Precision medicine in microbiology: personalizing antimicrobial and anti-inflammatory treatments in people with cystic fibrosis

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- Let's take a closer look at these issues

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Speed - whole genome sequencing for antimicrobial susceptibility testing

Clinical Sample



bacteria on selective media

Predicting antimicrobial susceptibilities for *Escherichia coli* and *Klebsiella pneumoniae* isolates using whole genomic sequence data

N. Stoesser^{1,2*}, E. M. Batty³, D. W. Eyre¹, M. Morgan², D. H. Wyllie⁴, C. Del Ojo Elias¹, J. R. Johnson⁵, A. S. Walker¹, T. E. A. Peto¹ and D. W. Crook^{1,2}

Prediction of *Staphylococcus aureus* Antimicrobial Resistance by Whole-Genome Sequencing

N. C. Gordon,^a J. R. Price,^b K. Cole,^b R. Everitt,^c M. Morgan,^d J. Finney,^a A. M. Kearns,^e B. Pichon,^e B. Young,^a D. J. Wilson,^a M. J. Llewelyn,^b J. Paul,^f T. E. A. Peto,^a D. W. Crook,^a A. S. Walker,^a T. Golubchik^a

Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing

The CRyPTIC Consortium and the 100,000 Genomes Project

Rapid antibiotic-resistance predictions from genome sequence data for *Staphylococcus aureus* and *Mycobacterium tuberculosis*

Phelim Bradley¹, N. Claire Gordon², Timothy M. Walker², Laura Dunn², Simon Heys¹, Bill Huang¹, Sarah Earle², Louise J. Pankhurst², Luke Anson², Mariateresa de Cesare¹, Paolo Piazza¹, Antonina A. Votintseva², Tanya Golubchik², Daniel J. Wilson^{1,2}, David H. Wyllie², Roland Diel³, Stefan Niemann^{4,5}, Silke Feuerriegel^{4,5}, Thomas A. Kohl⁴, Nazir Ismail^{6,7}, Shaheed V. Omar⁶, E. Grace Smith⁸, David Buck¹, Gil McVean¹, A. Sarah Walker^{2,9}, Tim E.A. Peto^{2,9}, Derrick W. Crook^{2,9,10} & Zamin Iqbal¹

Evaluation of Machine Learning and Rules-Based Approaches for Predicting Antimicrobial Resistance Profiles in Gram-negative Bacilli from Whole Genome Sequence Data

Mitchell W. Pesesky^{1†}, Tahir Hussain^{1,2†}, Meghan Wallace³, Sanket Patel³, Saadia Andleeb², Carey-Ann D. Burnham^{3,4*} and Gautam Dantas^{1,3,5,6*}

Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinIONTM sequencing

Minh Duc Cao^{1†}, Devika Ganesamoorthy^{1†}, Alysha G. Elliott¹, Huihui Zhang¹, Matthew A. Cooper¹ and Lachlan J.M. Coin^{1,2*}



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Speed - whole genome sequencing for antimicrobial susceptibility testing

- Potential is enormous
- Downside: focus on *known* resistance mechanisms
- Downside: prediction of gene expression in *in vivo* situation based on whole-genome sequencing is very difficult at best
- This means that acurately predicting a bacterial phenotype will not always be possible

• However, most methods based on growth – time to result: min. 1-2 days, often more

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Biofilm phenotype is not taken into account!











S. aureus



P. aeruginosa

Biofilm tolerance contributes to therapy failure



Persistence contributes to failure of therapy



Fauvart, ..., Michiels, 2011

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What is the effect in vivo?

In vivo PK/PD in a mouse model of biofilm lung infections



Bjarnsholt et al. Nat Rev Drug Discov 2013 12:791-808

What is the effect *in vivo*?



[Antibiotic]

- However, most methods based on growth time to result: min. 1-2 days, often more
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- Lack of correlation between *in vitro* results and efficiacy *in vivo* low predictive value
- Let's take a closer look at these issues
- Now what about the host? Does the host influence the outcome of an antimicrobial treatment?



Chronic lung infections by *P. aeruginosa* are caused by biofilms in the lung mucosa

(Thomas Bjarnsholt, Peter O. Jensen, Niels Hoiby)



3-D lung cell cultures mimic key features of the *in vivo* tissue

Architecture

Barrier function

Polarity

Multicellular complexity



Carterson et al, 2005. Infect Immun; Barrila et al. 2010, Nat Rev Microbiol; Crabbé et al, 2011. Cell Microbiol; Crabbé et al. 2014. Pathog Dis



Monolayer (A549 lung epithelial cells)

Microcarrier beads (Collagen I – coated)

(175 µm)

3-D lung cell cultures using the rotating wall vessel (RWV) technology



Carterson et al, 2005. Infect Immun; Barrila et al, 2010. Nat Rev Microbiol



Monolayer (A549 lung epithelial cells)



3-D lung cell cultures using the rotating wall vessel (RWV) technology



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Biofilm-like structures on 3-D lung cells







6

Log biofilm inhibition (CFU/mL)

3D cells influence antibiotic efficacy: ↑ efficacy aminoglycosides

 \downarrow efficacy colistin



P. aeruginosa biofilms on 3D-A549 cells

Crabbé et al. 2017. Sci Rep.

Does the host influence bacterial tolerance?



What causes this potentiating effect?



What causes this potentiating effect?



What causes this potentiating effect?



Crabbé et al, PLoS Path, 2019

Wrap-up - what about the host?

- Also the host produces (secreted) compounds that influence biofilm susceptibility
- This interaction between pathogen and host likely can have a significant impact on the efficacy of antimicrobial therapy
- Clinical implications unclear
- What about patient-to-patient variation and its impact?
- We need to expand our model and way of thinking



Wrap-up - what about the host?

- Also the host produces (secreted) compounds that influence biofilm susceptibility
- This form of 'communication' likely can have a significant impact on the efficacy of antimicrobial therapy
- Clinical implications unclear
- What about patient-to-patient variation and its impact?
- We need to expand our model and way of thinking
- What about influence of bacteria on the host? Role of commensals and the microbiome



Nature Reviews | Genetics

The Lung Microbiota of Healthy Mice Are Highly Variable, Cluster by Environment, and Reflect Variation in Baseline Lung Innate Immunity

Robert P. Dickson^{1,2}, John R. Erb-Downward¹, Nicole R. Falkowski¹, Ellen M. Hunter¹, Shanna L. Ashley¹, and Gary B. Huffnagle^{1,3,4,5}



Culture-Independent Analysis of Pediatric Bronchoalveolar Lavage Specimens

Philip Zachariah^{1,2*}, Chanelle Ryan^{1,3*‡}, Sruti Nadimpalli^{1§}, Gina Coscia^{1||}, Michelle Kolb^{1‡}, Hannah Smith¹, Marc Foca¹, Lisa Saiman^{1,2}, and Paul J. Planet^{1,2,3,4,5‡}1



Do commensal bacteria mediate the inflammatory response of the host to pathogens?

An *in vivo*-like 3D-model of lung epithelial cells (A549) is used





¹Barrila *et al*, 2010, Nat Rev Microbiol 8(11)

Lung epithelial cells are infected with various CF lung microbiome members

Pseudomonas aeruginosa PAO1 Staphylococcus aureus SP123 Streptococcus anginosus LMG 14696 Achromobacter xylosoxidans LMG 26680 Gemella haemolysans LMG 18984 Rothia mucilaginosa DSM 20746



Rothia mucilaginosa

- Gram positive coccus
- Facultative anaerobic (aerotolerant)
- Usually encapsulated with a small amount of polysaccharide
- Normal flora of the oral cavity and upper respiratory tract
- Forms biofilms

Classification	
Kingdom	Bacteria
Phylum	Actinobacteria
Class	Actinobacteria
Order	Actinomycetales
Family	Micrococcaceae
Genus	Rothia
Species	R. mucilaainosa



Screening of effect of various bacteria on IL-8 response induced by *P. aeruginosa* PAO1



Negative control = Uninfected 3-D A549 cells

PAO1 = Pseudomonas aeruginosa PAO1

S = Staphylococcus aureus SP123

St = *Streptococcus anginosus* LMG 14696

A = Achromobacter xylosoxidans LMG 26680

G = Gemella haemolysans LMG 18984

R = *Rothia mucilaginosa* DSM 20746

Screening of effect of various bacteria on IL-8 response induced by *P. aeruginosa* PAO1



R. mucilaginosa lowers the PAO1-induced IL-8 response in 3-D A549 cells

Effect of *R. mucilaginosa* on IL-8 response

All data point to involvement of (inhibition of) the NF-κB pathway

Wrap-up – does the lung microbiome influence the host?

- Yes!
- *R. mucilaginosa* lowers the pathogen-induced IL-8 response in lung epithelial cells
- XXXX

Ongoing work: developing a personalized approach for antimicrobial susceptibility testing in cystic fibrosis



Ongoing work: developing a personalized approach for antimicrobial susceptibility testing in cystic fibrosis

Conventional susceptibility assay



Minimal inhibitory concentration (MIC)

XNot personalized

XPoor predictor for *in vivo* susceptibility

XNo guarantee for clinical success

Approach: Mimic each patient in the lab

 Genetic background (CFTR mutation)



Develop 3D patient-specific models derived from nasal epithelial cells

• Lung microbiome



Use patient-specific microbiome + *P. aeruginosa* derived from sputum

Approach: Mimic each patient in the lab

Personalized antibiotic susceptibility profile

Conventional susceptibility assay



Minimal inhibitory concentration (MIC)

- XNot personalized
- XPoor predictor for *in vivo* susceptibility
 - XNo guarantee for clinical success

Personalized susceptibility assays



Biofilm eradicating concentration (BEC)





Better predictor for in vivo susceptibility



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