

Archive ouverte UNIGE

https://archive-ouverte.unige.ch

Article professionnel

Article

2014

Published version

Open Access

This is the published version of the publication, made available in accordance with the publisher's policy.

Staphylococcus aureus: the innocent culprit?

van Belkum, Alex; Schrenzel, Jacques

How to cite

VAN BELKUM, Alex, SCHRENZEL, Jacques. Staphylococcus aureus: the innocent culprit? In: Infection, genetics and evolution, 2014, vol. 21, p. 509. doi: 10.1016/j.meegid.2013.09.001

This publication URL: https://archive-ouverte.unige.ch/unige:40274

Publication DOI: <u>10.1016/j.meegid.2013.09.001</u>

© This document is protected by copyright. Please refer to copyright holder(s) for terms of use.

ELSEVIER

Contents lists available at ScienceDirect

Infection, Genetics and Evolution

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



Editorial

Staphylococcus aureus: The innocent culprit?



Staphylococcus aureus is a ubiquitous bacterial species colonizing skin and mucous membranes in humans and a variety of other host animals. The frequency with which *S. aureus* is encountered as an innocent colonizer suggests that there may be mutual profitability for both the guest and the host: more that 60% of all humans are culture positive when cross sectional studies are performed and essentially 100% of humans are sero-positive for a diversity of staphylococcal antigens. This shows that we all meet and interact with this bacterial species and that we mount a humoral and probably also a cellular immune response against a spectrum of its antigens including proteins that are considered real virulence factors. It is not clear whether humans profit from colonization and in which way the bacteria select the anatomical sites of colonization. The bacterial preference for the nasal (vestibulum nasi) niche remains an enigma.

To date there is only sparse information on the relevance of the human humoral immune responses with regard to their protective status when the colonizer causes invasive infections. The latter happens often when immunity of the host is harmed or when big wound surfaces or other predisposing factors are available. This shows that additional research into the pathophysiology of both colonization and infection by S. aureus is urgently required. This urgency is becoming even more apparent if the current development and evolution of multi-antibiotic resistance in this bacterial species is considered. The risk of infection, 80% of which is endogenous in its source, in combination with reduced antibiotic susceptibility and hence reduced therapeutic options, is still excessive in susceptible humans and resulting infections are increasingly difficult to treat. This clearly shows that staphylococcology (remember this new discipline!) still is an important science from both the fundamental and clinical perspective.

This special issue of Infection, Genetics and Epidemiology is fully dedicated to *S. aureus* and its evolution, epidemiology, infectiology and biology. In about a dozen of publications various aspects of the interactions between humans and bacterial cells are highlighted. The fundamental aspects and our current limitations with regard to human and veterinary bacterial carriage and subsequent risks of human infection are discussed in papers by Sollid et al. and Verkade et al. Virulence factors, primarily those proteins forming the family of staphylococcal toxins, are reviewed by Broeker

et al. The evolution of virulence as a whole is presented by Peleg et al. It is well known that bacteriophages help shape bacterial evolution and this will also reflect upon the human host: this important phenomenon is discussed by Wolz and colleagues. In addition, S. aureus has a diverse range of phenotypes among which the small colony variant (SCV) type. The importance of such presentations is reviewed by Kahl et al. The other manuscript deals with genuine in vivo evolution of S. aureus bacteria. The ways in which S. aureus adapts to various environmental challenges are the core of the current issue and evolution of bacteria during colonization and infection is reviewed by Fitzgerald and colleagues. More specifically, genetic variation as can be captured during outbreaks of infections and, hence, transmission of bacteria between hosts is the topic of the paper by Lindsay et al. The last two papers deal with the evolution of drug resistant strains of S. aureus. Methicillin resistant strains deriving from hospital or community acquired infections will be compared (DeLeo et al.) whereas the development of vancomycin resistance will be discussed by Howden and colleagues.

In all, this issue provides the reader with a timely overview of the information that is currently available with relevance to the *in vivo* evolution of *S. aureus*. We wish you pleasant reading and to enjoy our shared passion for staphylococology!

> Alex van Belkum BioMérieux, Microbiology R&D, 3, Route de Port Michaud, La Balme les Grottes, France Mobile: +33 609487905.

> > E-mail address: alex.vanbelkum@biomerieux.com

Jacques Schrenzel*

Geneva University Hospitals, Bacteriology & Genomics Laboratories, Rue
Gabrielle-Perret-Gentil 4, CH-1211 Geneva, Switzerland

* Tel.: +41 22 372 7308; fax: +41 22 372 7304.

E-mail address: jacques.schrenzel@genomic.ch

Available online 7 September 2013