

From the clinic: The changing profession of the clinical microbiologist

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ESCMID Postgraduate Technical Workshop
Clinical bioinformatics for microbial genomics and metagenomics
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Disclosure

- Research project and InnoSwiss grant with Resistell AG (Switzerland)

Backgrounds and Purpose



Is the profession of clinical microbiologist changing?

❖ Backgrounds:

- Clinical microbiology is a field in constant **evolution**
- Increasing **technological** opportunities
- Growing emphasis on **societal** issues

❖ Purpose:

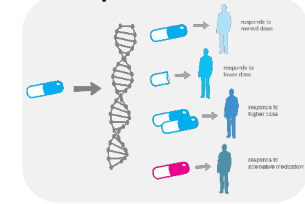
- Reflection on changes in the **profession**? Changes in the **approaches**?
Changes in the **perimeter** of CM

Plan

- 1. Brief history**
- 2. New technologies**
- 3. Positioning of the microbiologist**
- 4. Phenotypic microbiology: ongoing improvements**
- 5. Epidemiology**
- 6. Ethical challenges in genomic approaches to infectious disease**
- 7. Molecular & NGS: opportunity for new approaches or new applications?**
- 8. Conclusions**

Brief history

Societal changes
Big data, personalized
medicine, equity, parity,
responsibilities



Word "Microbiology", Louis Pasteur: the study of living organisms of microscopic size

"Microbes"

Koch bacillus
Koch postulate

1860 1878 1884-1890

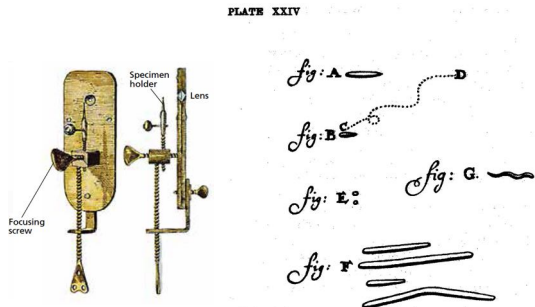
Improvement of phenotypic methods



1663-1685

Microscopy
Spermatozoids
Infusoria
Animalcules

A. van Leeuwenhoek



Broth



Potato



Petri dish

1990

Automates
AST
Blood culture



2000-2019

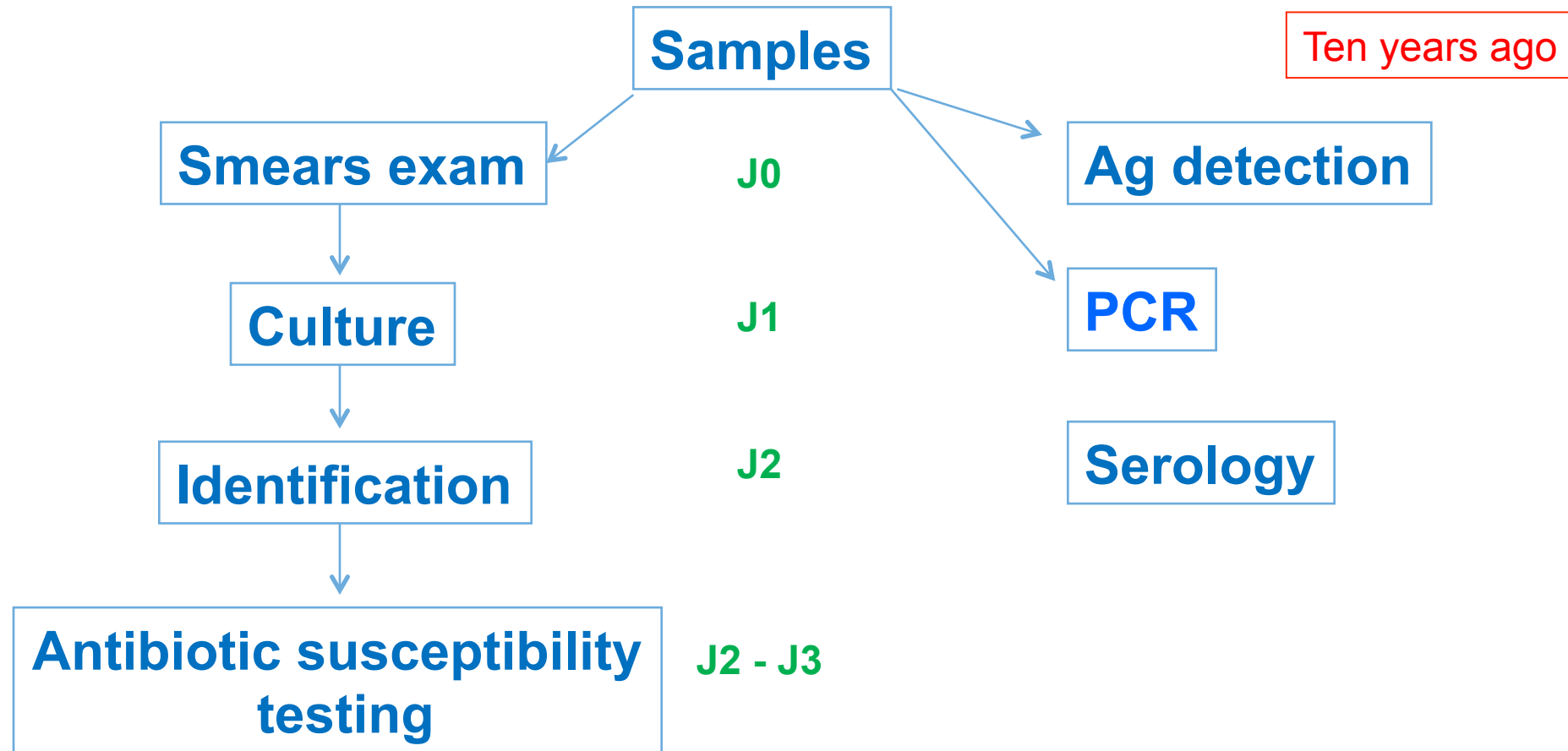
Molecular diagnostic
MALDI-TOF MS
Automation
NGS



?

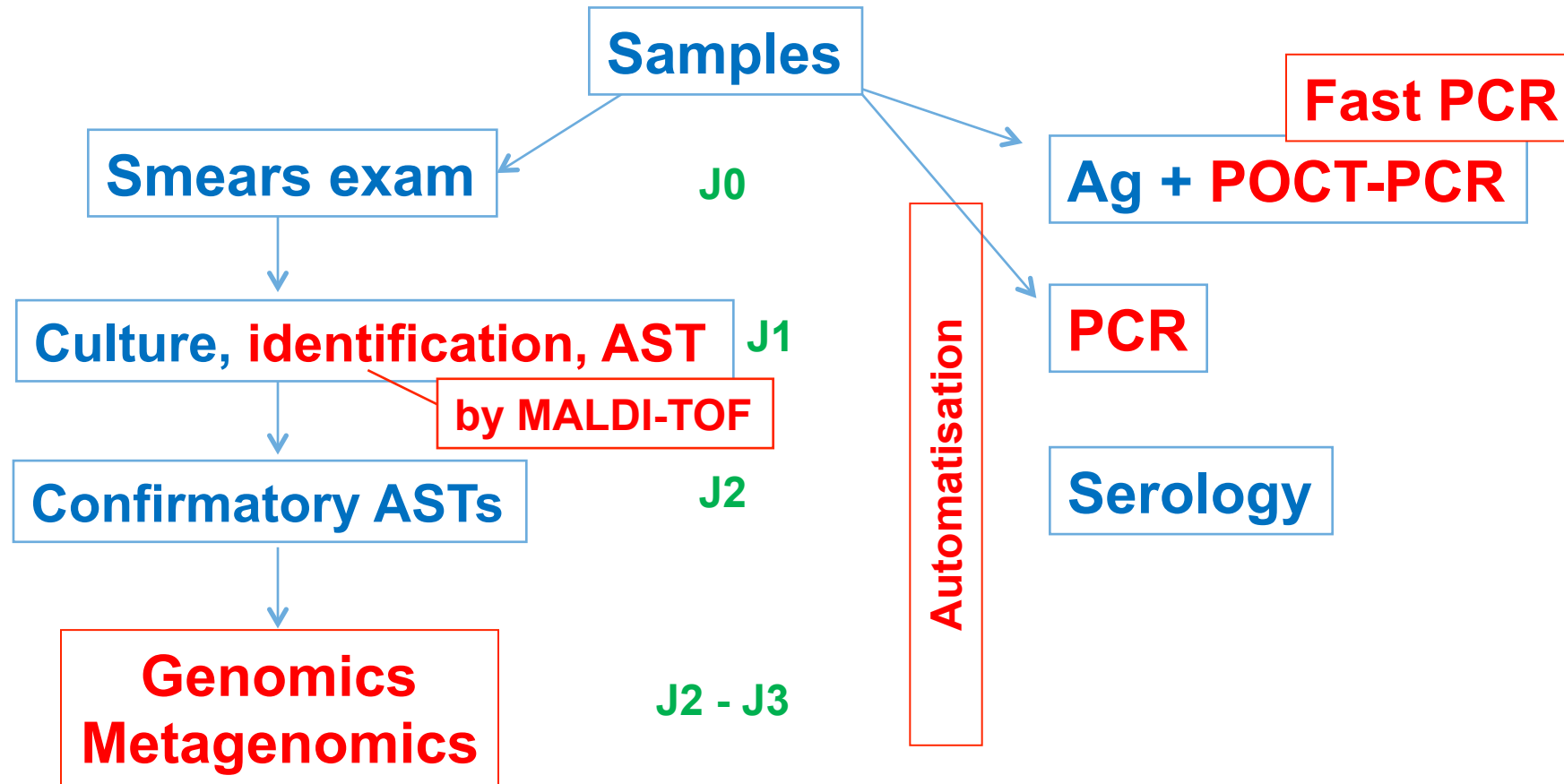
Approach in clinical microbiology

Technological opportunities of the past 10 years



Approach in clinical microbiology

Technological opportunities of the past 10 years



More information, more rapidly

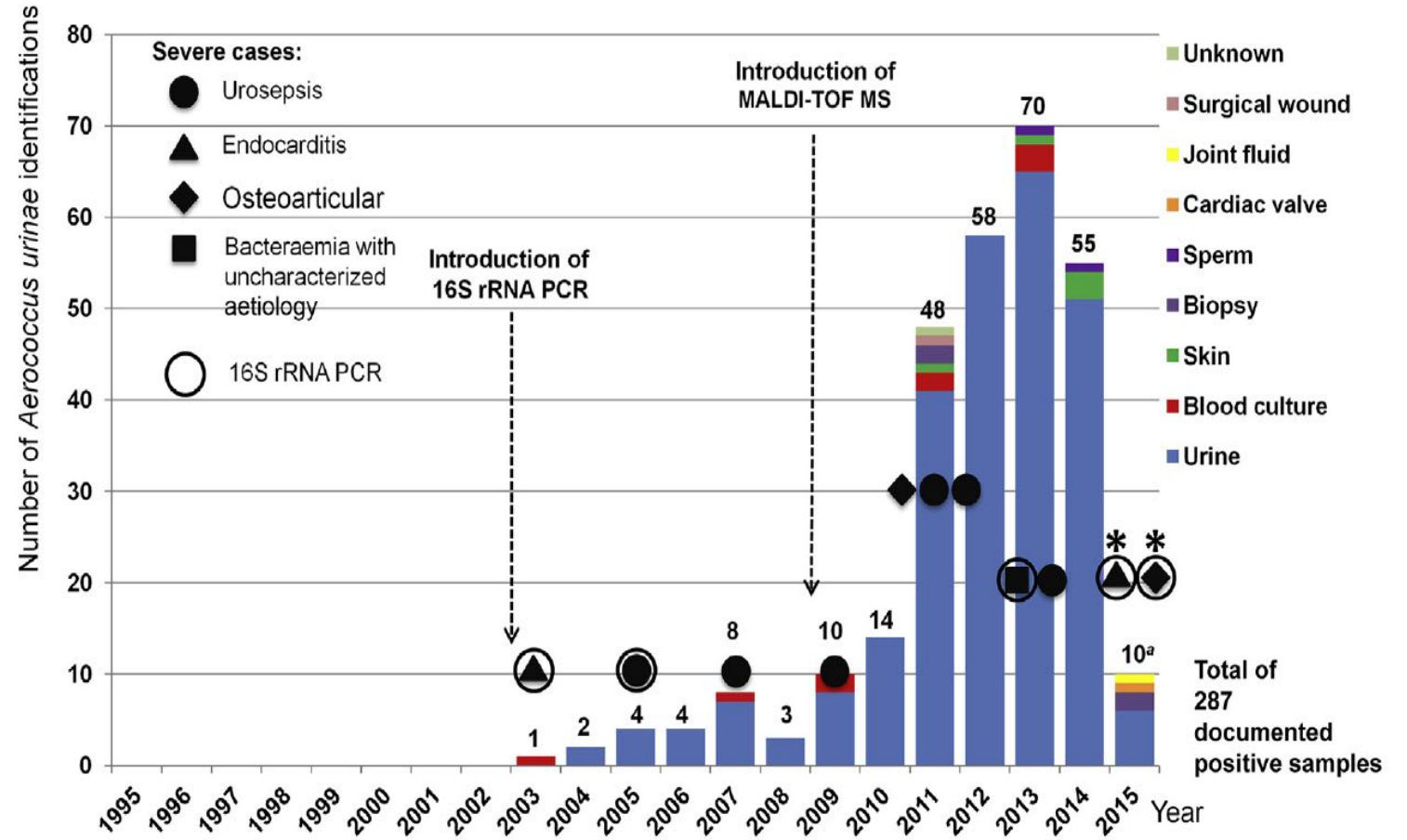
Pathogens identification

Impact of new technologies

- *Aerococcus urinae*
 - Gram positive cocci, pairs and clusters
 - α -haemolytic
- Identification hampered by morphotype ambiguity with streptococci or coagulase-negative staphylococci.
- Rarely identified before 2009.
- Identification improved by 16S rRNA PCR and MALDI-TOF MS



Significant pathogenic potential that should not be neglected (bloodstream infections, osteoarticular Infections etc ...)

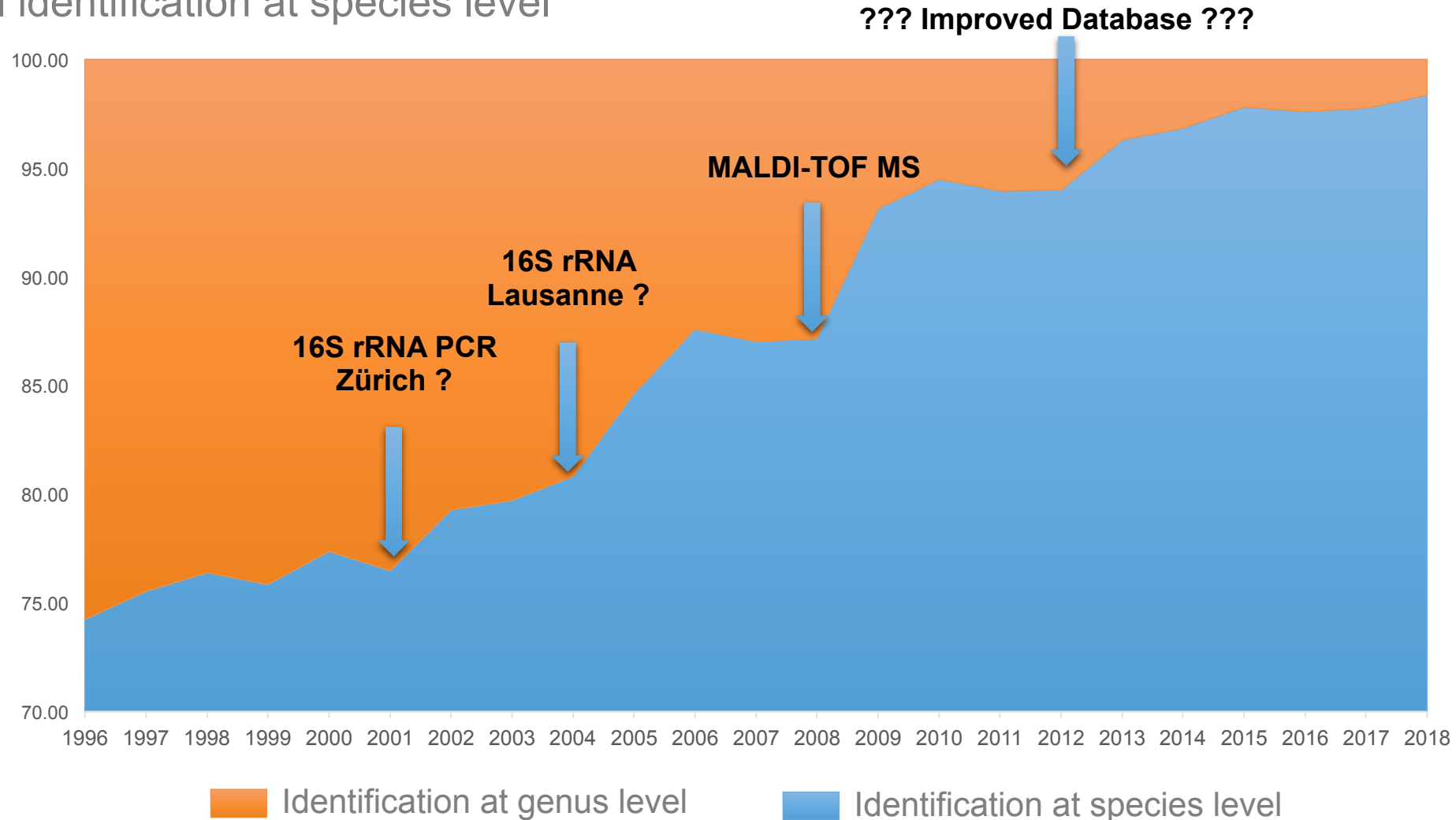


^a First trimester of 2015

Pathogens identification

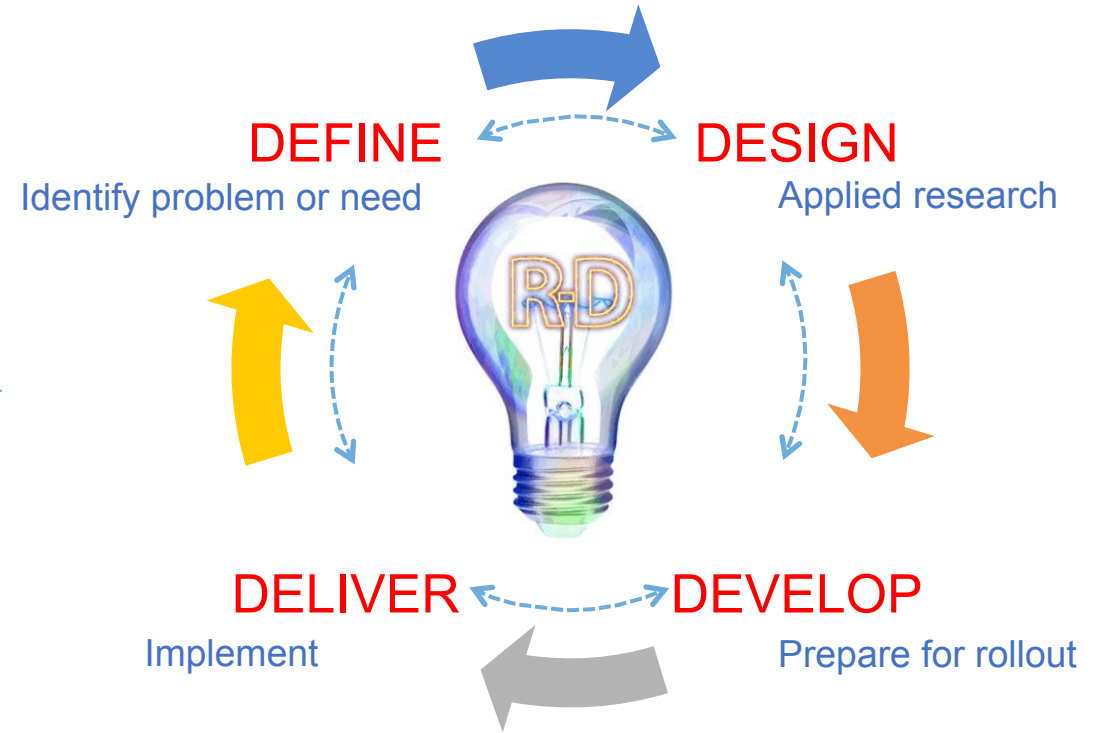
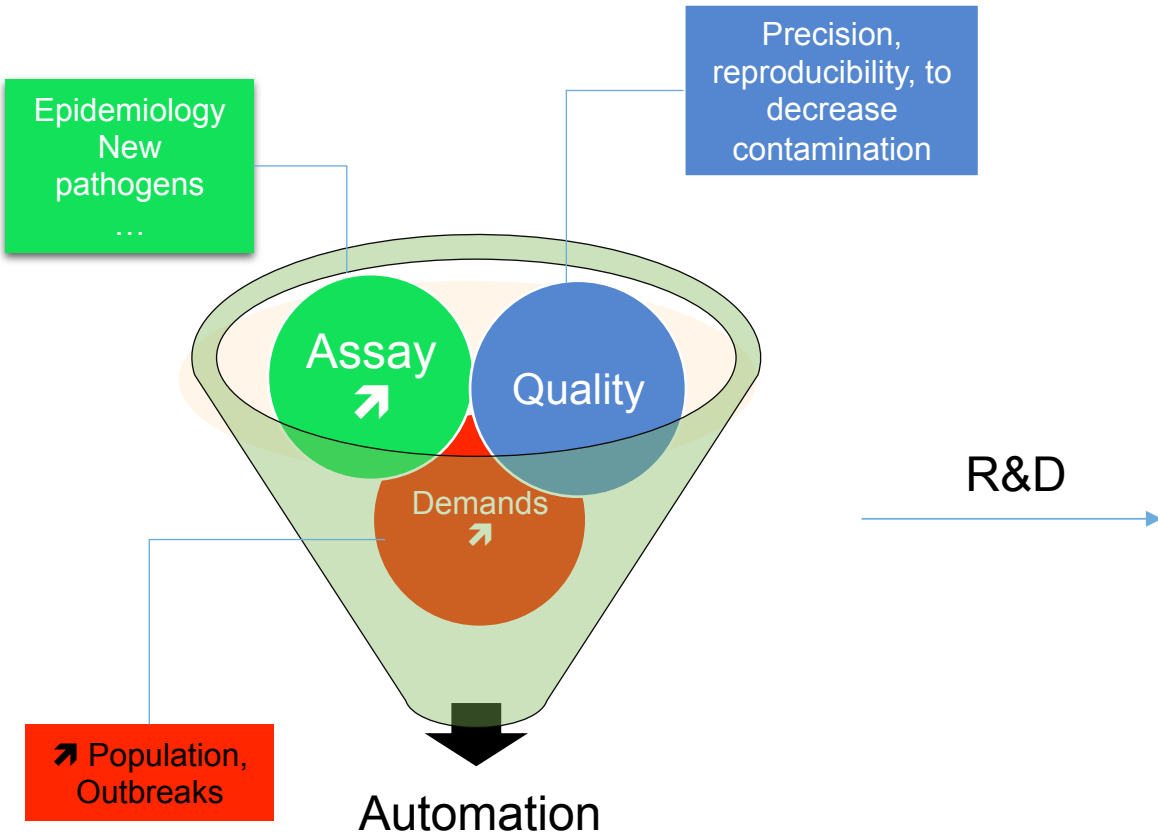
Impact of new technologies

Successful identification at species level



Courtesy of Dre Alix Coste

Importance of Research and Development



Importance of Research and Development

In-house automated molecular diagnostic platform

- M. pneumoniae*
- C. pneumoniae*
- L. pneumophila*
- M. tuberculosis complex*
- B. pertussis*
- B. parapertussis*
- N. meningitidis*
- L. monocytogenes*
- H. influenzae*
- C. trachomatis*
- N. gonorrhoeae*
- B. henselae*
- B. quintana*
- M. hominis*
- A. fumigatus*
- Bacillus anthracis*
- Plasmodium sp*
- Toxoplasma gondii*
- eubactérienne
- panmycobactérienne
- panfongique
- Influenza A/B
- RSV A/B
- HSV/VZV
- HHV6
- HPV
- Parvovirus B19
- CMV
- EBV
- Candida sp.*
- Rickettsia sp.*

TAT 48-72 hours

TAT 24-48 hours

6-24 hours

ACTIVITY

2007

2008

2009

2010

2011

2012

2013

2014

2015

2016

2017

S. pneumoniae
JC virus
BK virus
Norovirus
HMPV

C. burnetii
Acantamoeba
Haemophilus sp.
Pneumocystis
Coronavirus
Parainfluenza
Picornavirus

HDV
HBV
Influenza H1N1
GeneXpert EV

Brucella sp.

T. whipplei
Leishmania
Pan chlamydia
HHV8
HEV
GX Mtbc/Rif
GX Flu A/H1N1/B

L28B
Diminution TAT

S. aureus PVL
S. aureus mecC
F. tularensis
Yersinia pestis
Anaplasma sp

C. psittaci
C. abortus
N. gonorrhoeae
GX Flu A/B/RSV
GX Noro

C extraction
Fast PCR HM

Aspergillus sp.
A. terreus
A. flavus
A. niger

Kingella kingae
Zika virus
Measle

< 2007



MagNA Pure LC
ADN

EasyMag
ARN

GeneXpert

MagNA Pure 96
ADN/ARN

FAST real time
PCR

2x HAMILTON

2X Quantstudio

BD-MAX

Fastfinder
(informatique)

Research and development to introduce new tests and to achieve automation

Importance of Research and Development



Ebola



Measles

- Reactivity and Pertinence
 - development and innovation that fit with (local) needs of the laboratories
 - Epidemiology change
 - Emerging pathogens
 - Outbreaks
- Clinical microbiologist
 - Stay up to date
 - Follow up after the introduction of new tests
 - Translational studies with physicians
 - To determine the added value of new tests
 - The needs for new tests
 - How to interpret



Institut Pasteur

Microbes and Infection xx (2017) 1–7

www.elsevier.com/locate/micinf

Original article

Genomics of the new species *Kingella negevensis*: diagnostic issues and identification of a locus encoding a RTX toxin

Kingella negevensis

Onya Opota ^{a,*}, Sacha Laurent ^{a,1}, Trestan Pillonel ^a, Marie Léger ^b, Sabrina Trachsel ^b, Guy Prod'homme ^a, Katia Jaton ^a, Gilbert Greub ^{a,c,*}

Clinical Microbiology and Infection 24 (2018) 548.e5–548.e8



Contents lists available at ScienceDirect

Clinical Microbiology and Infection

journal homepage: www.clinicalmicrobiologyandinfection.com



Research note

Novel *Tropheryma* species in a lung biopsy sample from a kidney transplant recipient[☆]

A. Vankeerberghen ^{1,*}, S. Jonckheere ¹, H. De Raeye ², R. Caluwe ³, H. De Beenhouwer ¹

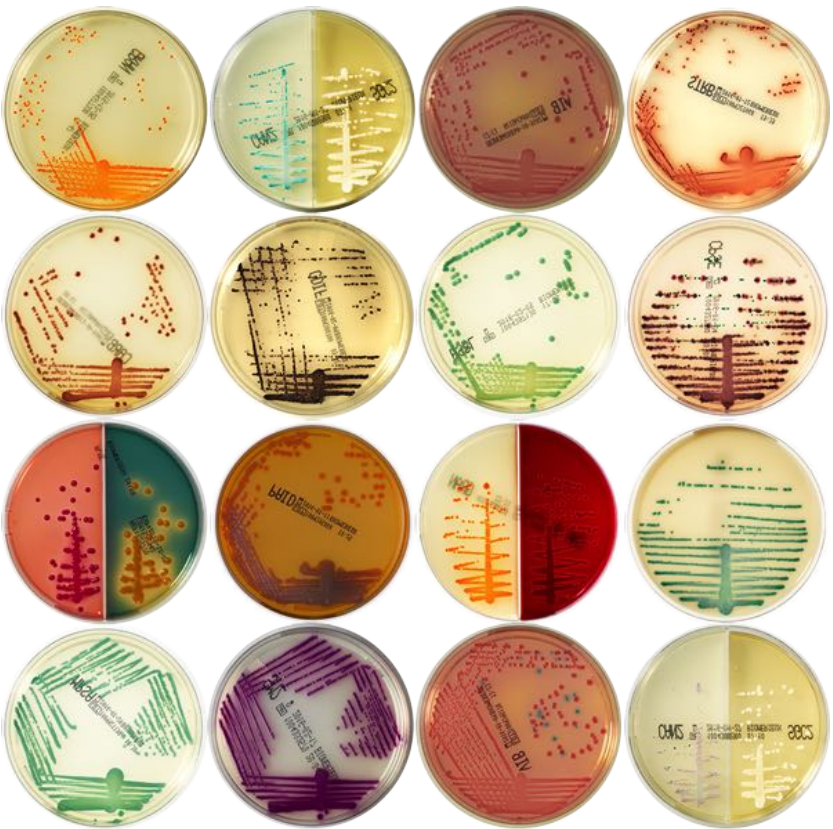
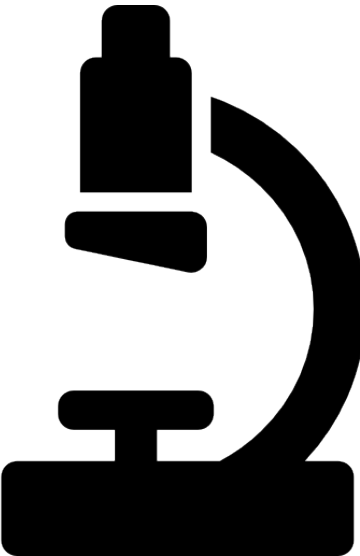
¹ Laboratory of Clinical Microbiology, OLV Hospital Aalst, Aalst, Belgium

² Department of Pathology, OLV Hospital Aalst, Aalst, Belgium

³ Department of Nephrology, OLV Hospital Aalst, Aalst, Belgium

Tropheryma sp.

Ongoing development in phenotypic microbiology



Ongoing development in phenotypic microbiology

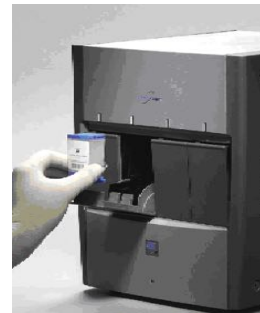
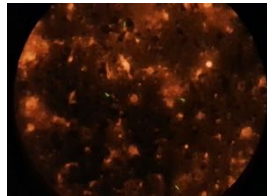


TIME TO RESULT

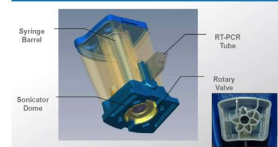
2 hours
Respiratory specimens

6-24hours
Any specimens

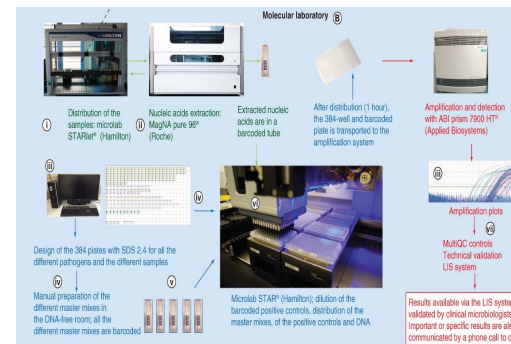
6-8 weeks



Cartridge Design and Operating Principle



Xpert MTB/RIF
TAT 2h, emergency, 7/7
Xpert MTB/RIF (Cepheid)
Specific detection of *Mtbc*
Sensitivity +++
Detection of resistance marker (*rpoB*)



In-house developed automated Molecular Dx platform

TAT 6-24h, opening hours, 5 days/7

Specific detection of *Mtbc*

Sensitivity +++

- Batches, High throughput
- +/- Coast effective
- Specialized lab

Added value of molecular assay Xpert MTB/RIF compared to sputum smear microscopy to assess the risk of tuberculosis transmission in a low-prevalence country. Opota O, Senn L, Prod'hom G, Mazza-Stalder J, Tissot F, Greub G and Jatou K *Clin Microbiol Infect* 2016; **22**: 613-9.

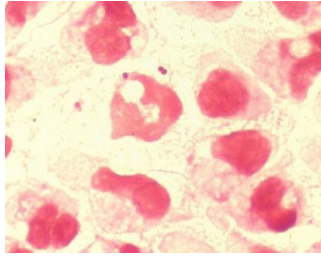
The rapid molecular test Xpert MTB/RIF ultra: Towards improved tuberculosis diagnosis and rifampicin resistance detection. Opota O, Mazza-Stalder J, Greub G, Jatou K. *Clin Microbiol Infect* 2019.

Ongoing development in phenotypic microbiology

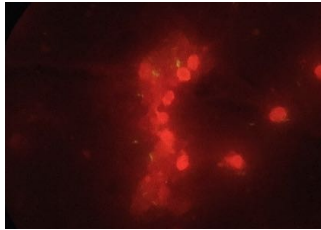
MICROSCOPY

MOLECULAR BIOLOGY

GRAM for CSF



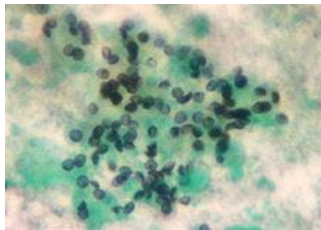
Auramine/Ziehl staining for mycobacteria



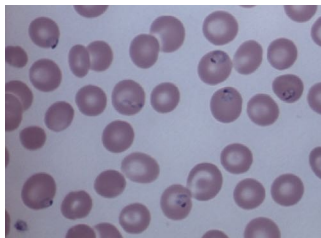
+

AUTOMATED MICROSCOPY

Silver staining for PCP



Thin smear for malaria



Ongoing development in phenotypic microbiology

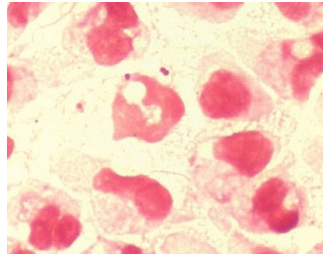
MICROSCOPY

MOLECULAR BIOLOGY

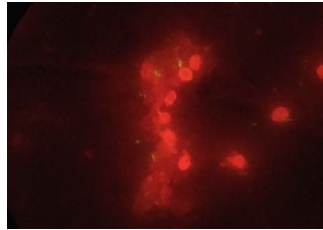


AUTOMATED MICROSCOPY

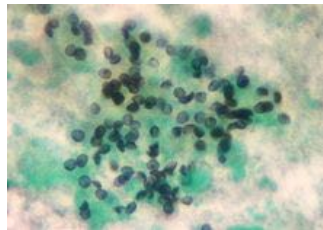
GRAM for CSF



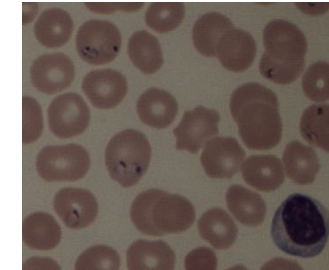
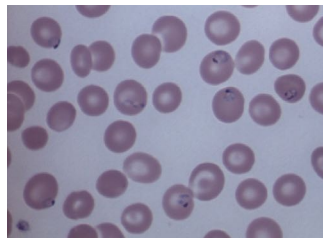
Auramine/Ziehl staining for mycobacteria



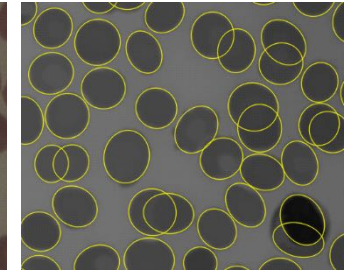
Silver staining for PCP



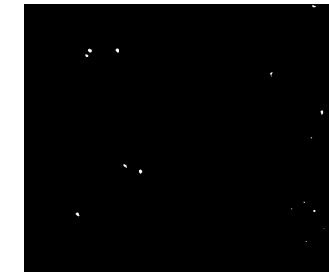
Thin smear for malaria



1. Original image



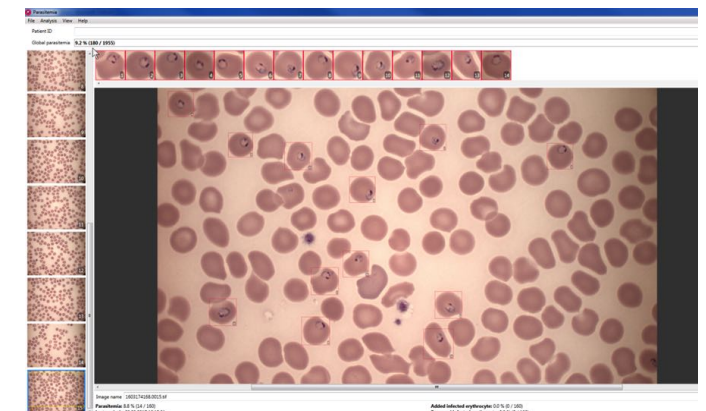
2. Finding location of cells by ellipsis matching.



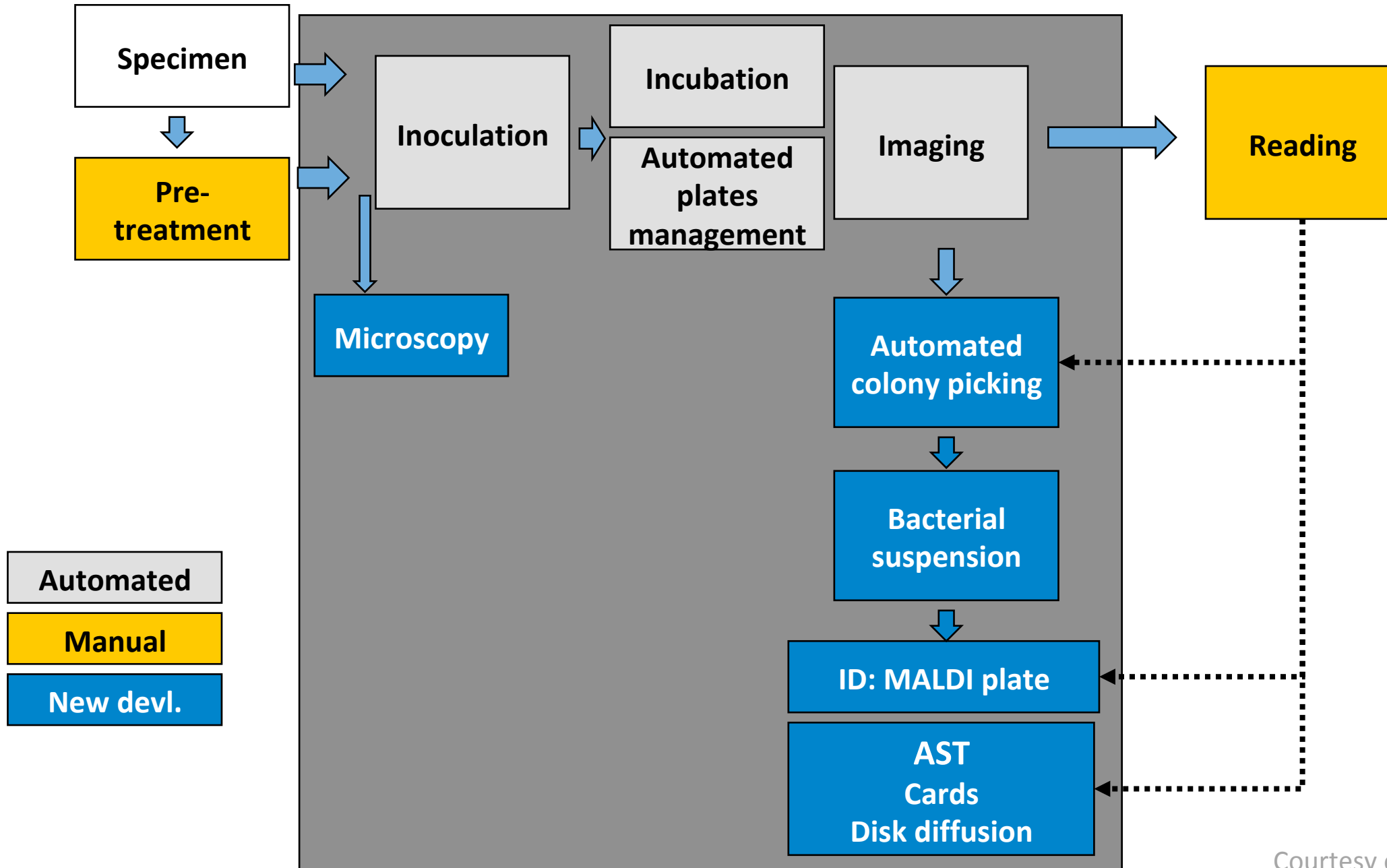
3. Segmentation of parasites and other stained elements.



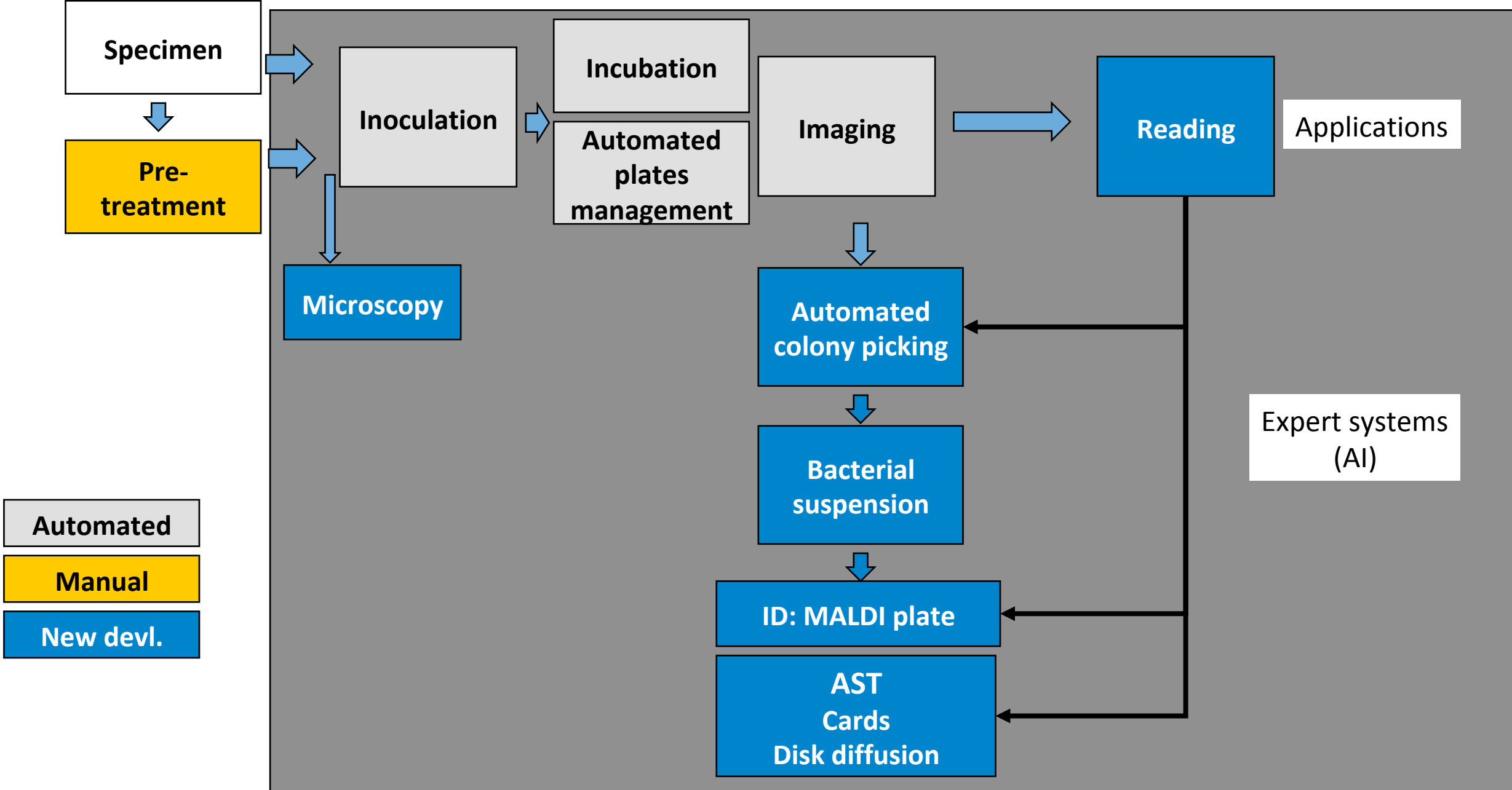
4. Classification of cells and computation of the parasitemia. Blue cross: healthy cells, red cross: infected cells, black cross: other elements



Full automation in Bacteriology



Full automation in Bacteriology



Ongoing development in phenotypic microbiology

Additional improvement of laboratory productivity?



Development of intelligent algorithms

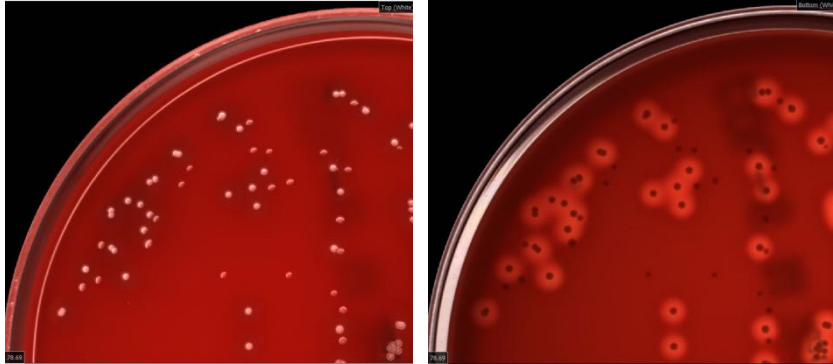
Ongoing projects

- Automated quantification
- **Automated identification (Imaging identification)**
- Automated processing
-

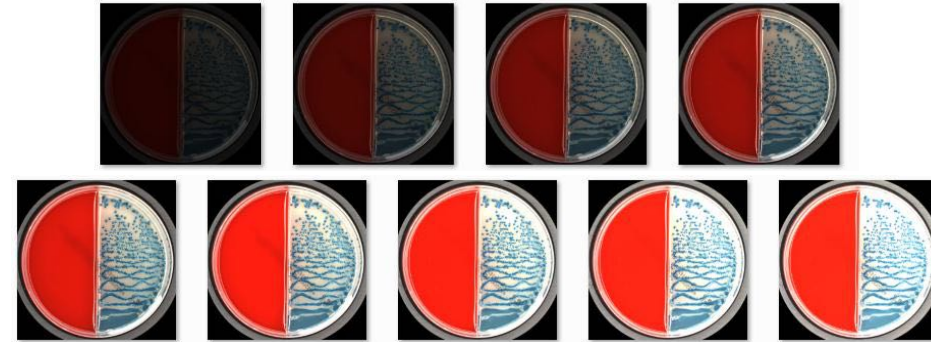
Imaging identification

Visible and invisible light characteristics

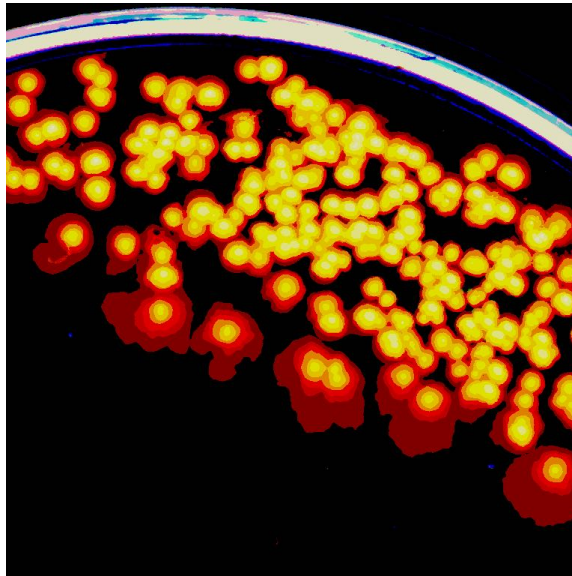
Illumination sources



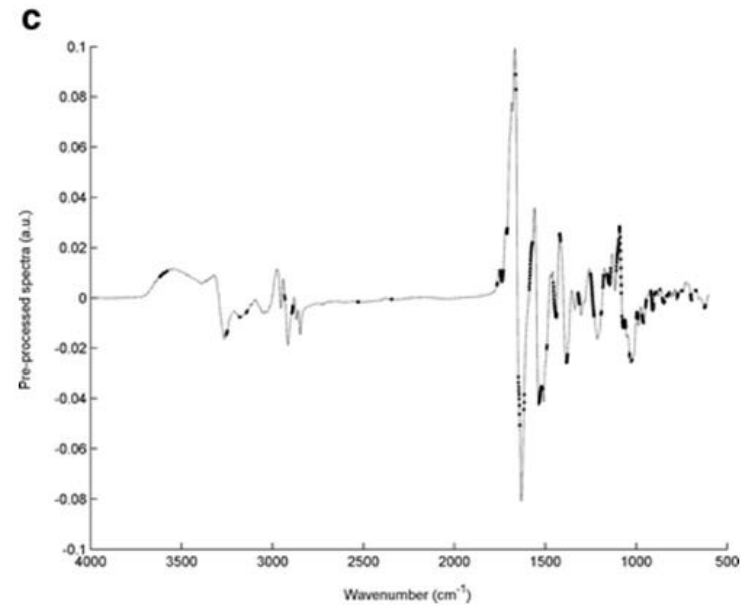
Optimal illumination (pixel, channel)



Growth pattern

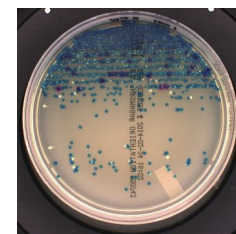
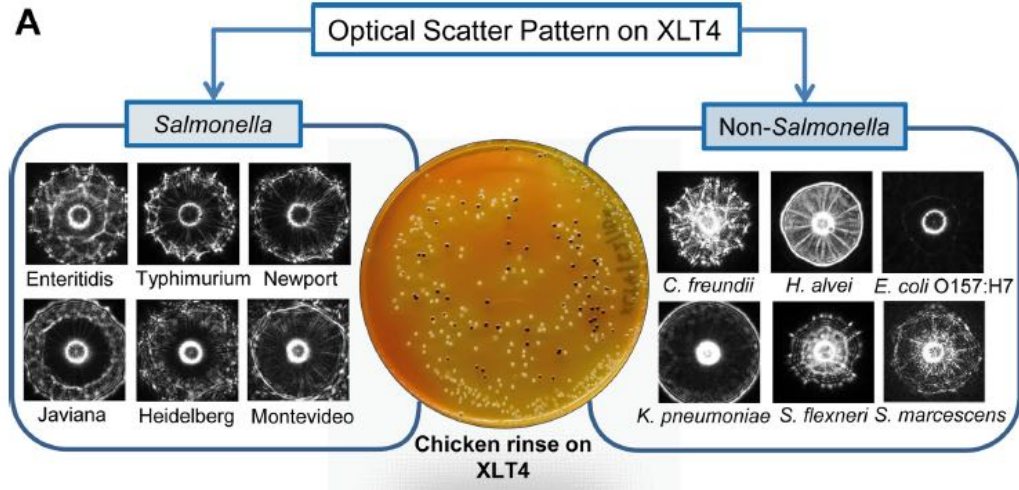
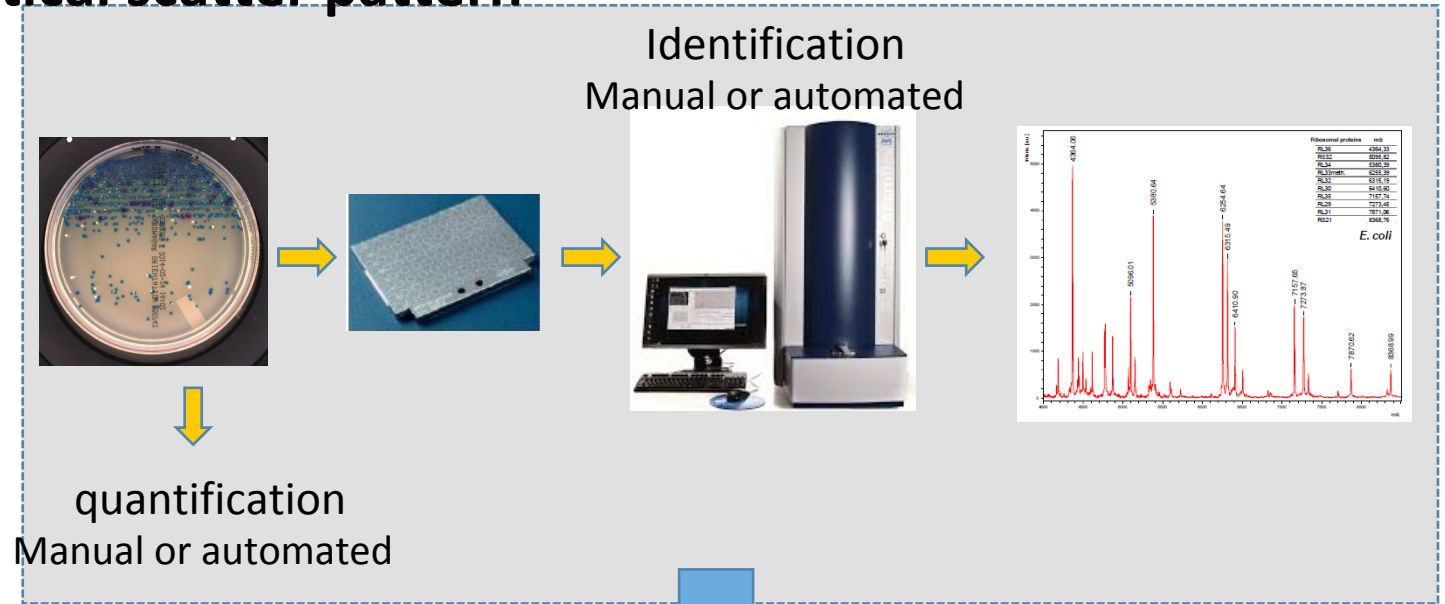


Fourier transform infrared (FT-IR) spectroscopy

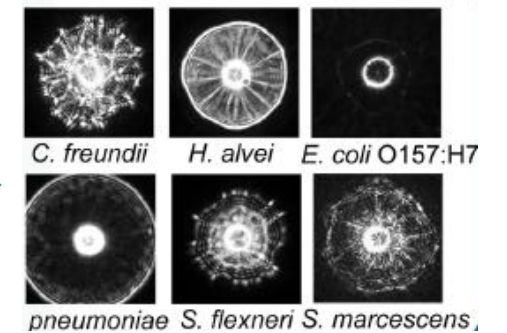


Imaging identification

Optical scatter pattern



Automated identification
and quantification



Ongoing development in phenotypic microbiology

Rapid drug susceptibility test

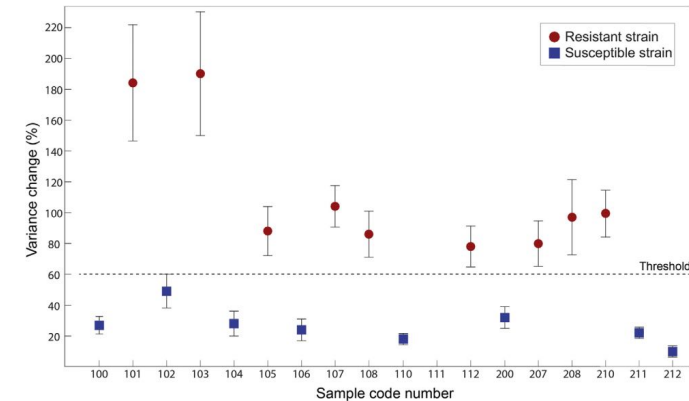
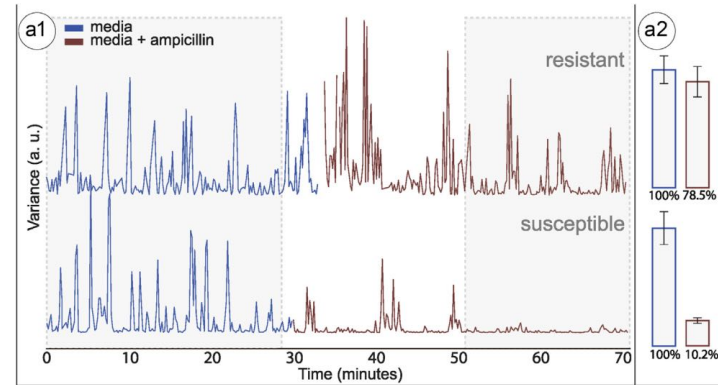
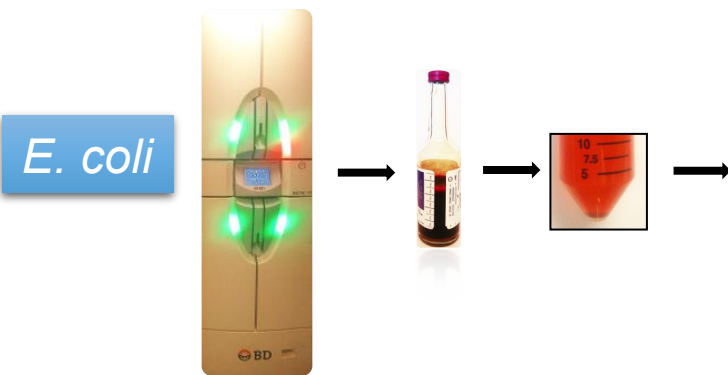
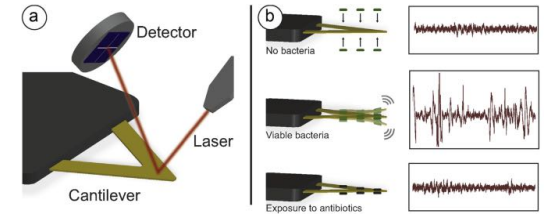
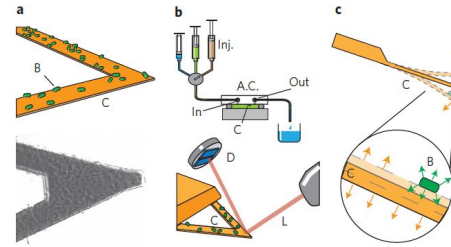
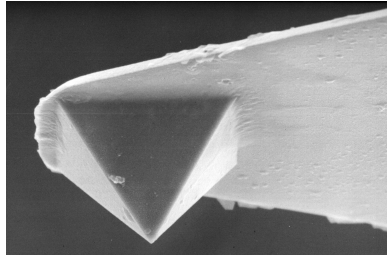
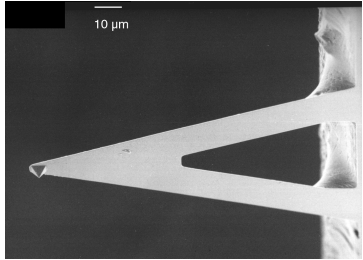
- Immunochromatographic tests
- Enzymatic, Colorimetric tests
- MALDI-TOF MS
- Imaging of bacterial growth
- Nanomotion AST



Ongoing development in phenotypic microbiology

Rapid drug susceptibility test

Bacteria nanomotion: Movement as a read-out for antibiotic susceptibility test



Elapsed time < 3 hours

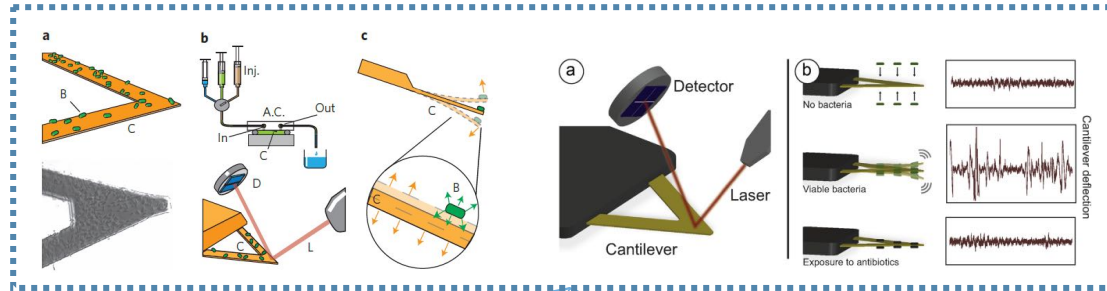
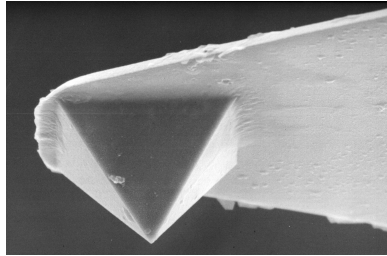
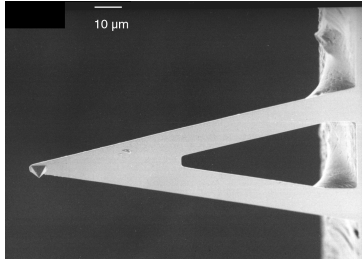
Longo, G., et al. 2013. Rapid detection of bacterial resistance to antibiotics using AFM cantilevers as nanomechanical sensors. Nat Nanotechnol 8:522-6.

Stupar, P., O. Opota, et al. 2017. Nanomechanical sensor applied to blood culture pellets: a fast approach to determine the antibiotic susceptibility

Ongoing development in phenotypic microbiology

Rapid drug susceptibility test

Bacteria nanomotion: Movement as a read-out for antibiotic susceptibility test



Eucaryotics

Yeast

Fast growing

Fastidious growing

Mycobacteria

Intracellular?

E. coli

K. pneumoniae

S. aureus

...

Bordetella pertussis

Mycobacterium abscessus

Mycobacterium BCG (Bacillus Calmette-Guerin)

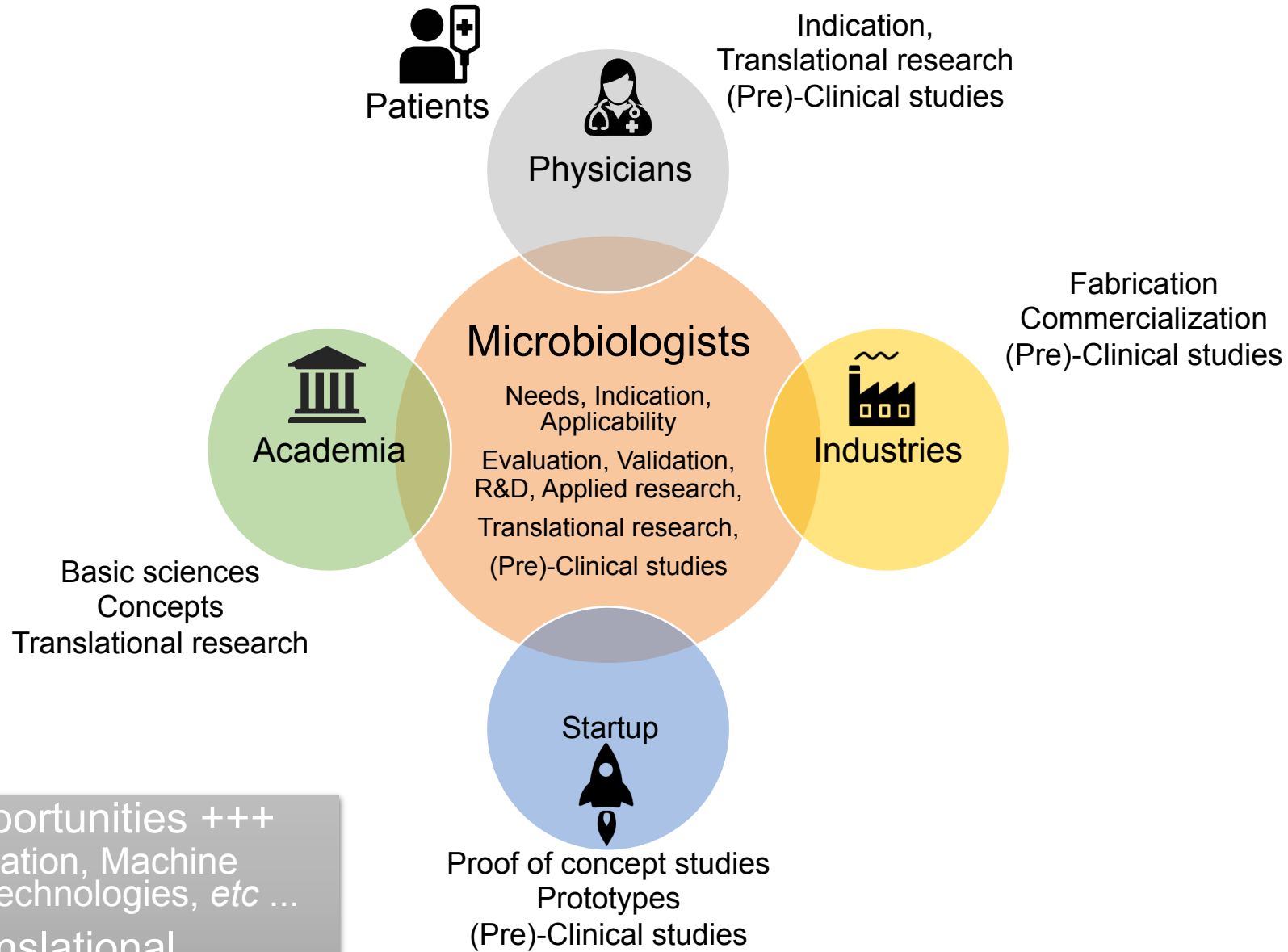
Stupar, P., O. Opota, et al. 2017. "Nanomechanical sensor applied to blood culture pellets: a fast approach to determine the antibiotic susceptibility against agents of bloodstream infections." Clin Microbiol Infect 23(6): 400-405.

Kasas, S., et al., 2018. "AFM contribution to unveil pro- and eukaryotic cell mechanical properties." Semin Cell Dev Biol 73: 177-187.

Villalba, M. et al., 2018. "Nanomotion Detection Method for Testing Antibiotic Resistance and Susceptibility of Slow-Growing Bacteria." Small 14(4).

Mustazzolu, A., et al., 2019. "A Rapid Unraveling of the Activity and Antibiotic Susceptibility of Mycobacteria." Antimicrob Agents Chemother 63(3).

Positioning of the Microbiologist



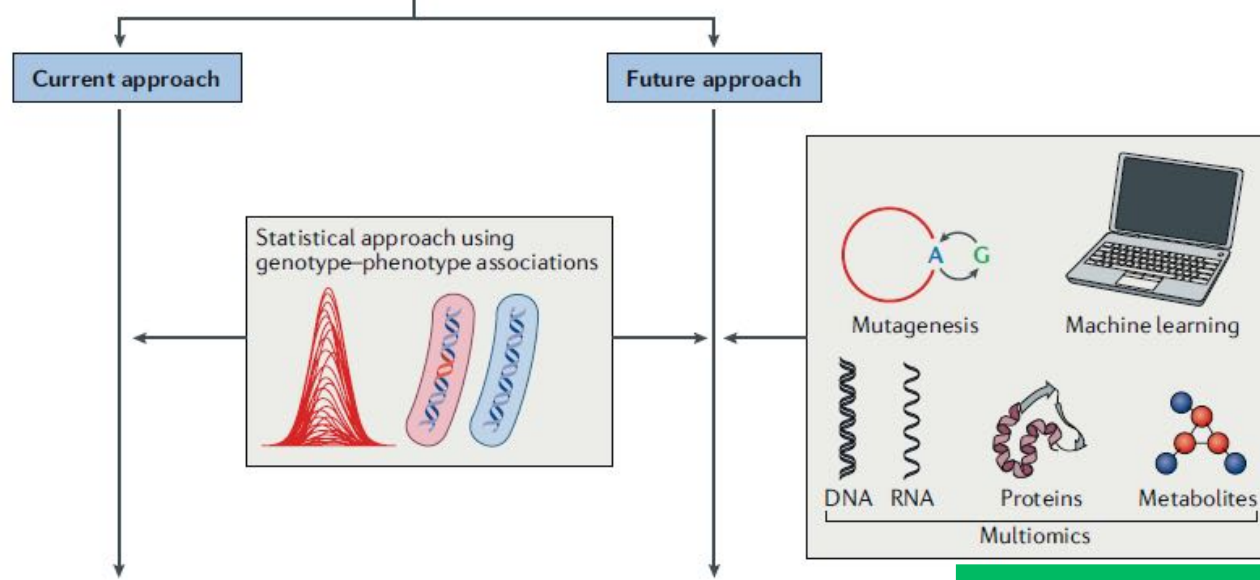
- Technological opportunities +++
 - Imaging, Automation, Machine learning, Nanotechnologies, etc ...
- Importance of translational research

Future of phenotypic microbiology

Current and potential approaches for determining resistance-related polymorphisms

Input whole genome sequencing data

	Strain 1	Strain 2	Strain 3	Strain 4
Lineage	4	3	1	<i>M. bovis</i>
<i>rpoB</i> mutation	Ser450Leu	Ser450Leu	Ser450Leu	Gln429Ala
<i>pncA</i> mutation	Val130Gly	Val130Gly	Arg123Gly	Gly108Ser
Phenotype	RIF resistant PZA resistant	RIF resistant PZA resistant	RIF resistant PZA susceptible	RIF susceptible PZA resistant



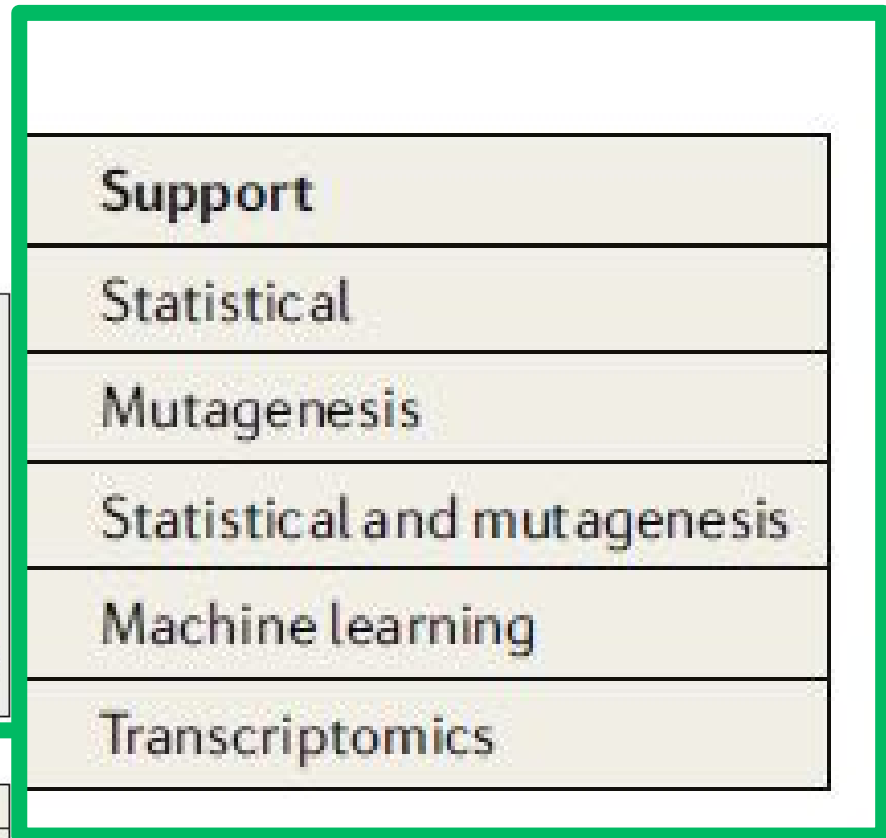
Resistance detected using a statistical approach

Gene	Mutation	Drug
<i>rpoB</i>	Ser450Leu	RIF
<i>pncA</i>	Val130Gly	PZA

Extended knowledge base

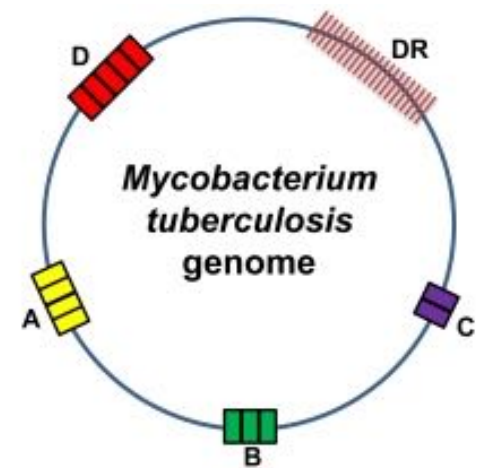
Gene	Mutation	Drug	Phenotype	Support
<i>rpoB</i>	Ser450Leu	RIF	Resistant	Statistical
<i>rpoB</i>	Gln429Ala	RIF	Susceptible	Mutagenesis
<i>pncA</i>	Val130Gly	PZA	Resistant	Statistical and mutagenesis
<i>pncA</i>	Arg123Gly	PZA	Susceptible	Machine learning
<i>pncA</i>	Gly108Ser	PZA	Resistant	Transcriptomics

Importance of result reporting!



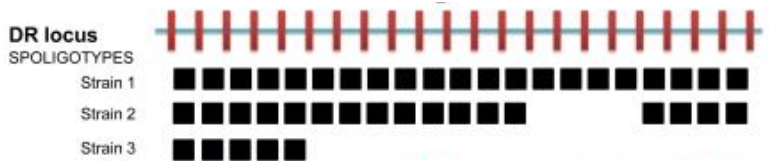
Meehan, C. J., et al. 2019. "Whole genome sequencing of *Mycobacterium tuberculosis*: current standards and open issues." *Nature Reviews Microbiology* 17(9): 533-545.

Epidemiology



Spoligotyping

Sp (acers) oligo (nucléotides) typing
Présence ou absence de spacer (n=43)

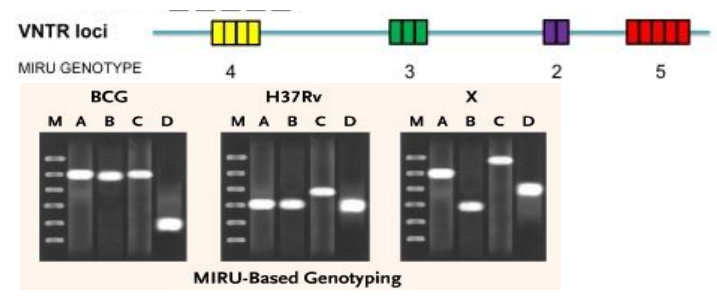


Spacer	1	5	10	15	20	25	30	35	40	43	Species
1	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
2	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
3	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
4	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
5	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
6	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
7	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
8	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
9	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
10	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
11	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
12	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
13	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
14	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
15	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
16	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
17	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
18	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
19	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
20	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
21	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
22	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
23	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
24	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
25	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
26	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
27	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
28	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
29	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
30	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
31	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
32	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
33	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
34	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
35	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
36	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
37	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
38	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
39	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
40	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
41	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
42	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
43	■	■	■	■	■	■	■	■	■	■	<i>M. tuberculosis</i>
44	□	□	□	□	□	□	□	□	□	□	<i>M. bovis</i>
45	■	■	■	■	■	■	■	■	■	■	<i>M. bovis</i>
46	■	■	■	■	■	■	■	■	■	■	<i>M. bovis</i>
47	■	■	■	■	■	■	■	■	■	■	<i>M. bovis</i>
48	■	■	■	■	■	■	■	■	■	■	<i>M. bovis</i>
49	□	□	□	□	□	□	□	□	□	□	Incomplete
50	□	□	□	□	□	□	□	□	□	□	Incomplete
51	□	□	□	□	□	□	□	□	□	□	Incomplete
52	□	□	□	□	□	□	□	□	□	□	Incomplete
53	□	□	□	□	□	□	□	□	□	□	Incomplete
54	□	□	□	□	□	□	□	□	□	□	Incomplete

MIRU-VNTR

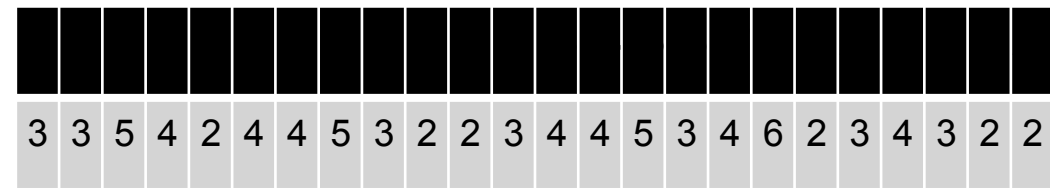
Mycobacterial interspersed repetitive units-variable number tandem repeats

Comparaison du nombre de répétitions (24 locus)

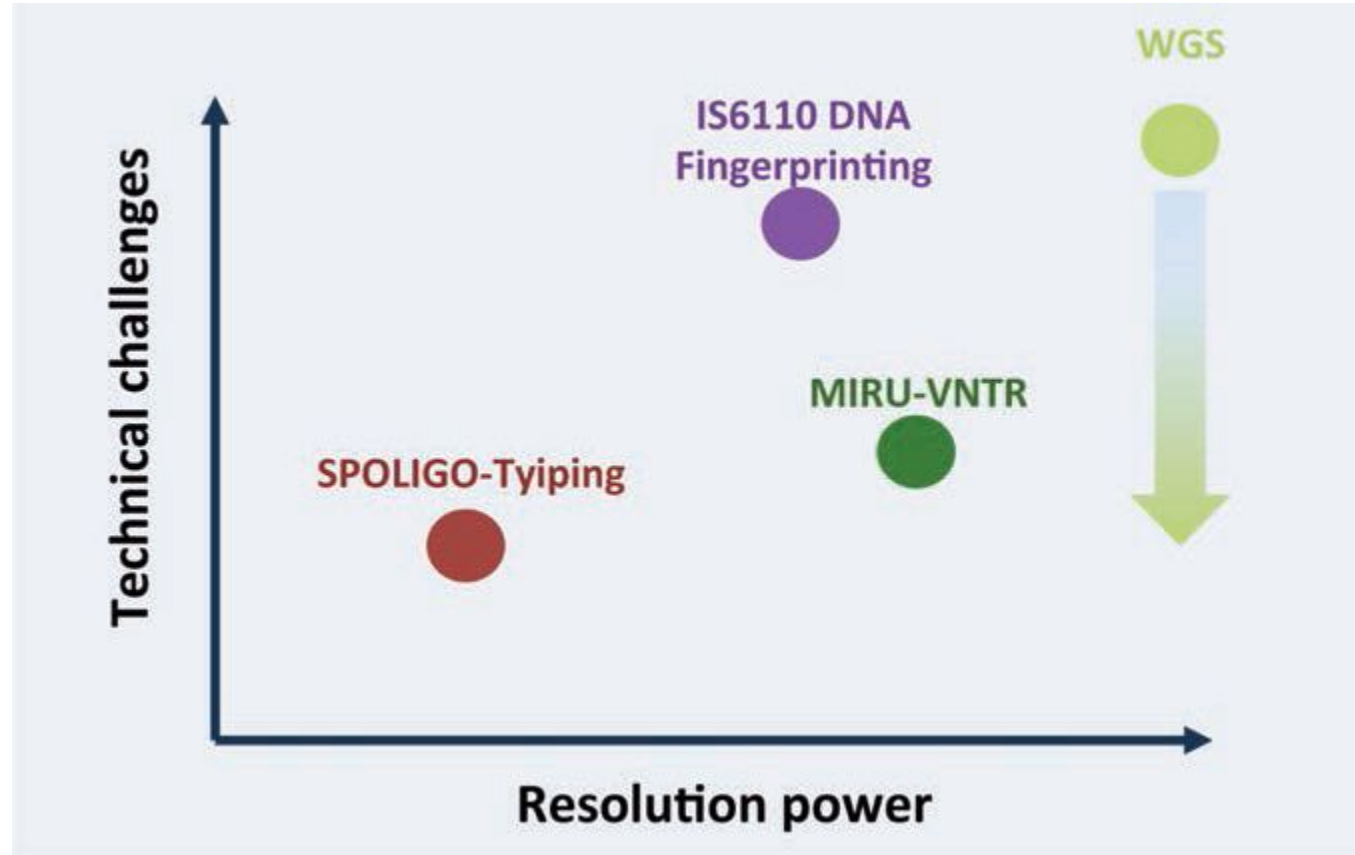


Locus

Repetitive number

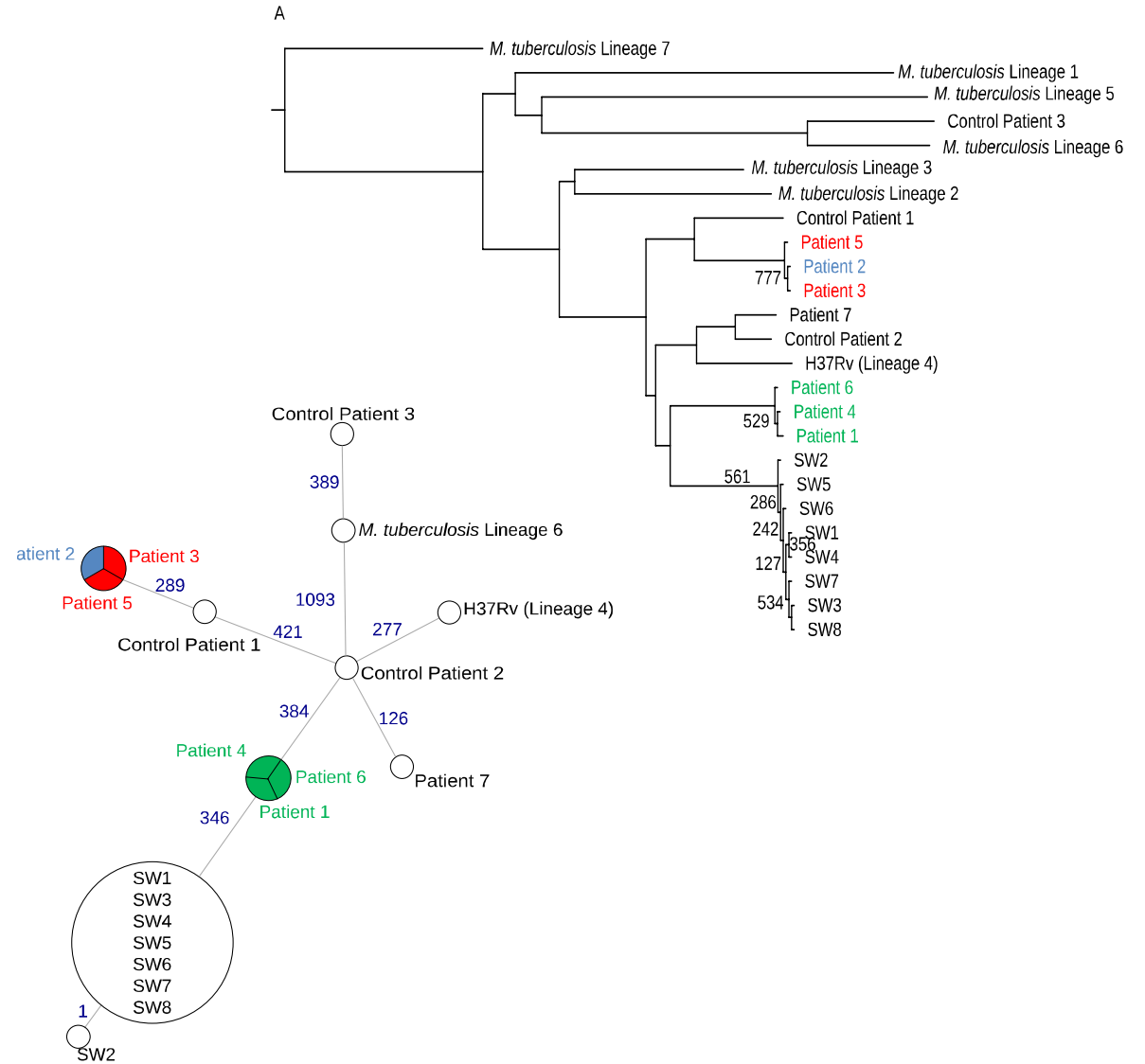
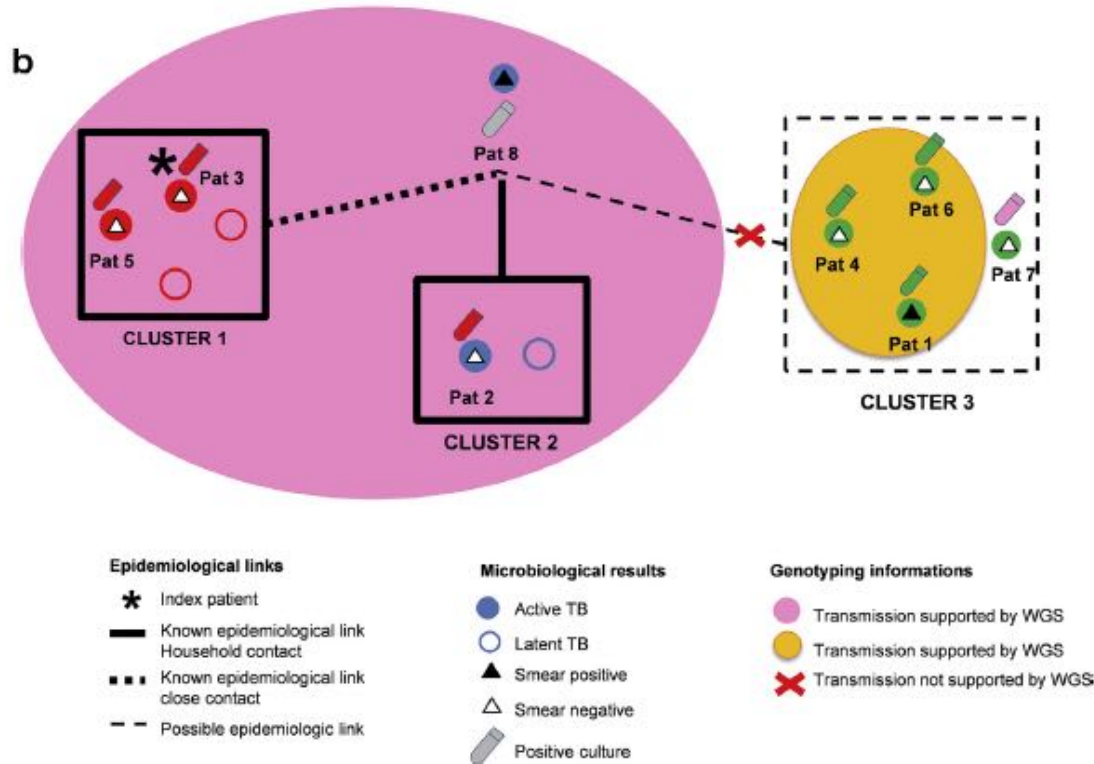
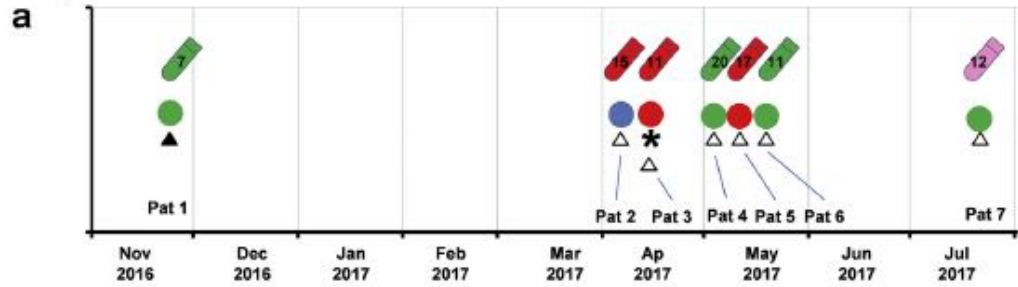


Epidemiology



Different methods used in molecular typing of *Mycobacterium tuberculosis* (Cannas et al, 2016)

Epidemiology



Zakham, F., S. Laurent, A. L. Esteves Carreira, A. Corbaz, C. Bertelli, E. Masserey, L. Nicod, G. Greub, K. Jaton, J. Mazza-Stalder and O. Opota (2019). "Whole-genome sequencing for rapid, reliable and routine investigation of *Mycobacterium tuberculosis* transmission in local communities." *New Microbes and New Infections* 31: 100582.

Investigation of an International Outbreak of MDR-TB among patients arriving from the Horn of Africa



30 may 2016:
German Mycobacteria reference center
→ independant investigation of a **possible outbreak** of MDR-TB in Germany

29 April 2016:
Zurich Reference Center for Mycobacteria →
Investigation of a possible **national outbreak** of MDR-TB due to **other reports in Switzerland**

- ❖ From Feb. 2016 to **April 2017**
- ❖ **29 patients diagnose with MDR-TB**
- ❖ **7 European countries**
- ❖ Patients coming from Somalia, Eritrea, Djibouti Ethiopia and Soudan
- ❖ Resistance to : rifampicin, isoniazid, ethambutol, pyrazinamide and capreomycine

2016

2017

31 Dec 2015:
Induced sputum
Positive culture (29 days),
MDR-TB
Mutation *rpoB*
Mutation *katG*

20 June 2016:
Bronchial aspirate Asp.
Positive culture (20 days),
MDR-TB
Mutation *rpoB*
Mutation *katG*

14 Oct. 2016:
Sputum
PCR positive (~300 DNA copies/ml)
Xpert MTB/RIF positif
***rpoB* mutation détecté**

Investigation of an International Outbreak of MDR-TB among patients arriving from the Horn of Africa

Added-value of WGS-based molecular epidemiology

CLINICAL DATA

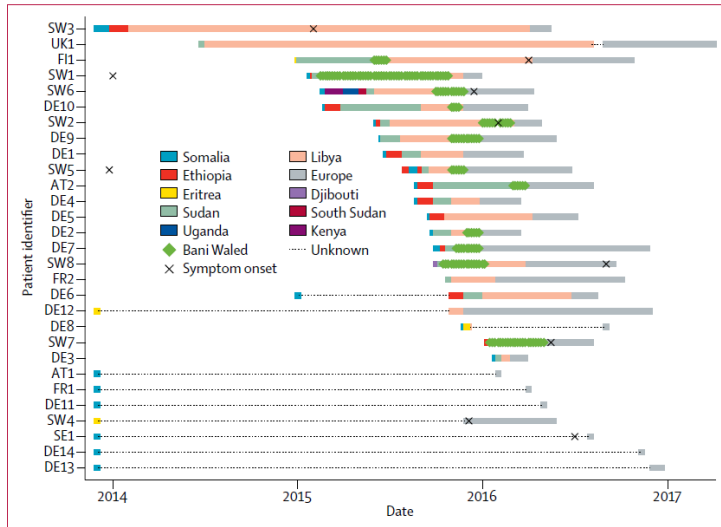


Figure 2: Timeline of patient journeys until diagnosis. The 1st of each month is shown as the country entry date. Subsequent countries visited in the same month are presented at 5-day intervals.

EPIDEMIOLOGICAL DATA

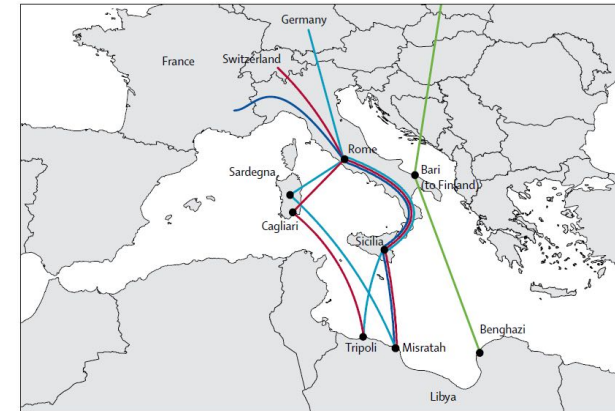
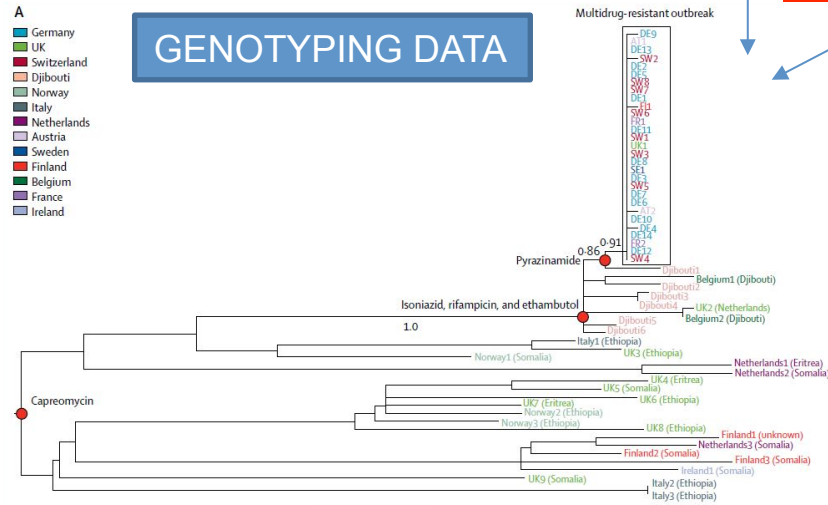


Figure 3: Reported migration routes through Italy of 29 outbreak patients with a documented migration route, August, 2014, to February, 2017

Rapid and reliable understanding of the situation

GENOTYPING DATA



Walker TM, Merker M, Knoblauch AM, Helbling P, Schoch OD, van der Werf MJ, et al. **A cluster of multidrug-resistant *Mycobacterium tuberculosis* among patients arriving in Europe from the horn of africa: A molecular epidemiological study.** *The Lancet Infectious Diseases* 2018.



Ethical Challenges in Genomic Approaches to Infectious Disease



EUROPEAN SOCIETY OF
MYCOBACTERIOLOGY

European Society of Mycobacteriology
Valencia, Spain
July 1, 2019

ETHICAL CHALLENGES IN GENOMIC APPROACHES TO INFECTIOUS DISEASE:

THE USE OF WHOLE GENOME SEQUENCING IN TB SURVEILLANCE

ERIC T. JUENGST, PHD

CENTER FOR BIOETHICS

UNIVERSITY OF NORTH CAROLINA, CHAPEL HILL

[HTTP://BIOETHICS.UNC.EDU](http://bioethics.unc.edu)

- Four illustrative cases and the ethical considerations they highlight
- Eight key considerations for developing anticipatory policies and practices
- Round table discussion and audience feedback.

Ethical Challenges in Genomic Approaches to Infectious Disease

European Society of Mycobacteriology
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ETHICAL CHALLENGES IN GENOMIC
APPROACHES TO INFECTIOUS DISEASE:

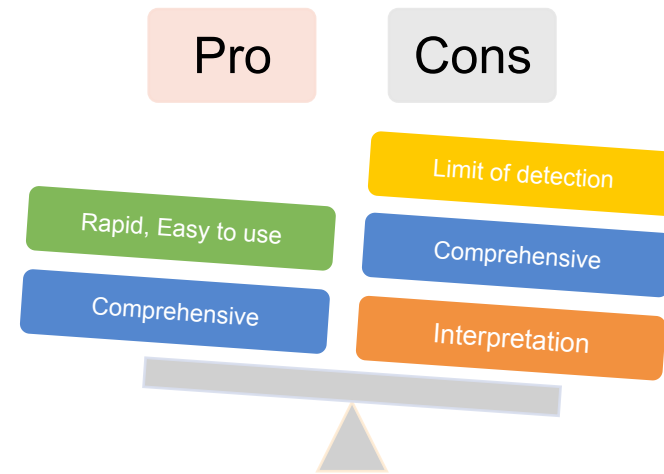
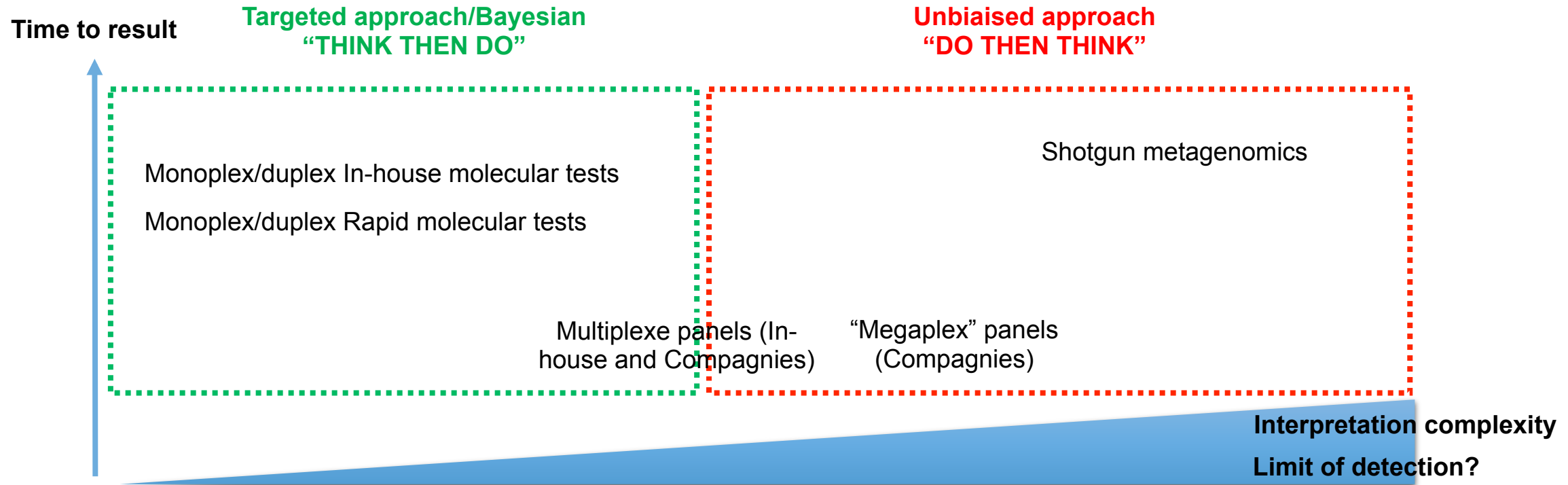
THE USE OF WHOLE GENOME SEQUENCING IN TB SURVEILLANCE

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- **8 key points for discussion**

- Public health mandate for actionable real-time Mtb WGS
- Mtb WGS without individual consent
- Promoting social justice and global solidarity
- Insuring confidentiality and security
- Two-step data sharing between public health institutions
- Personal disclosure and group interest: building patient partnerships
- Privacy and consent in disclosure of transmission events
- Professional transparency in public communication.

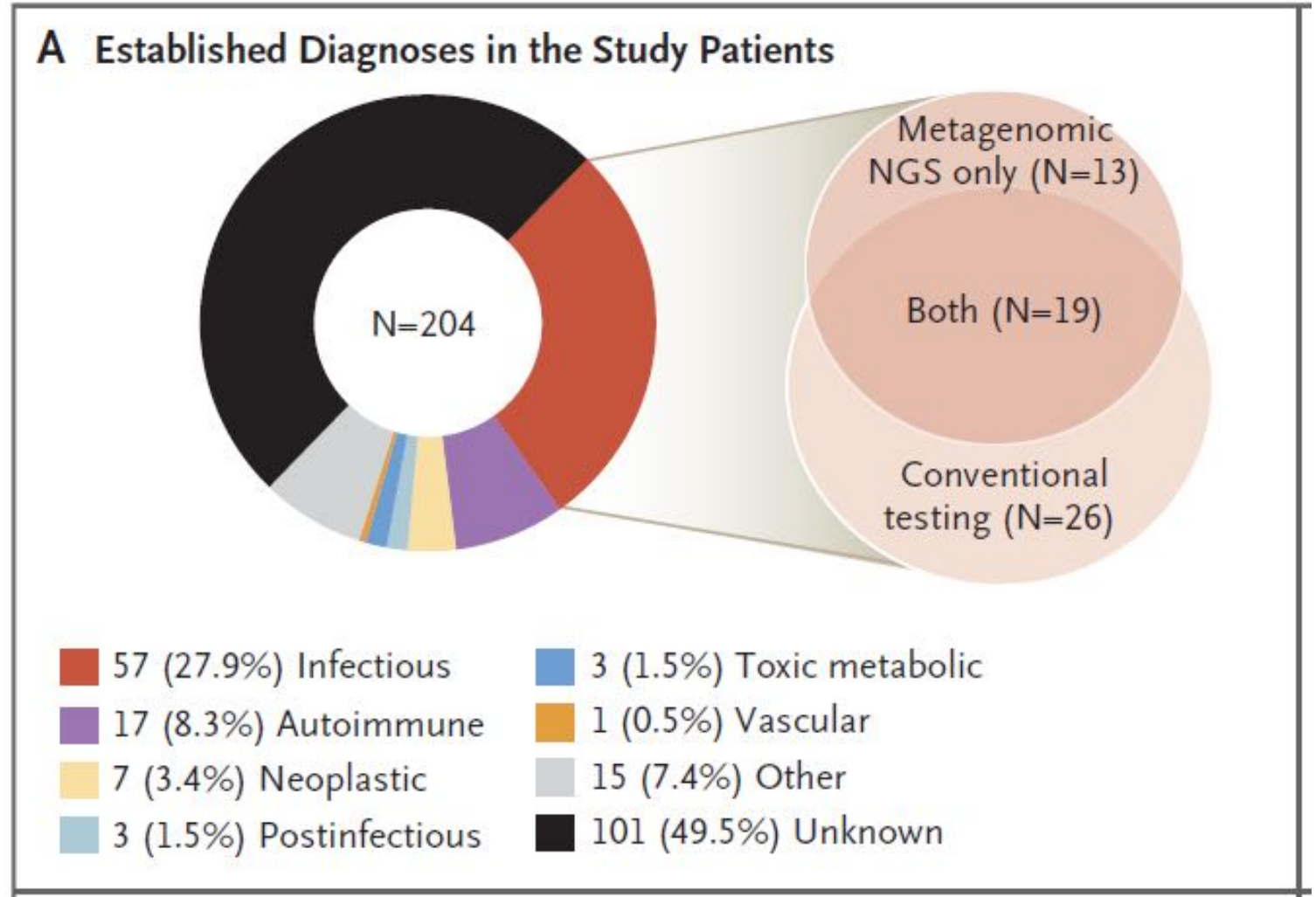
New approaches in clinical microbiology?



New approach in clinical microbiology?

Shotgun meta-GEN for pathogen detection and identification

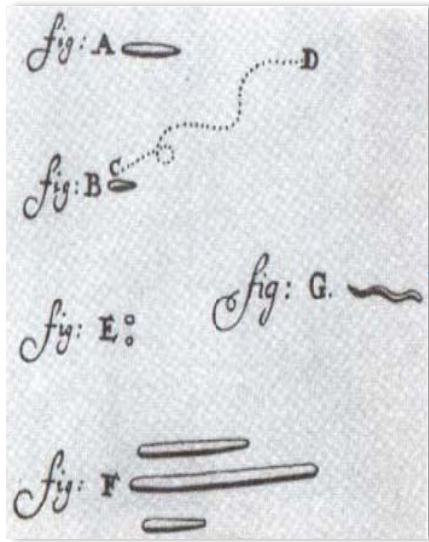
- Backgrounds:
 - Encephalitis of unknown etiology: **32%–75%**.
- Methods
 - 204 specimens, conventional culture and molecular methods versus shotgun metagenomics
- Results
 - Conventional methods + NGS resulted in **49.5%** of unknown etiology
- Conclusions:
 - Added value +/-
 - Need other studies/other syndromes
 - Other indication of metagenomics



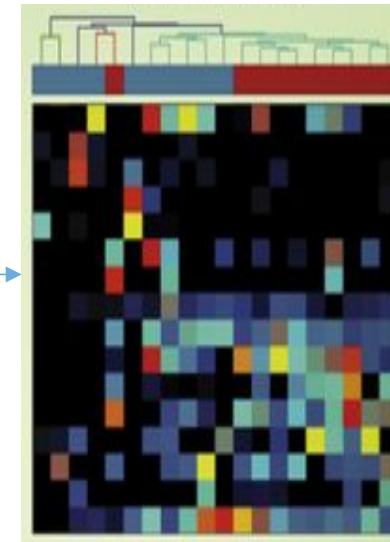
Wilson, et al., 2019. "Clinical Metagenomic Sequencing for Diagnosis of Meningitis and Encephalitis." *N Engl J Med* **380**(24): 2327-2340.

New approaches in clinical microbiology?

Microbial species



van Leeuwenhoek
1683



Microbial species
Microbes functions/pathways
Host cells response

Quince et al. 2017.

Same approaches?
Same objectives?
Same applications?

New applications,
New approaches

Microbiology

Clinical
microbiology

Identification

Resistance

Carriage

Prognosis

Anticipation

Personalized clinical
microbiology

Immune status

Infection course

Epidemiology

Severity

Forensic

...?

+

Conclusions

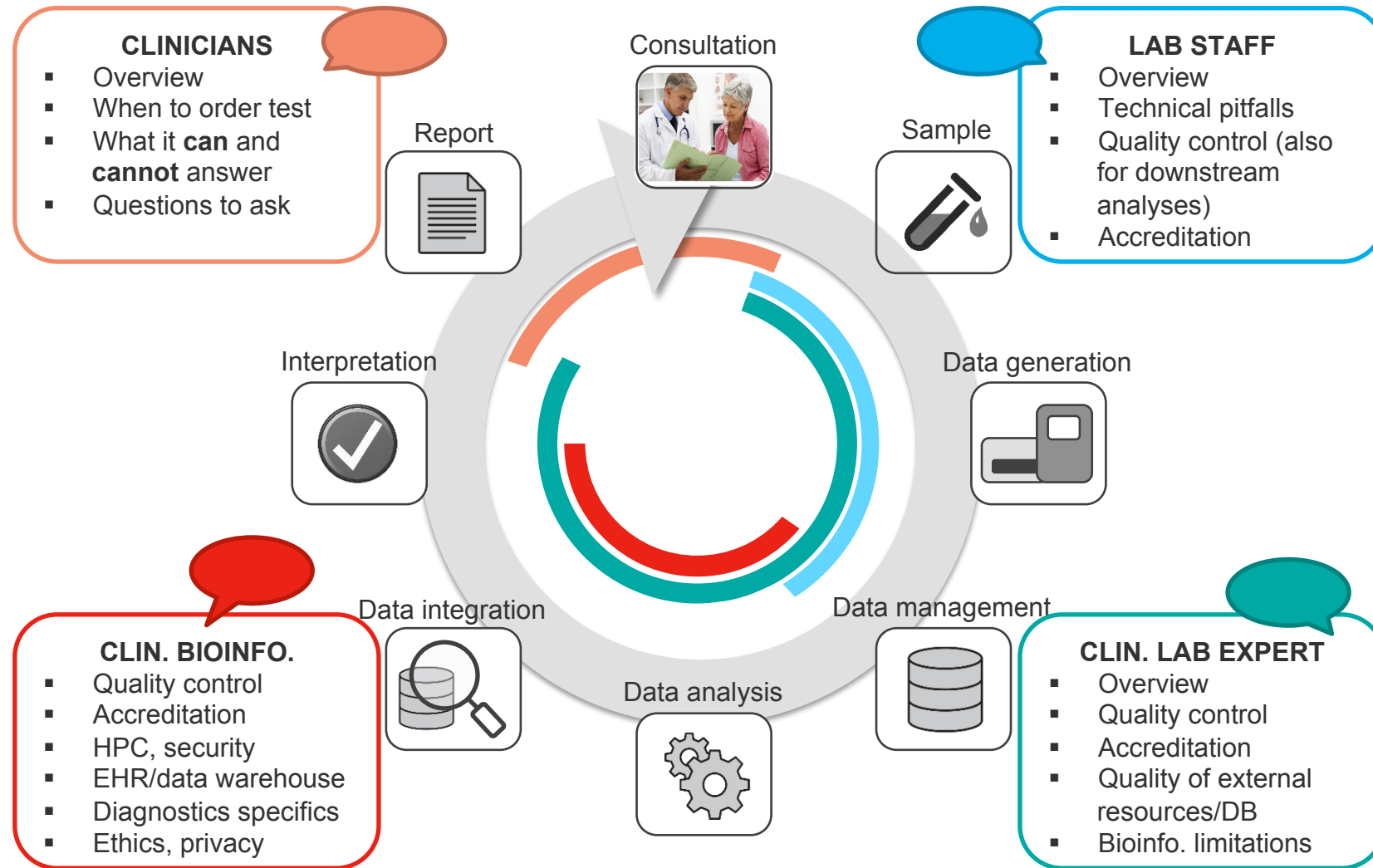
❖ Clinical Microbiologist

- is not only a service provider
- participates in the prescription of the biologic analysis and can, by dialoguing with the clinician, modulate this one. REMIC (Referential of Medical Microbiology of the French Society of Microbiology).

❖ Importance of training to maintain knowledge and skills

- expertise for dialogue
- to anticipate future changes

Conclusions



Examples of profile-specific training needs (not exhaustive)

Dre Aitana Lebrand

Conclusions

- ❖ Management of increasing informations
- ❖ Important role of the CM
 - Data management
 - Data interpretation integration
 - Reporting results
- ❖ New approaches? New tools?
 - Digitalization and infectious diseases to improving patient outcome in the age of big data
- ❖ Societal and ethical Challenges
 - Personalized medicine
 - Genomic approaches to infectious disease



	<p>Contact</p> <p>Administrative Secretariat Dr Giulia De Angelis Fondazione Policlinico Universitario A. Gemelli - IRCCS, Università Cattolica del S. Cuore Institute of Microbiology Largo A. Gemelli 8 00167 Rome, Italy precisionmedicinerome2019@gmail.com</p>	 <p>ESCMID MANAGING INFECTIONS PROMOTING SCIENCE</p> <p>ESCMID Postgraduate Education Course Second Course on Precision Medicine</p> <p>Rome, Italy 26 – 28 September 2019</p>	<p>ESCMID Postgraduate Education Course Second Course on Precision Medicine</p> <p>Organiser • ESCMID Faculty Commission</p> <p>Course Coordinators • Prof. Maurizio Sanguinetti, Rome, Italy • Dr Alexandra Mailles, Saint Maurice, France • Dr Angela Huttner, Geneva, Switzerland • Dr Giulia De Angelis, Rome, Italy</p> <p>Course Objectives Upon completion of this course, participants will be able to:</p> <ul style="list-style-type: none">• Understand the pharmacokinetic and epidemiologic heterogeneity in patient populations traditionally excluded from clinical studies such as the critically ill, the elderly, those with renal insufficiency, the obese, and female patients• Understand the evidence (or lack thereof) for medical decision-making in these populations• Explore both the limits and the strengths of current "one-size-fits-all" guidelines• Understand the clinical implications of variations in local epidemiology, microbiota, and regional perceptions regarding antimicrobial use• Explore the clinical evidence for recommended durations of antimicrobial therapy• Understand the variation in pharmacokinetics across populations• Explore the ethical dilemmas in antimicrobial decision-making (the individual versus society)
<p>Target Audience Clinicians or clinical microbiologists who are confronted in their practice to the need to address the specificity of their patient to achieve the best possible management.</p> <p>Faculty Members Marlijn Adbo, Hamburg, Germany Werner C. Albrich, St. Gallen, Switzerland Julia Bielecki, Basel, Switzerland Pierre-Vincent Bocthod, Lausanne, Switzerland Susanna Esposito, Perugia, Italy Angela Huttner, Geneva, Switzerland Benedikt Huttner, Geneva, Switzerland Jeroen Schaeten, Nijmegen, Netherlands Simon Le Hello, Caen, France Alexandra Mailles, Saint-Maurice, France Marco Rinaldi Oggioni, Leicester, United Kingdom Patricia Favese, La Tronche, France Maurizio Sanguinetti, Rome, Italy Christoph Skovak, Marburg, Germany Marc J. Struelens, Stockholm, Sweden Thomas Grenholm Tängdén, Uppsala, Sweden Henri Van Werkhoven, Utrecht, Netherlands Noemie Wagner, Geneva, Switzerland</p>	 <p>ESCMID EUROPEAN SOCIETY OF CLINICAL MICROBIOLOGY AND INFECTIONS (ESCAI)</p>		

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Prof. Eric Juengst,

Pneumology Service, CHUV

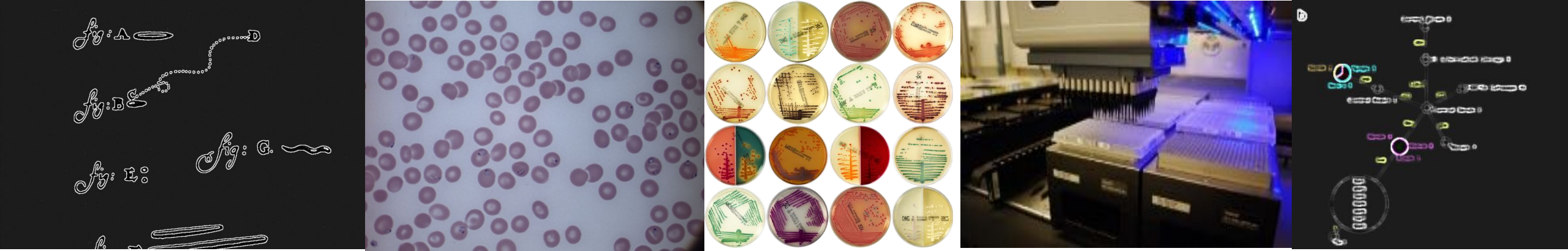
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Dr Petar Stupar

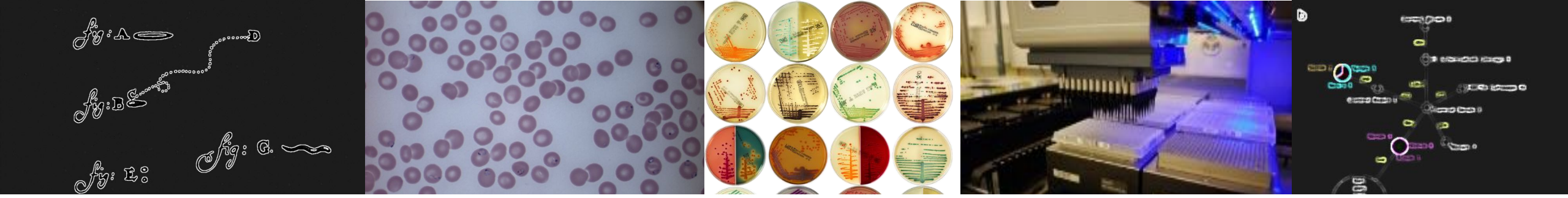


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“Education is the passport to the future, for tomorrow belongs to those who prepare for it today” Malcolm X (Malcolm Little)





From the clinic: The changing profession of the clinical microbiologist

Dr Onya Opota, PhD., CM.

Diagnostic department, Institute of Microbiology
Lausanne hospital university, Switzerland

ESCMID Postgraduate Technical Workshop
Clinical bioinformatics for microbial genomics and metagenomics
Lausanne, 9 September 2019

