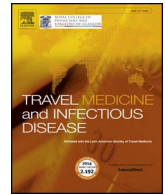




Contents lists available at ScienceDirect

Travel Medicine and Infectious Disease

journal homepage: www.elsevier.com/locate/tmaid

The role of ‘filth flies’ in the spread of antimicrobial resistance

Francis C. Onwugamba^a, J. Ross Fitzgerald^b, Kateryn Rochon^c, Luca Guardabassi^d, Abraham Alabi^{e,f}, Stefan Kühne^g, Martin P. Grobusch^{e,f,h}, Frieder Schaumburg^{a,*}^a Institute of Medical Microbiology, University Hospital Münster, Münster, Germany^b The Roslin Institute, University of Edinburgh, Edinburgh, UK^c Department of Entomology, University of Manitoba, Winnipeg, Canada^d Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg, Denmark^e Centre de Recherches Médicales de Lambaréné (CERMEL), Lambaréné, Gabon^f Institut für Tropenmedizin, Eberhard Karls Universität Tübingen, Deutsches Zentrum für Infektionsforschung, Tübingen, Deutschland, Germany^g Julius Kühn Institute, Federal Research Centre for Cultivated Plants, Kleinmachnow, Germany^h Center of Tropical Medicine and Travel Medicine, Department of Infectious Diseases, Division of Internal Medicine, Academic Medical Center, University of Amsterdam, Amsterdam, The Netherlands

ARTICLE INFO

Keywords:

Diptera

Antimicrobial resistance

Transmission

Bacteria

ABSTRACT

Background: ‘Filth flies’ feed and develop in excrement and decaying matter and can transmit enteric pathogens to humans and animals, leading to colonization and infection. Considering these characteristics, ‘filth flies’ are potential vectors for the spread of antimicrobial resistance (AMR). This review defines the role of flies in the spread of AMR and identifies knowledge gaps.

Methods: The literature search (original articles, reviews indexed for PubMed) was restricted to the English language. References of identified studies were screened for additional sources.

Results: ‘Filth flies’ are colonized with antimicrobial-resistant bacteria of clinical relevance. This includes extended spectrum beta-lactamase-, carbapenemase-producing and colistin-resistant (*mcr-1* positive) bacteria. Resistant bacteria in flies often share the same genotypes with bacteria from humans and animals when their habitat overlap. The risk of transmission is most likely highest for enteric bacteria as they are shed in high concentration in excrements and are easily picked up by flies. ‘Filth flies’ can ‘bio-enhance’ the transmission of AMR as bacteria multiply in the digestive tract, mouthparts and regurgitation spots.

Conclusion: To better understand the medical importance of AMR in flies, quantitative risk assessment models should be refined and fed with additional data (e.g. vectorial capacity, colonization dose). This requires targeted ecological, epidemiological and *in vivo* experimental studies.

1. Introduction

“According to our best sanitarians”, Samuel Miller reported to the Massachusetts Association of Boards of Health in 1914 “flies breed disease” and concluded: “The fly is a curse.” [1]. So-called ‘filth flies’ have been linked to faecal-oral transmission of bacteria [2], fungi [3,4], parasites [5,6] and viruses [7,8] (Fig. 1). ‘Filth flies’ are defined as flies that use excrement and decaying matter for nutrition and oviposition [9]. All medically relevant ‘filth flies’ have some characteristics in common: they are coprophagic (feeding on animal manure and human faeces) or omnivorous, synanthropic (living in association with humans) and endophilic (preferring in-house dwelling) [10]. Of over 125,000 species belonging to the order Diptera (true flies) at least two main families of ‘filth flies’ are involved in the transmission of

medically important pathogens namely *Muscidae*, and *Calliphoridae* [5,11]. Moreover, these flies have a great potential to contribute to the dissemination of bacteria (e.g. enteric pathogens and commensal bacteria) due to their remarkable ability to move freely between different habitats and overcome long flight distances (5–7 km) [12–16]. Therefore, it is likely that they play a role in the spread of antimicrobial resistance (AMR) between animals and humans. Recent reports have shown that the fly gut provides a suitable environment for carriage of antimicrobial resistant bacteria and horizontal transfer of AMR genes [17,18].

Mathematical models are suitable tools to assess the risk bacterial transmission. The quantitative microbial risk assessment (QMRA) is frequently used in food production processes to evaluate food safety. The four stages of QMRA are hazard identification (e.g. population at

* Corresponding author. Institute of Medical Microbiology, University Hospital Münster, Domagkstr. 10, 48149 Münster, Germany.
E-mail address: frieder.schaumburg@ukmuenster.de (F. Schaumburg).

<https://doi.org/10.1016/j.tmaid.2018.02.007>

Received 20 December 2017; Received in revised form 12 February 2018; Accepted 19 February 2018

1477-8939/ © 2018 The Authors. Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Abbreviations

AMR	antimicrobial resistance	ESBL	extended-spectrum beta-lactamase
CFU	colony forming units	MLST	multilocus sequence typing
CRE	carbapenem-resistant <i>Enterobacteriaceae</i>	MRSA	methicillin-resistant <i>Staphylococcus aureus</i>
GCP-ICH	Good Clinical Practice-International Conference of	PFGE	pulsed field gel electrophoresis
		QMRA	quantitative microbial risk assessment

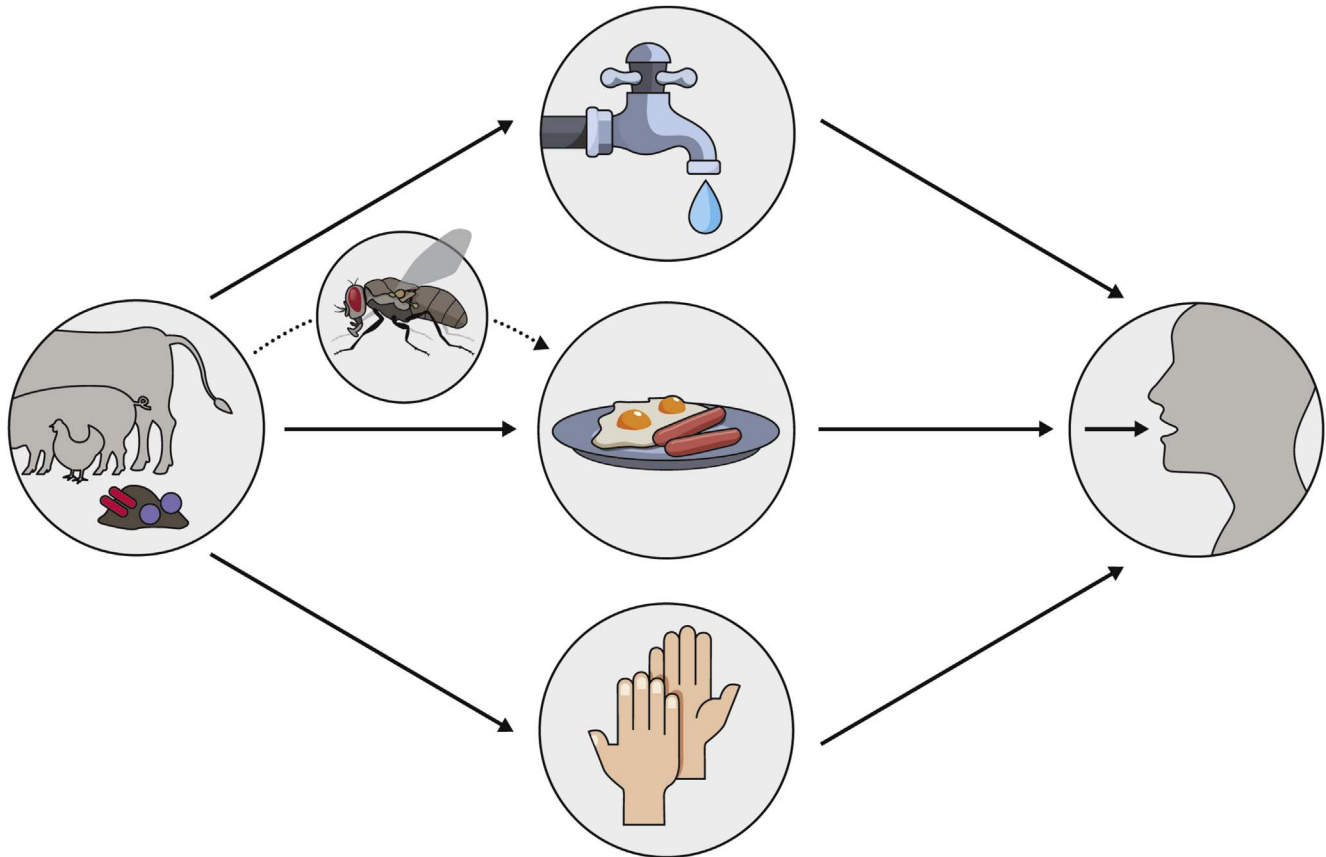


Fig. 1. Pathways of faecal-oral transmission. Pathogens from faeces can be transmitted to humans or animals through drinking water, food or hands (smear infection). Flies can enhance the contamination of food, as no direct contact of food and faeces is necessary.

risk to acquire a certain pathogen), dose-response (e.g. exposure dose to health outcomes), exposure (i.e. pathways of microbes to reach the population) and risk characterization (i.e. probability of an health outcome after exposure) [19]. Such a QMRA has been developed for the transmission of resistant bacteria from poultry to humans through flies [20].

In their review, Zurek and Gosh already described the colonization of insects in general with antimicrobial resistant bacteria and suggested that flies play a role in the spread of antimicrobial resistant bacteria between livestock and urban areas [21]. In our review we built on this work by giving an updated epidemiological picture of AMR with a special focus on ‘filth flies’ and on emerging antimicrobial resistance phenotypes of clinical relevance (e.g. extended-spectrum beta-lactamase (ESBL)-producing *Enterobacteriaceae*, carbapenem- and colistin resistant Gram-negative bacteria, see Supplement and Table A1 for methods). We identified knowledge gaps and suggest topics for future research initiatives.

2. Occurrence and fate of medically relevant bacteria in ‘filth flies’

Flies can carry medically relevant bacteria on the surface of their exoskeleton (e.g. legs, mouthparts) and in the alimentary canal (Table A2). Consequently, bacterial transmission can occur through

regurgitation, defecation or translocation from the exoskeleton (Figs. 1 and 2) [2]. The ingestion of flies by insectivores could be an additional route of transmission [22]. Finally, degrading flies can contaminate the environment with antimicrobial-resistant bacteria. Numerous studies assessed bacterial colonization in pooled fly samples [12,23–25]. However, this approach is inappropriate to measure the actual prevalence in individual flies.

It is methodically simple to analyze the prevalence of bacteria on the body surface (washing off the microbiota from the exoskeleton) separately from the intestine (dissection of the alimentary canal after surface disinfection) [26]. The available studies applied different pathogen detection methods (e.g. PCR, culture, selective media, and broth enrichment). Therefore, the carrier rates should be compared cautiously.

According to a study analyzing individual flies (*Muscidae*, *Calliphoridae*) collected from urban restaurants in the USA, similar colonization rates were found in the intestine compared to the exoskeleton for *Salmonella enterica* (6 vs. 1%) and *Listeria monocytogenes* (3 vs. 1%) using a PCR-based system [27]. However, the majority of studies analyzed bacterial colonization of the body surface only. Very high rates were found for *Klebsiella* spp. (51.9%), *Escherichia coli* (32.1%) and *Pseudomonas aeruginosa* (26.9%) in flies collected from fresh-food markets, garbage piles, restaurants, school cafeterias and rice paddies in

Download English Version:

<https://daneshyari.com/en/article/8743891>

Download Persian Version:

<https://daneshyari.com/article/8743891>

[Daneshyari.com](https://daneshyari.com)