaining the blood cultures. For example, coagulase-negative staphylococci are commonly isolated and treated as contaminants because they are generally normal skin flora. On that premise, the patient does not associate with catheters or vascular prostheses.

1.2 Problem Statement

There are approximately 600 post-mortem cases per year in Hospital Kuala Lumpur, and PMM tests are indicated to rule out infections caused by a bacterial pathogen. However, occasionally culture results with isolated mixed growth of bacteria pose challenges in interpreting the PMM examination results. When there is mixed growth in the culture, true infection or contamination is unable to be determined when the source of bacteria is undetermined. Contamination can be due to inappropriate handling of specimens while collecting them. Furthermore, the true pathogen may be neglected, and this has made it more difficult to determine the possible cause of death.

Sampling site and the relevant skin flora are recommended to take into account for the interpretation of PMM examination results (Nordin, 2018). In order to deal with the possible contamination problem, it seems critical to know the skin microbiome of early cadavers. The skin microbiome can not only exclude contaminants, but can also help to determine the PMI. There are a few studies about the skin microbiome from cadavers; however, those studies mostly included cadavers with PMIs of more than 24 hours (Johnson et al., 2016; Metcalf et al., 2013). It is rare to have studies focus on cadavers with a PMI of less than 24 hours.

Therefore, this study aims to determine the commonly found skin flora on early cadavers. The outcome of this study can prevent misinterpretation in certain deaths of skin flora as

pathogens in post-mortem blood culture that may result from the contamination of the needle. It is necessary to know the normal skin flora of the early cadavers in order to help with the contamination problem.

1.3 Research Questions

- a. What type of skin flora will be present on early cadavers within 24 hours of time since death?
- b. What is the relationship between types of skin flora and anatomical sites as well as post-mortem interval?

1.4 Research Objectives

1.4.1 General Objective

To determine the bacterial profiles of skin flora on early cadavers

1.4.2 Specific Objectives

- i. To study the bacterial profiles of skin flora collected from neck and femoral sites on early cadavers.
- ii. To compare the differences of bacterial profiles collected from neck and femoral sites
- iii. To study the dynamic pattern of the flora profiles in relation to duration of earliest documented time of death to sampling time.

1.5 Hypothesis

There are different microorganisms appearing at different anatomical sites at different times of death.

REFERENCES

- Aguilera-Arreola, M. G., Ostria-Hernández, M. L., Albarrán-Fernández, E., Juárez-Enriquez, S. R., Majalca-Martínez, C., Rico-Verdín, B., Ruiz, E. A., Ruiz-Palma, M., Morales-García, M. R., & Contreras-Rodríguez, A. (2018). Correct Identification of *Ochrobactrum anthropi* From Blood Culture Using 16rRNA Sequencing: A First Case Report in an Immunocompromised Patient in Mexico. *Frontiers in Medicine*, 5.
- Amar, Y., Lagkouvardos, I., Silva, R. L., Ishola, O. A., Foesel, B. U., Kublik, S., Schöler, A., Niedermeier, S., Bleuel, R., Zink, A., Neuhaus, K., Schlöter, M., Biedermann, T., & Köberle, M. (2021). Pre-digest of unprotected DNA by Benzonase improves the representation of living skin bacteria and efficiently depletes host DNA. *Microbiome*, 9(1), 1-14.
- Anderson, M. J. (2001). A new method for non-parametric multivariate analysis of variance. *Austral Ecology*, 26(1), 32-46.
- Atakro, C. A., Addo, S. B., Aboagye, J. S., Blay, A. A., Amoa-Gyarteng, K. G., Menlah, A., Garti, I., Agyare, D. F., Junior, K. K., & Sarpong, L. (2019). Nurses' and Medical Officers' Knowledge, Attitude, and Preparedness Toward Potential Bioterrorism Attacks. *SAGE Open Nursing*, 5, 2377960819844378.
- Bay, L., Barnes, C. J., Fritz, B. G., Thorsen, J., Restrup, M., Rasmussen, L., Sørensen, J. K., Hesselvig, A. B., Odgaard, A., Hansen, A. J., & Bjarnsholt, T. (2020). Universal Dermal Microbiome in Human Skin. *MBio*, 11(1).
- Benbow, M. E., Pechal, J. L., Lang, J. M., Erb, R., & Wallace, J. R. (2015). The Potential of High-throughput Metagenomic Sequencing of Aquatic Bacterial Communities to Estimate the Postmortem Submersion Interval. *Journal of Forensic Sciences*, 60(6), 1500–1510.
- Bhatia, M., Mishra, B., Thakur, A., Dogra, V., & Loomba, P. S. (2016). Concept of forensic microbiology and its applications. *SMU Med J*, 3(1), 275-294.
- Bjerre, R. D., Hugerth, L. W., Boulund, F., Seifert, M., Johansen, J. D., & Engstrand, L. (2019). Effects of sampling strategy and DNA extraction on human skin microbiome investigations. *Scientific Reports*, 9(1).
- Blaser, M. J., Dominguez-Bello, M. G., Contreras, M., Magris, M., Hidalgo, G., Estrada, I., Gao, Z., Clemente, J. C., Costello, E. K., & Knight, R. (2013). Distinct cutaneous bacterial assemblages in a sampling of South American Amerindians and US residents. *The ISME Journal*, 7(1), 85–95.
- Burns, E. M., Ahmed, H., Isedeh, P. N., Kohli, I., Van Der Pol, W., Shaheen, A., Muzaffar, A. F., Al-Sadek, C., Foy, T. M., Abdelgawwad, M. S., Huda, S., Lim, H. W., Hamzavi, I., Bae, S., Morrow, C. D., Elmets, C. A., & Yusuf, N. (2019). Ultraviolet radiation, both UVA and UVB, influences the composition of the skin microbiome. *Experimental Dermatology*, 28(2), 136–141.

- Burton, J. L., Saegeman, V., Arribi, A., Rello, J., Andreoletti, L., Cohen, M. C., Fernandez-Rodriguez, A., & ESGFOR Joint Working Group of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) Study Group of Forensic and Postmortem Microbiology and the European Society of Pathology. (2019). Postmortem microbiology sampling following death in hospital: an ESGFOR task force consensus statement. *Journal of Clinical Pathology*, 72(5), 329–336.
- Byrd, A. L., Belkaid, Y., & Segre, J. A. (2018). The human skin microbiome. *Nature Reviews. Microbiology*, 16(3), 143–155.
- Can, I., Javan, G. T., Pozhitkov, A. E., & Noble, P. A. (2014). Distinctive thanatomicrobiome signatures found in the blood and internal organs of humans. *Journal of Microbiological Methods*, 106, 1–7.
- Caporaso, J. G., Lauber, C. L., Walters, W. A., Berg-Lyons, D., Lozupone, C. A., Turnbaugh, P. J., Fierer, N., & Knight, R. (2011). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proceedings of the National Academy of Sciences of the United States of America*, 108 Suppl 1(supplement_1), 4516–4522.
- Castillo, D. E., Nanda, S., & Keri, J. E. (2019). Propionibacterium (Cutibacterium) acnes Bacteriophage Therapy in Acne: Current Evidence and Future Perspectives. *Dermatology and Therapy*, 9(1), 19–31.
- Christoffersen S. (2015). The importance of microbiological testing for establishing cause of death in 42 forensic autopsies. *Forensic Science International*, 250, 27–32.
- Cocariu, E. A., Mageriu, V., Stăniceanu, F., Bastian, A., Socoliuc, C., & Zurac, S. (2016). Correlations Between the Autolytic Changes and Postmortem Interval in Refrigerated Cadavers. *Romanian Journal of Internal*, 54(2), 105–112.
- Cosseau, C., Romano-Bertrand, S., Duplan, H., Lucas, O., Ingrassia, I., Pigasse, C., Roques, C., & Jumas-Bilak, E. (2016). *Proteobacteria* from the human skin microbiota: Species-level diversity and hypotheses. *One Health (Amsterdam, Netherlands)*, 2, 33–41.
- D'Aleo, F., Bonanno, R., Bianco, G., & Trunfio, A. (2017). Postmortem microbiology as a routine tool for legal-medicine in Italy: is it time?. *Microbiologia Medica*, 32(2).
- Damann, F. E., Williams, D. E., & Layton, A. C. (2015). Potential Use of Bacterial Community Succession in Decaying Human Bone for Estimating Postmortem Interval. *Journal of Forensic Sciences*, 60(4), 844–850.
- DeBruyn, J. M., & Hauther, K. A. (2017). Postmortem succession of gut microbial communities in deceased human subjects. *PeerJ*, 5, e3437.

- Deel, H., Bucheli, S. R., Belk, A. D., Ogden, S., Lynne, A. M., Carter, D., Knight, R., & Metcalf, J. L. (2020). Using microbiome tools for estimating the postmortem interval. In *Elsevier eBooks* (pp. 171–191). Elsevier BV.
- DeSantis, T. Z., Hugenholtz, P., Larsen, N., Rojas, M., Brodie, E. L., Keller, K., Huber, T., Dalevi, D., Hu, P., & Andersen, G. L. (2006). Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Applied and Environmental Microbiology*, 72(7), 5069–5072.
- Desmond, A.U., Nicholas, O., & Emmanuel, O.O. (2018). Microbial Forensics: Forensic Relevance of the Individual Person's Microbial Signature. *The International Journal of Life-Sciences Scientific Research*, 4(5): 2037-2043.
- Dong, K., Xin, Y., Cao, F., Huang, Z., Sun, J., Peng, M., Liu, W., & Shi, P. (2019). Succession of oral microbiota community as a tool to estimate postmortem interval. *Scientific Reports*, 9(1).
- Dréno, B., Araviiskaia, E., Berardesca, E., Gontijo, G., Sanchez Viera, M., Xiang, L. F., Martin, R., & Bieber, T. (2016). Microbiome in healthy skin, update for dermatologists. *Journal of the European Academy of Dermatology and Venereology : JEADV*, 30(12), 2038–2047.
- Driessen, R., Latten, B., Bergmans, D., Hulsewe, R., Holtkamp, J., van der Horst, I., Kubat, B., & Schnabel, R. M. (2021). Clinical diagnoses vs. autopsy findings in early deceased septic patients in the intensive care: a retrospective cohort study. *Virchows Archiv : An International Journal of Pathology*, 478(6), 1173–1178.
- Edgar R. C. (2013). UPARSE: highly accurate OTU sequences from microbial amplicon reads. *Nature Methods*, 10(10), 996–998.
- Edmonds-Wilson, S. L., Nurinova, N. I., Zapka, C. A., Fierer, N., & Wilson, M. (2015). Review of human hand microbiome research. *Journal of Dermatological Science*, 80(1), 3–12.
- Fernández-Rodríguez, A. (2019). Post-mortem microbiology: Sampling and interpretation. In *Investigation of Sudden Infant Death Syndrome* (pp. 100–105). Cambridge University Press.
- Fernández-Rodríguez, A., Burton, J. L., Andreoletti, L., Alberola, J., Fornes, P., Merino, I., Martínez, M. J., Castillo, P., Sampaio-Maia, B., Caldas, I. M., Saegeman, V., Cohen, M. C., & ESGFOR and the ESP (2019). Post-mortem microbiology in sudden death: sampling protocols proposed in different clinical settings. *Clinical microbiology and infection : the official publication of the European Society of Clinical Microbiology and Infectious Diseases*, 25(5), 570–579.
- Fernández-Rodríguez, A., Cohen, M. C., Lucena, J., Van de Voorde, W., Angelini, A., Ziyade, N., & Saegeman, V. (2015). How to optimise the yield of forensic and clinical post-mortem microbiology with an adequate sampling: a proposal for

standardisation. *European Journal of Clinical Microbiology & Infectious Diseases* : official publication of the European Society of Clinical Microbiology, 34(5), 1045–1057.

- Fierer, N., Lauber, C. L., Zhou, N., McDonald, D., Costello, E. K., & Knight, R. (2010). Forensic identification using skin bacterial communities. *Proceedings of the National Academy of Sciences of the United States of America*, 107(14), 6477–6481.
- Finley, S. J., Benbow, M. E., & Javan, G. T. (2015). Microbial communities associated with human decomposition and their potential use as postmortem clocks. *International Journal of Legal Medicine*, 129(3), 623–632.
- García, M. G., Pérez-Cárceles, M. D., Osuna, E., & Legaz, I. (2020). Impact of the Human Microbiome in Forensic Sciences: a Systematic Review. *Applied and Environmental Microbiology*, 86(22).
- Goel A. K. (2015). Anthrax: A disease of biowarfare and public health importance. *World Journal of Clinical Cases*, 3(1), 20–33.
- Goldman L. (2018). Autopsy 2018: Still Necessary, Even if Occasionally Not Sufficient. *Circulation*, 137(25), 2686–2688.
- Grice, E. A., & Segre, J. A. (2011). The skin microbiome. *Nature Reviews. Microbiology*, 9(4), 244–253.
- Grice, E. A., Kong, H. H., Conlan, S., Deming, C. B., Davis, J., Young, A. C., NISC Comparative Sequencing Program, Bouffard, G. G., Blakesley, R. W., Murray, P. R., Green, E. D., Turner, M. L., & Segre, J. A. (2009). Topographical and temporal diversity of the human skin microbiome. *Science (New York, N.Y.)*, 324(5931), 1190–1192.
- Grogan, M. D., Bartow-McKenney, C., Flowers, L., Knight, S. A., Uberoi, A., & Grice, E. A. (2019). Research techniques made simple: profiling the skin microbiota. *Journal of Investigative Dermatology*, 139(4), 747-752.e1.
- Gupta, V. K., Paul, S., & Dutta, C. (2017). Geography, ethnicity or subsistence-specific variations in human microbiome composition and diversity. *Frontiers in Microbiology*, 8, 1162.
- Hagiya, H., Ohnishi, K., Maki, M., Watanabe, N., & Murase, T. (2013). Clinical characteristics of *Ochrobactrum anthropi* bacteremia. *Journal of Clinical Microbiology*, 51(4), 1330–1333.
- Heo, C. C., Mohamad, A. M., Ahmad Firdaus, M. S., Jeffery, J., & Baharudin, O. (2007). A preliminary study of insect succession on a pig carcass in a palm oil plantation in Malaysia. *Tropical Biomedicine*, 24(2), 23–27.

- Hospodsky, D., Pickering, A. J., Julian, T. R., Miller, D., Gorthala, S., Boehm, A. B., & Peccia, J. (2014). Hand bacterial communities vary across two different human populations. *Microbiology (Reading, England)*, 160(Pt 6), 1144–1152.
- Hu, X., Chang, L., Wang, Z., Liu, G., Hu, Z., & Li, N. (2020). Age- and Sex-Linked Bacterial Community Variation and Function Prediction from Insoles of Healthy Chinese Population. *Indian Journal of Microbiology*, 60(2), 222–229.
- Huang, S., Haiminen, N., Carrieri, A. P., Hu, R., Jiang, L., Parida, L., Russell, B., Allaband, C., Zarrinpar, A., Vázquez-Baeza, Y., Belda-Ferre, P., Zhou, H., Kim, H. C., Swafford, A. D., Knight, R., & Xu, Z. Z. (2020). Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. *MSystems*, 5(1).
- Humez, S., Delteil, C., Maurage, C. A., Torrents, J., Capuani, C., Tuchtan, L., & Piercecchi, M. D. (2019). Does the medical autopsy still have a place in the current diagnostic process? A 6-year retrospective study in two French University hospitals. *Forensic Sci Med Pathol* 15, 564–569.
- Hyde, E. R., Haarmann, D. P., Lynne, A. M., Bucheli, S. R., & Petrosino, J. F. (2013). The living dead: bacterial community structure of a cadaver at the onset and end of the bloat stage of decomposition. *PloS One*, 8(10), e77733.
- Hyde, E. R., Haarmann, D. P., Petrosino, J. F., Lynne, A. M., & Bucheli, S. R. (2015). Initial insights into bacterial succession during human decomposition. *International Journal of Legal Medicine*, 129(3), 661–671.
- Jain, T., Nema, V., Gupta, M., Kumawat, R., Singhal, P. K., Chaubey, G., Kango, N., & Shrivastava, P. (2020). A pilot study on showcasing the forensic relevance of skin microflora. *Research Square*.
- Javan, G. T., & Finley, S. J. (2018). What Is the “Thanatobiome” and What Is Its Relevance to Forensic Investigations?. In *Forensic Ecogenomics* (pp. 133-143). Elsevier.
- Javan, G. T., Finley, S. J., Abidin, Z., & Mulle, J. G. (2016). The thanatobiome: a missing piece of the microbial puzzle of death. *Frontiers in Microbiology*, 7, 225.
- Jegan C., Mangayarkarasi V., Rukadikar Ar., Anandi V. (2019). Prevalence of pathogens causing bacteraemia in tertiary care hospital. *Indian J Microbiol Res*, 6(1), 6-10.
- Johnson, H. R., Trinidad, D. D., Guzman, S., Khan, Z., Parziale, J. V., DeBruyn, J. M., & Lents, N. H. (2016). A Machine Learning Approach for Using the Postmortem Skin Microbiome to Estimate the Postmortem Interval. *PloS One*, 11(12), e0167370.
- Jugé, R., Rouaud-Tinguely, P., Breugnot, J., Servaes, K., Grimaldi, C., Roth, M. P., Coppin, H., & Closs, B. (2018). Shift in skin microbiota of Western European women across aging. *Journal of Applied Microbiology*, 125(3), 907–916.

- Kabir, B., Naik, D., Kumar, V.P., & Bhas, G. (2016). Awareness and knowledge about bioterrorism among medical students at a University in Malaysia. *Malaysian Applied Biology*, 45(2), 63–67.
- Khalid, N., Zainun, K. A., Hisham, S., Mazan, N. I., & Amin Nordin, S. (2018). Group B streptococcus infection in a sudden unexpected death of infancy - the importance of microbiological investigation at post-mortem. *Tropical Biomedicine*, 35(3), 604–609.
- Kim, H. J., Kim, J. J., Myeong, N. R., Kim, T., Kim, D., An, S., Kim, H., Park, T., Jang, S. I., Yeon, J. H., Kwack, I., & Sul, W. J. (2019). Segregation of age-related skin microbiome characteristics by functionality. *Scientific Reports*, 9(1), 1–11.
- Klindworth, A., Pruesse, E., Schweer, T., Peplies, J., Quast, C., Horn, M., & Glöckner, F. O. (2013). Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. *Nucleic Acids Research*, 41(1), e1.
- Klompas, M., Ochoa, A., Ji, W., McKenna, C., Clark, R., Shenoy, E. S., Hooper, D., Rhee, C., & CDC Prevention Epicenters Program (2020). Prevalence of Clinical Signs Within Reference Ranges Among Hospitalized Patients Prescribed Antibiotics for Pneumonia. *JAMA Network Open*, 3(7), e2010700.
- Kodama, W. A., Xu, Z., Metcalf, J. L., Song, S. J., Harrison, N., Knight, R., Carter, D. O., & Happy, C. B. (2019). Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. *Journal of Forensic Sciences*, 64(3), 791–798.
- Lauber, C. L., Zhou, N., Gordon, J. I., Knight, R., & Fierer, N. (2010). Effect of storage conditions on the assessment of bacterial community structure in soil and human-associated samples. *FEMS Microbiology Letters*, 307(1), 80–86.
- Leung, M. H., Wilkins, D., & Lee, P. K. (2015). Insights into the pan-microbiome: skin microbial communities of Chinese individuals differ from other racial groups. *Scientific Reports*, 5(1), 1–16.
- Martinez, R. M., & Wolk, D. M. (2016). Bloodstream infections. *Microbiology Spectrum*, 4(4).
- Meisel, J. S., Hannigan, G. D., Tyldsley, A. S., SanMiguel, A. J., Hodkinson, B. P., Zheng, Q., & Grice, E. A. (2016). Skin Microbiome Surveys Are Strongly Influenced by Experimental Design. *The Journal of Investigative Dermatology*, 136(5), 947–956.
- Metcalf J. L. (2019). Estimating the postmortem interval using microbes: Knowledge gaps and a path to technology adoption. *Forensic Science International. Genetics*, 38, 211–218.
- Metcalf, J. L., Wegener Parfrey, L., Gonzalez, A., Lauber, C. L., Knights, D., Ackermann, G., Humphrey, G. C., Gebert, M. J., Van Treuren, W., Berg-Lyons,

- D., Keepers, K., Guo, Y., Bullard, J., Fierer, N., Carter, D. O., & Knight, R. (2013). A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. *ELife*, 2, e01104.
- Metcalf, J. L., Xu, Z. Z., Bouslimani, A., Dorrestein, P., Carter, D. O., & Knight, R. (2017). Microbiome Tools for Forensic Science. *Trends in Biotechnology*, 35(9), 814–823.
- Metcalf, J. L., Xu, Z. Z., Weiss, S., Lax, S., Van Treuren, W., Hyde, E. R., Song, S. J., Amir, A., Larsen, P., Sangwan, N., Haarmann, D., Humphrey, G. C., Ackermann, G., Thompson, L. R., Lauber, C., Bibat, A., Nicholas, C., Gebert, M. J., Petrosino, J. F., Reed, S. C., ... Knight, R. (2016). Microbial community assembly and metabolic function during mammalian corpse decomposition. *Science (New York, N.Y.)*, 351(6269), 158–162.
- Micallef M. J. (2018). The autopsy and diagnosis of pulmonary thrombo-embolism. *Forensic Science, Medicine, and Pathology*, 14(2), 241–243.
- Miller, J. M., Binnicker, M. J., Campbell, S., Carroll, K. C., Chapin, K. C., Gilligan, P. H., Gonzalez, M. D., Jerris, R. C., Kehl, S. C., Patel, R., Pritt, B. S., Richter, S. S., Robinson-Dunn, B., Schwartzman, J. D., Snyder, J. W., Telford, S., 3rd, Theel, E. S., Thomson, R. B., Jr, Weinstein, M. P., & Yao, J. D. (2018). A Guide to Utilization of the Microbiology Laboratory for Diagnosis of Infectious Diseases: 2018 Update by the Infectious Diseases Society of America and the American Society for Microbiology. *Clinical Infectious Diseases : an official publication of the Infectious Diseases Society of America*, 67(6), e1–e94.
- Mustapha, N. A., Hu, A., Yu, C. P., Sharuddin, S. S., Ramli, N., Shirai, Y., & Maeda, T. (2018). Seeking key microorganisms for enhancing methane production in anaerobic digestion of waste sewage sludge. *Applied Microbiology And Biotechnology*, 102(12), 5323–5334.
- Na, J.Y., Park, J.H., Ham, S.H., Kim, H.S., Park, J.T. (2016). A Comparative Study of Postmortem Bacterial Culture and Identification Methods. *Korean Journal of Legal Medicine*, 40(2), 55-60.
- Nannan Panday, R. S., Wang, S., van de Ven, P. M., Hekker, T., Alam, N., & Nanayakkara, P. (2019). Evaluation of blood culture epidemiology and efficiency in a large European teaching hospital. *Plos One*, 14(3), e0214052.
- Noriki, S., Iino, S., Kinoshita, K., Fukazawa, Y., Inai, K., Sakai, T., & Kimura, H. (2019). Pathological analysis of cadavers for educational dissection by using postmortem imaging. *Pathology International*, 69(10), 580–600.
- Ogai, K., Nagase, S., Mukai, K., Iuchi, T., Mori, Y., Matsue, M., Sugitani, K., Sugama, J., & Okamoto, S. (2018). A Comparison of Techniques for Collecting Skin Microbiome Samples: Swabbing Versus Tape-Stripping. *Frontiers in Microbiology*, 9, 2362.

- Oh, J., Byrd, A. L., Park, M., NISC Comparative Sequencing Program, Kong, H. H., & Segre, J. A. (2016). Temporal Stability of the Human Skin Microbiome. *Cell*, 165(4), 854–866.
- Oliveira, M., & Amorim, A. (2018). Microbial forensics: new breakthroughs and future prospects. *Applied Microbiology and Biotechnology*, 102(24), 10377–10391.
- Palmiere, C., Egger, C., Prod'Hom, G., & Greub, G. (2016). Bacterial Translocation and Sample Contamination in Postmortem Microbiological Analyses. *Journal of Forensic Sciences*, 61(2), 367–374.
- Pantopikou K & Papasotiriou I (2017). Detection and Identification of Bacterial Contamination in Blood Samples from Cancer Patients. *Arch Clin Microbiol*, 8(3), 1-5.
- Park, J., Kim, S. J., Lee, J. A., Kim, J. W., & Kim, S. B. (2017). Microbial forensic analysis of human-associated bacteria inhabiting hand surface. *Forensic Science International: Genetics Supplement Series*, 6, e510-e512.
- Pechal, J. L., Crippen, T. L., Benbow, M. E., Tarone, A. M., Dowd, S., & Tomberlin, J. K. (2014). The potential use of bacterial community succession in forensics as described by high throughput metagenomic sequencing. *International Journal of Legal Medicine*, 128(1), 193–205.
- Pechal, J. L., Crippen, T. L., Tarone, A. M., Lewis, A. J., Tomberlin, J. K., & Benbow, M. E. (2013). Microbial community functional change during vertebrate carrion decomposition. *PloS One*, 8(11), e79035.
- Pechal, J. L., Schmidt, C. J., Jordan, H. R., & Benbow, M. E. (2018). A large-scale survey of the postmortem human microbiome, and its potential to provide insight into the living health condition. *Scientific Reports*, 8(1), 1-15.
- Perez Perez, G. I., Gao, Z., Jourdain, R., Ramirez, J., Gany, F., Clavaud, C., Demande, J., Breton, L., & Blaser, M. J. (2016). Body Site Is a More Determinant Factor than Human Population Diversity in the Healthy Skin Microbiome. *PloS One*, 11(4), e0151990.
- Petry N. M. (2002). A comparison of young, middle-aged, and older adult treatment-seeking pathological gamblers. *The Gerontologist*, 42(1), 92–99.
- Phan, K., Barash, M., Spindler, X., Gunn, P., & Roux, C. (2020). Retrieving forensic information about the donor through bacterial profiling. *International Journal of Legal Medicine*, 134(1), 21–29.
- Prast-Nielsen, S., Tobin, A. M., Adamzik, K., Powles, A., Hugerth, L. W., Sweeney, C., Kirby, B., Engstrand, L., & Fry, L. (2019). Investigation of the skin microbiome: swabs vs. biopsies. *The British Journal of Dermatology*, 181(3), 572–579.

- Procopio, N., Lovisolio, F., Sguazzi, G., Ghignone, S., Voyron, S., Migliario, M., Renò, F., Sellitto, F., D'Angiolella, G., Tozzo, P., Caenazzo, L., & Gino, S. (2021). "Touch microbiome" as a potential tool for forensic investigation: A pilot study. *Journal of Forensic and Legal Medicine*, 82, 102223.
- Qiao, Z., Huang, S., Leng, F., Bei, Y., Chen, Y., Chen, M., Hu, Y., Huang, Y., & Xiang, Q. (2021). Analysis of the Bacterial Flora of Sensitive Facial Skin Among Women in Guangzhou. *Clinical, Cosmetic and Investigational Dermatology*, 14, 655–664.
- R Core Team (2020). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. <https://www.R-project.org/>
- Rashidi, N. H. M., Azahar, A., Ibrahim, R., & Zakariah, S. Z. (2020). Persistent Community-acquired *Ochrobactrum anthropi* Bacteremia in Severe Dengue Infection: A Case Report. *Malaysian Journal of Medicine and Health Sciences*, 16(201).
- Rastogi, N., & Mathur, P. (2017). *Ochrobactrum anthropi*: An emerging pathogen causing meningitis with sepsis in a neurotrauma patient. *Journal of Infection in Developing Countries*, 11(9), 733–735.
- Riedel S. (2014). The value of postmortem microbiology cultures. *Journal of Clinical Microbiology*, 52(4), 1028–1033.
- Saegeman, V., Cohen, M. C., Alberola, J., Ziyade, N., Farina, C., ESCMID Study Group for Forensic and Postmortem Microbiology, Cornaglia, G., & Fernández-Rodríguez, A. (2017). How is post-mortem microbiology appraised by pathologists? Results from a practice survey conducted by ESGFOR. *European Journal of Clinical Microbiology & Infectious Diseases: Official Publication of the European Society of Clinical Microbiology*, 36(8), 1381–1385.
- Saegeman, V., Cohen, M. C., Burton, J. L., Martinez, M. J., Rakislova, N., Offiah, A. C., & Fernandez-Rodriguez, A. (2021). Microbiology in minimally invasive autopsy: best techniques to detect infection. ESGFOR (ESCMID study group of forensic and post-mortem microbiology) guidelines. *Forensic Science, Medicine, and Pathology*, 17(1), 87–100.
- Samaras, S., & Hoptroff, M. (2020). The Microbiome of Healthy Skin. *Skin Microbiome Handbook: From Basic Research to Product Development*, 1-32.
- SanMiguel, A., & Grice, E. A. (2015). Interactions between host factors and the skin microbiome. *Cellular and Molecular Life Sciences*, 72(8), 1499–1515.
- Schmedes, S. E., Sajantila, A., & Budowle, B. (2016). Expansion of Microbial Forensics. *Journal of Clinical Microbiology*, 54(8), 1964–1974.
- Schmedes, S. E., Woerner, A. E., & Budowle, B. (2017). Forensic Human Identification Using Skin Microbiomes. *Applied and Environmental Microbiology*, 83(22).

- Shi, X. Y., Wang, J., Zhang, W. N., Zhao, M., Ju, J., Li, X. Y., Lu, Q., Wang, B., & Zou, L. P. (2021). Cesarean Section Due to Social Factors Affects Children's Psychology and Behavior: A Retrospective Cohort Study. *Frontiers in Pediatrics*, 8, 586957.
- Shibagaki, N., Suda, W., Clavaud, C., Bastien, P., Takayasu, L., Iioka, E., Kurokawa, R., Yamashita, N., Hattori, Y., Shindo, C., Breton, L., & Hattori, M. (2017). Aging-related changes in the diversity of women's skin microbiomes associated with oral bacteria. *Scientific Reports*, 7(1), 1-10.
- Shojania, K. G., & Burton, E. C. (2008). The vanishing nonforensic autopsy. *The New England Journal of Medicine*, 358(9), 873–875.
- Steglińska, A., Jachowicz, A., Szulc, J., Adamiak, J., Otlewska, A., Pielech-Przybylska, K., & Gutarowska, B. (2019). Factors Influencing Microbiological Biodiversity of Human Foot Skin. *International Journal of Environmental Research and Public Health*, 16(18), 3503.
- Tekle, M., Legesse, M., Edao, B. M., Ameni, G., & Mamo, G. (2019). Isolation and identification of *Brucella melitensis* using bacteriological and molecular tools from aborted goats in the Afar region of north-eastern Ethiopia. *BMC Microbiology*, 19(1), 1-6.
- Teo, C. H., Pawita, A. H., Khairul, O., Atiah Ayunni, A. G., & Noor Hazfalinda, H. (2013). Post mortem changes in relation to different types of clothing. *The Malaysian Journal of Pathology*, 35(1), 77–85.
- Tsokos, M., & Püschel, K. (2001). Postmortem bacteriology in forensic pathology: diagnostic value and interpretation. *Legal Medicine (Tokyo, Japan)*, 3(1), 15–22.
- Van Rensburg, J. J., Lin, H., Gao, X., Toh, E., Fortney, K. R., Ellinger, S., Zwickl, B., Janowicz, D. M., Katz, B. P., Nelson, D. E., Dong, Q., & Spinola, S. M. (2015). The Human Skin Microbiome Associates with the Outcome of and Is Influenced by Bacterial Infection. *MBio*, 6(5), e01315-15.
- Vargas-Robles, D., Gonzalez-Cedillo, C., Hernandez, A. M., Alcaraz, L. D., & Peimbert, M. (2020). Passenger-surface microbiome interactions in the subway of Mexico City. *PloS One*, 15(8), e0237272.
- Vázquez-Baeza, Y., Pirrung, M., Gonzalez, A., & Knight, R. (2013). EMPeror: a tool for visualizing high-throughput microbial community data. *Gigascience*, 2(1), 16.
- Ventura Spagnolo, E., Stassi, C., Mondello, C., Zerbo, S., Milone, L., & Argo, A. (2019). Forensic microbiology applications: A systematic review. *Legal Medicine (Tokyo, Japan)*, 36, 73–80.
- Vila, A., Pagella, H., Vera Bello, G., & Vicente, A. (2016). *Brucella suis* bacteremia misidentified as *Ochrobactrum anthropi* by the VITEK 2 system. *Journal of Infection in Developing Countries*, 10(4), 432–436.

- Watanabe, H., Nakamura, I., Mizutani, S., Kurokawa, Y., Mori, H., Kurokawa, K., & Yamada, T. (2018). Minor taxa in human skin microbiome contribute to the personal identification. *PloS One*, 13(7), e0199947.
- Wen, Y., Xiao, F., Wang, C., & Wang, Z. (2016). The impact of different methods of DNA extraction on microbial community measures of BALF samples based on metagenomic data. *American Journal of Translational Research*, 8(3), 1412–1425.
- Whickam, H., & Sievert, C. (2016). *ggplot2: Elegant Graphics for Data Analysis*. New York, NY : Springer Science+Business Media, LLC. <https://ggplot2.tidyverse.org>
- Wickham, H. (2007). Reshaping data with the reshape package. *Journal of Statistical Software*, 21(12), 1-20.
- Wilkins, D., Leung, M. H., & Lee, P. K. (2017). Microbiota fingerprints lose individually identifying features over time. *Microbiome*, 5(1), 1-9.
- Wise, N. M. (2021). *Determining Ideal Swab Type for Collection of the Microbiome for Forensic Identification Purposes* (Doctoral dissertation, Bowling Green State University).
- Yao, T., Han, X., Guan, T., Zhai, C., Liu, C., Liu, C., Zhu, B., & Chen, L. (2021). Exploration of the microbiome community for saliva, skin, and a mixture of both from a population living in Guangdong. *International Journal of Legal Medicine*, 135(1), 53–62.
- Ying, S., Zeng, D. N., Chi, L., Tan, Y., Galzote, C., Cardona, C., Lax, S., Gilbert, J., & Quan, Z. X. (2015). The Influence of Age and Gender on Skin-Associated Microbial Communities in Urban and Rural Human Populations. *PloS One*, 10(10), e0141842.
- Yu, D., Ininbergs, K., Hedman, K., Giske, C. G., Strålin, K., & Özenci, V. (2020). Low prevalence of bloodstream infection and high blood culture contamination rates in patients with COVID-19. *PloS One*, 15(11), e0242533.
- Zapka, C., Leff, J., Henley, J., Tittl, J., De Nardo, E., Butler, M., Griggs, R., Fierer, N., & Edmonds-Wilson, S. (2017). Comparison of Standard Culture-Based Method to Culture-Independent Method for Evaluation of Hygiene Effects on the Hand Microbiome. *MBio*, 8(2), e00093-17.
- Zhai, W., Huang, Y., Zhang, X., Fei, W., Chang, Y., Cheng, S., Zhou, Y., Gao, J., Tang, X., Zhang, X., & Yang, S. (2018). Profile of the skin microbiota in a healthy Chinese population. *The Journal of Dermatology*, 45(11), 1289–1300.