# MALDI-TOF/MS
## (Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry)
# en bactériologie clinique

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# Patiente de 25 ans

- Consutle son MT Jeudi 19.02 pour angine avec EF

- StrepA rapid-test: nég

- TTT Brufen-Dafalgan

- Samedi 21.02: CAU pour persistance angine+EF
    - Suspicion d'abcès rétro-amygdalien
    - CT-scan en urgence, hémocs puis Augmentin po

# Evolution

- Lundi 23.02: hémoc positive BG-

- ID par tests biochimiques / PCR Séquençage : 24h-72h

- Même jour, *Fusobacterium necrophorum* ID par MALDI-TOF/MS, la patiente est rentrée à domicile… »

- Décision de rappeler son médecin traitant pour qu'il contacte la patiente: suspicion de Lemierre?

# Patient de 67 ans

- Un patient de 67 ans est admis aux HUG suite à une altération de l'état général, 39°C, Antibio X
- Une paire d'hémoculture a été faite aux urgences plus d'autres examens
- Après 18h d'incubation un des deux flacons d'hémoculture s'est positivé
- L'examen direct montre au jour 0: Bâtonnets GRAM négatifs fusiformes

# ID Phénotypique

- Jour 1 : colonies « translucide » sur gélose au sang et chocolat agar, oxidase –

- Jour 2: Résultat Vitek2:
  - Good identification
  - %id= 89 *Sphingomonas paucimobilis*

# Jour 3

- ❑ Résultat API 20 E:
  - Bonne identification
  - %id= 93 T= 0.62
  - *Pasteurella pneumotropica*

- ❑ Résultat API 20 NE:
  - Bonne identification
  - %id= 96.3 T=0.6
  - *Mannheimia haemolytica / Pasteurella trehalosi*

# Jour 6… ID Moléculaire

- Résultat 16S-rDNA sequencing:
  - *Capnocytophaga sputigena*


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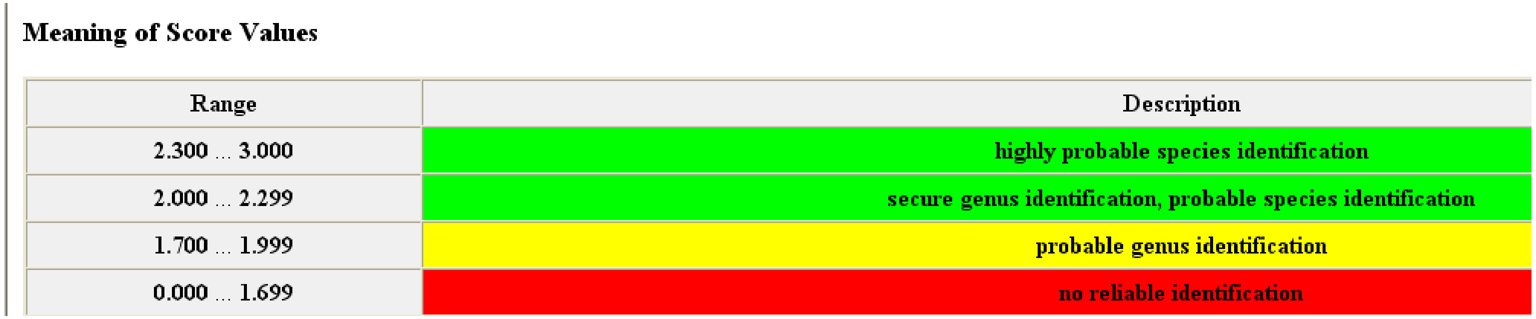
# Retour au jour 1: MALDI-TOF/MS

| Rank (Quality) | Matched Pattern | Score Value | NCBI Identifier |
|---|---|---|---|
| 1<br>(+) | Capnocytophaga ochracea DSM 7271_DSM | 1.847 | 1018 |
| 2<br>(-) | Capnocytophaga ochracea DSM 7272_DSM | 1.585 | 1018 |

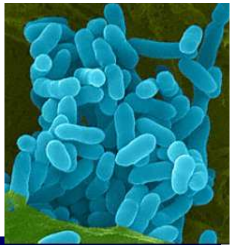


**Meaning of Score Values**

| Range | Description |
|---|---|
| 2.300 ... 3.000 | highly probable species identification |
| 2.000 ... 2.299 | secure genus identification, probable species identification |
| 1.700 ... 1.999 | probable genus identification |
| 0.000 ... 1.699 | no reliable identification |

# Need for speed?

# Need for speed?



- Monsieur H, 35 ans est admis aux HUG suite à un état fébrile, associé à des céphalées et douleur d’une loge rénale puis depuis une atteinte pulmonaire sévère avec choc septique.

- Anamnèse: Monsieur H était en vacances en Martinique, dans le village Le Vauclin.

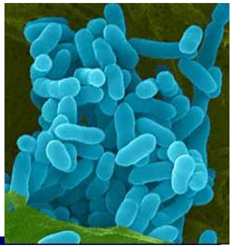
Tempête xynthia

- L'état du patient se dégrade rapidement et il décède après 3 jours d’hospitalisation.

# Jour 0

- ❑ Une paire d’hémoculture a été faite aux urgence plus d’autres examens
- ❑ L’examen direct montre au jour 1: Bâtonnets GRAM négatifs

# Jour 1



nalyte3

BRUKER

Analyte Name: 2501031407
Analyte Description:
Analyte ID: HE 9303 GS BAER
Analyte Creation Date/Time: 2010-11-26 17:17:33.375
Applied MSP Library(ies):
Applied Taxonomy Tree: Bruker Taxonomy

| Rank (Quality) | Matched Pattern | Score Value | NCBI Identifier |
|---|---|---|---|
| 1<br>( ++ ) | Burkholderia thailandensis DSM 13276T HAM | 2.045 | 57975 |
| 2<br>( - ) | Burkholderia anthina LMG 16670 HAM | 1.681 | 179879 |
| 3<br>( - ) | Burkholderia plantarii DSM 9509T HAM | 1.673 | 41899 |
| 4<br>( - ) | Burkholderia cepacia group 18875_1 CHB | 1.666 | 292 |
| 5<br>( - ) | Burkholderia cenocepacia LMG 12614 HAM | 1.655 | 95486 |
| 6<br>( - ) | Burkholderia cepacia DSM 7288T HAM | 1.636 | 292 |
| 7<br>( - ) | Burkholderia dolosa DSM 16088T HAM | 1.626 | 152500 |
| 8<br>( - ) | Hydrogenophaga flava B339 UFL | 1.538 | 65657 |
| 9<br>( - ) | Burkholderia vietnamiensis LMG 10929T HAM | 1.5 | 60552 |
| 10<br>( - ) | Burkholderia ambifaria LMG 11351 HAM | 1.498 | 152480 |

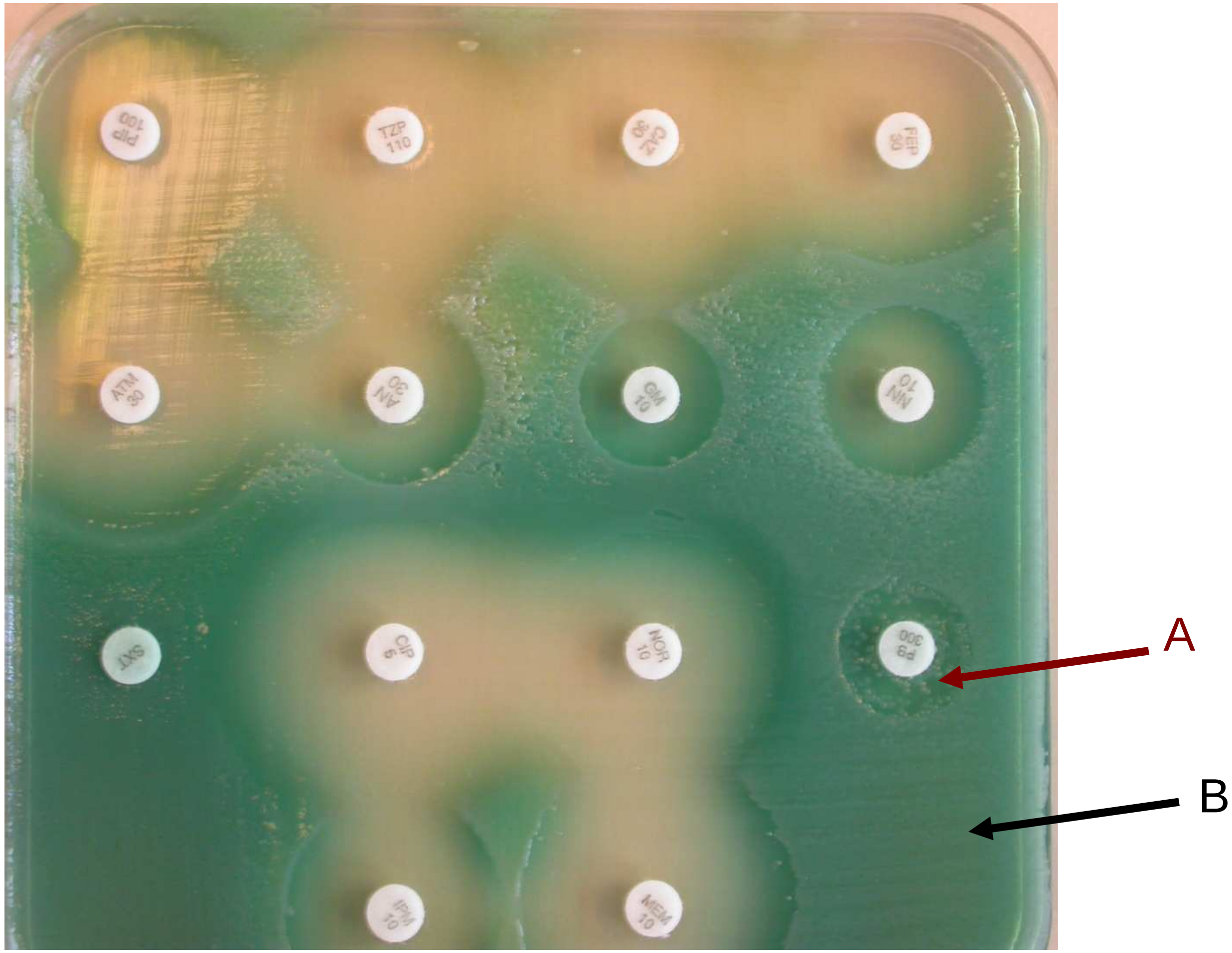
# 16S rRNA gene sequencing

- Séquence de 993pb, identique à *B. pseudomallei*.

- Une seule différence avec les 2 types de séquences de *B. mallei* connus (un C au lieu d'un T)

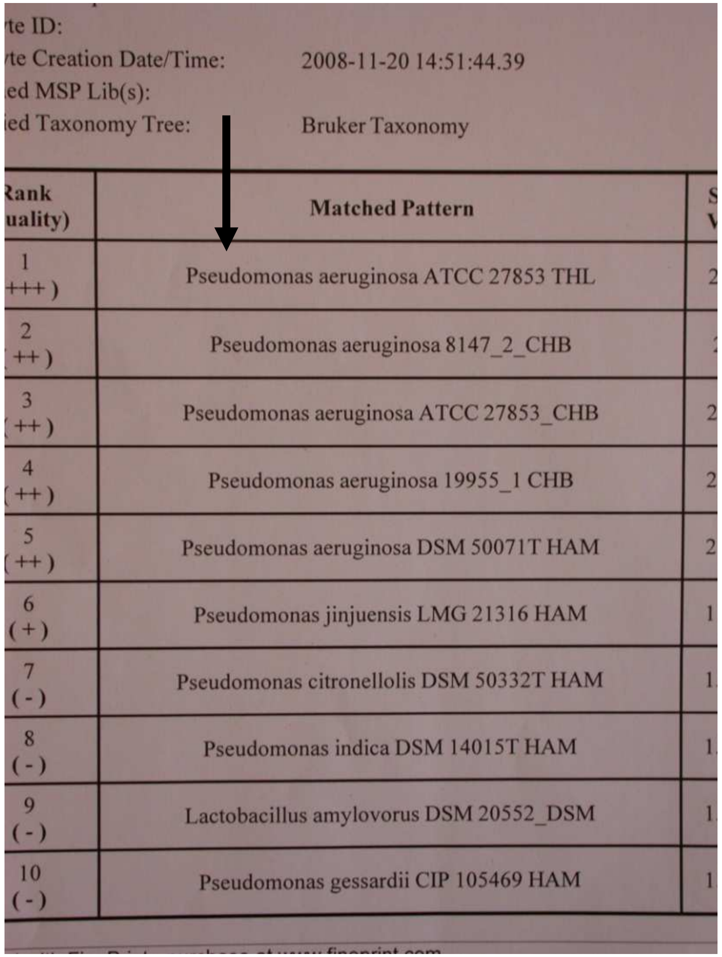
- Alignée avec des séquences de *B. pseudomallei, B. mallei* et *B. thailandensis* décrites dans l'article du JCM (Gee J.E., 2003,). La souche du patient H. présente 12 différences sur 993 bases avec *B. thailandensis.*

# Antibiogramme mixte



# Antibiogramme mixte

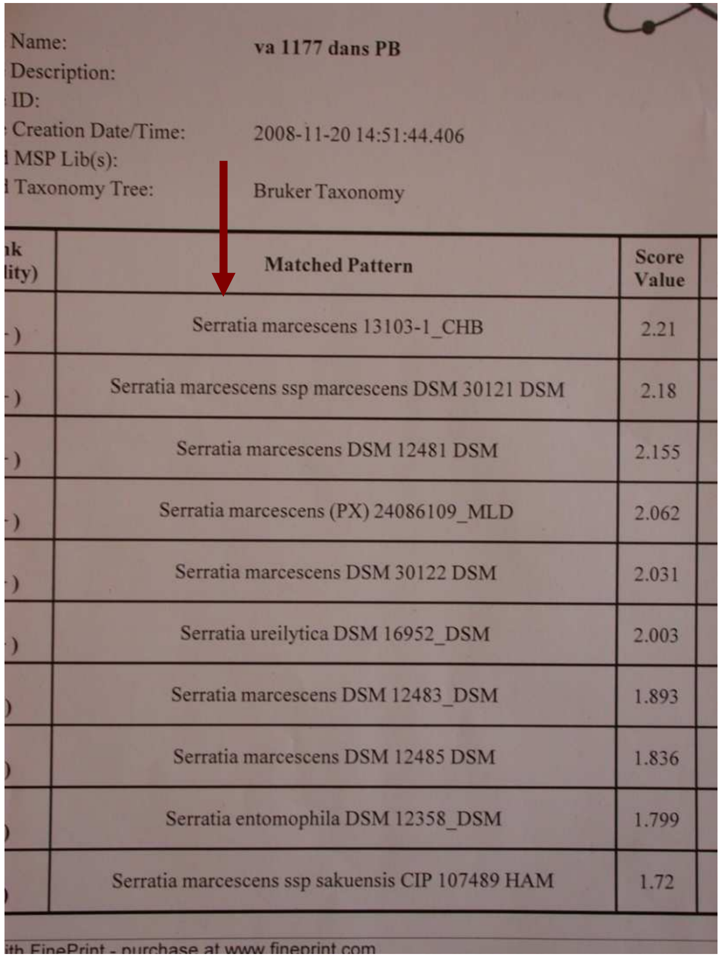
B



te ID:
te Creation Date/Time: 2008-11-20 14:51:44.39
ed MSP Lib(s):
ied Taxonomy Tree: Bruker Taxonomy

| Rank<br>uality) | Matched Pattern | S<br>V |
|---|---|---|
| 1<br>+++) | Pseudomonas aeruginosa ATCC 27853 THL | 2 |
| 2<br>++) | Pseudomonas aeruginosa 8147_2_CHB | |
| 3<br>(++) | Pseudomonas aeruginosa ATCC 27853_CHB | 2 |
| 4<br>(++) | Pseudomonas aeruginosa 19955_1 CHB | 2 |
| 5<br>(++) | Pseudomonas aeruginosa DSM 50071T HAM | 2 |
| 6<br>(+) | Pseudomonas jinjuensis LMG 21316 HAM | 1 |
| 7<br>(-) | Pseudomonas citronellolis DSM 50332T HAM | 1. |
| 8<br>(-) | Pseudomonas indica DSM 14015T HAM | 1. |
| 9<br>(-) | Lactobacillus amylovorus DSM 20552_DSM | 1. |
| 10<br>(-) | Pseudomonas gessardii CIP 105469 HAM | 1 |

A



Name: **va 1177 dans PB**
Description:
ID:
Creation Date/Time: 2008-11-20 14:51:44.406
MSP Lib(s):
Taxonomy Tree: Bruker Taxonomy

| k<br>lity) | Matched Pattern | Score Value |
|---|---|---|
| -) | Serratia marcescens 13103-1_CHB | 2.21 |
| -) | Serratia marcescens ssp marcescens DSM 30121 DSM | 2.18 |
| -) | Serratia marcescens DSM 12481 DSM | 2.155 |
| -) | Serratia marcescens (PX) 24086109_MLD | 2.062 |
| ) | Serratia marcescens DSM 30122 DSM | 2.031 |
| ) | Serratia ureilytica DSM 16952_DSM | 2.003 |
| ) | Serratia marcescens DSM 12483_DSM | 1.893 |
| ) | Serratia marcescens DSM 12485 DSM | 1.836 |
| ) | Serratia entomophila DSM 12358_DSM | 1.799 |
| ) | Serratia marcescens ssp sakuensis CIP 107489 HAM | 1.72 |

# Need for speed?

# Need for speed?

- Homme de 42 ans est admis au HUG suite à un état fébrile.
- Une paire d’hémoculture a été faite aux urgences plus d’autres examens
- L’examen direct montre au jour 1: CG+ en diplo et chainettes

# Need for speed?

**Analyte5**

BRUKER

Analyte Name: **3001721487**
Analyte Description:
Analyte ID: he 5569
Analyte Creation Date/Time: 2011-02-01 10:31:54.796
Applied MSP Library(ies):
Applied Taxonomy Tree: Bruker Taxonomy

| Rank (Quality) | Matched Pattern | Score Value | NCBI Identifier |
|---|---|---|---|
| 1<br>( ++ ) | Streptococcus pneumoniae ATCC 49619 THL | 2.04 | 1313 |
| 2<br>( ++ ) | Streptococcus pneumoniae besSt29 THL | 2.001 | 1313 |
| 3<br>( + ) | Streptococcus oralis DSM 20379 DSM | 1.854 | 1303 |
| 4<br>( + ) | Streptococcus pneumoniae DSM 14378 DSM | 1.839 | 1313 |
| 5<br>( + ) | Streptococcus pneumoniae DSM 11868 DSM | 1.81 | 1313 |
| 6<br>( + ) | Streptococcus oralis DSM 20395 DSM | 1.77 | 1303 |
| 7<br>( + ) | Streptococcus pneumoniae DSM 11866 DSM | 1.749 | 1313 |
| 8<br>( + ) | Streptococcus pseudopneumoniae DSM 18670T DSM | 1.738 | 257758 |
| 9<br>( + ) | Streptococcus oralis DSM 20627T DSM | 1.707 | 1303 |
| 10<br>( - ) | Streptococcus pneumoniae DSM 11865 DSM | 1.673 | 1313 |

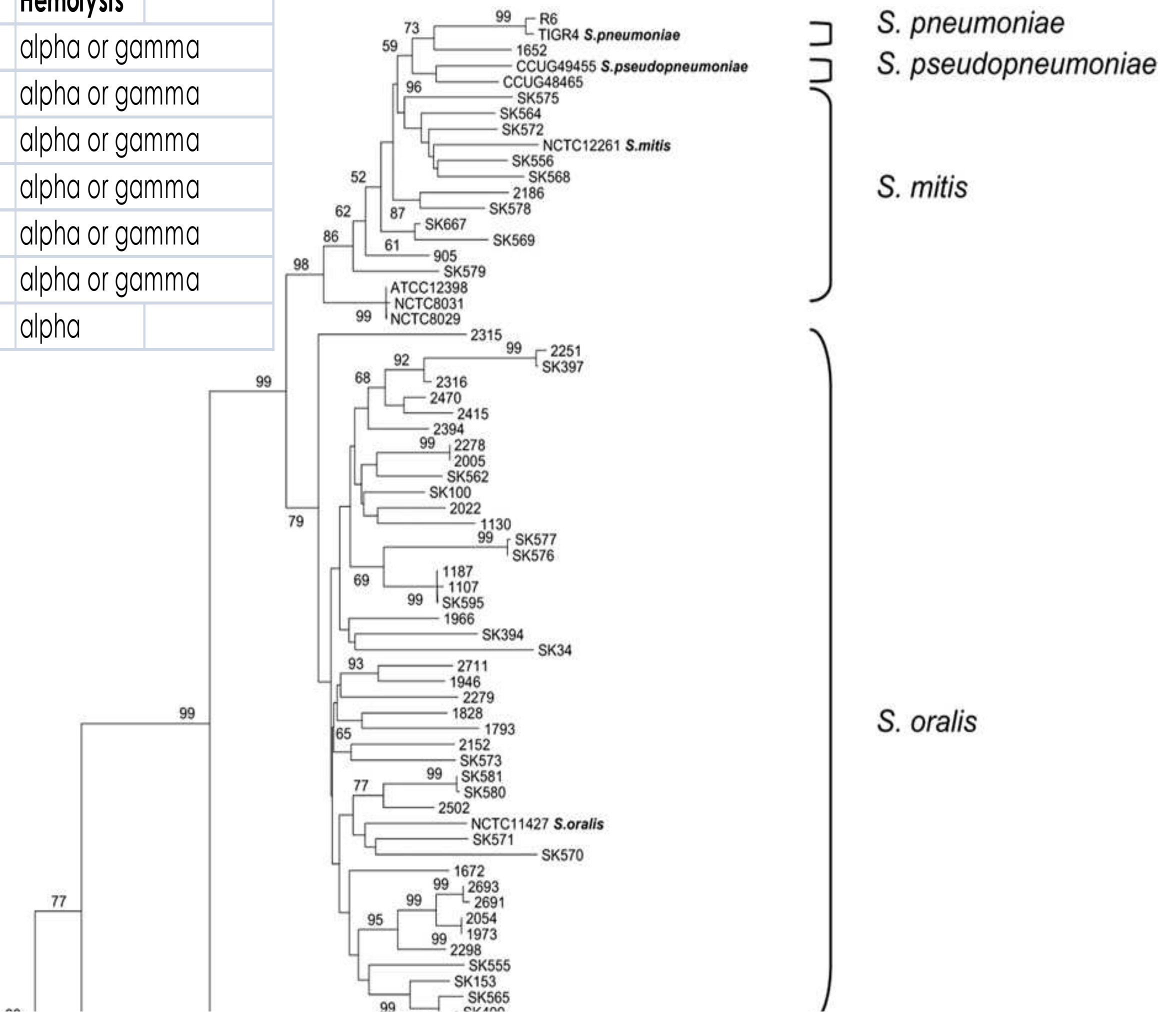
**Jour 2**
Optochine: Sensible
Pneumoagglutination: NEG

ID: *S. mitis*

Endocardite sur valve native

# *Streptococcus mitis* group

| **Streptococcus mitis group** | **Lancefield group** | **Hemolysis** |
|---|---|---|
| S. mitis | K, O or None at all | alpha or gamma |
| S. sanguinis | H or None at all | alpha or gamma |
| S. parasanguinis | None at all | alpha or gamma |
| S. oralis | None at all | alpha or gamma |
| S. infantis | None at all | alpha or gamma |
| S. gordonii | None at all | alpha or gamma |
| S. pneumoniae | None at all | alpha |

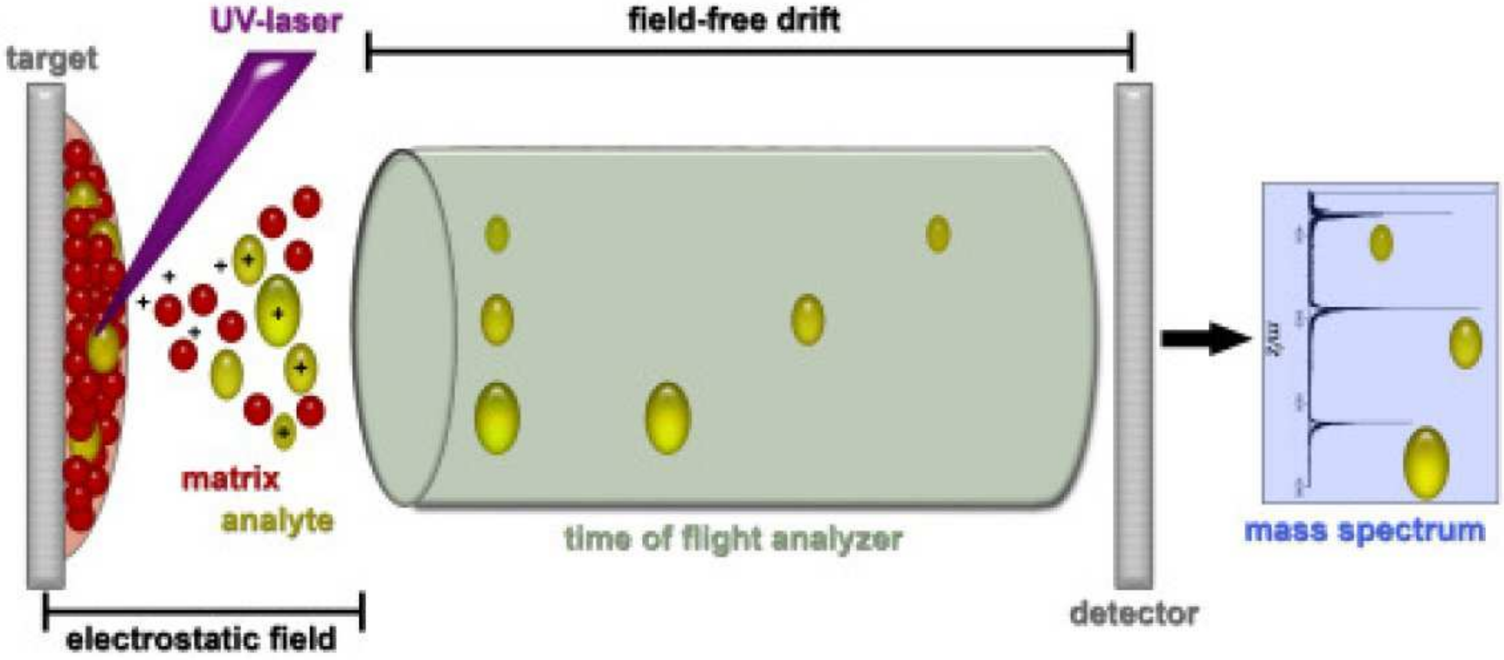


# The principle of MS…

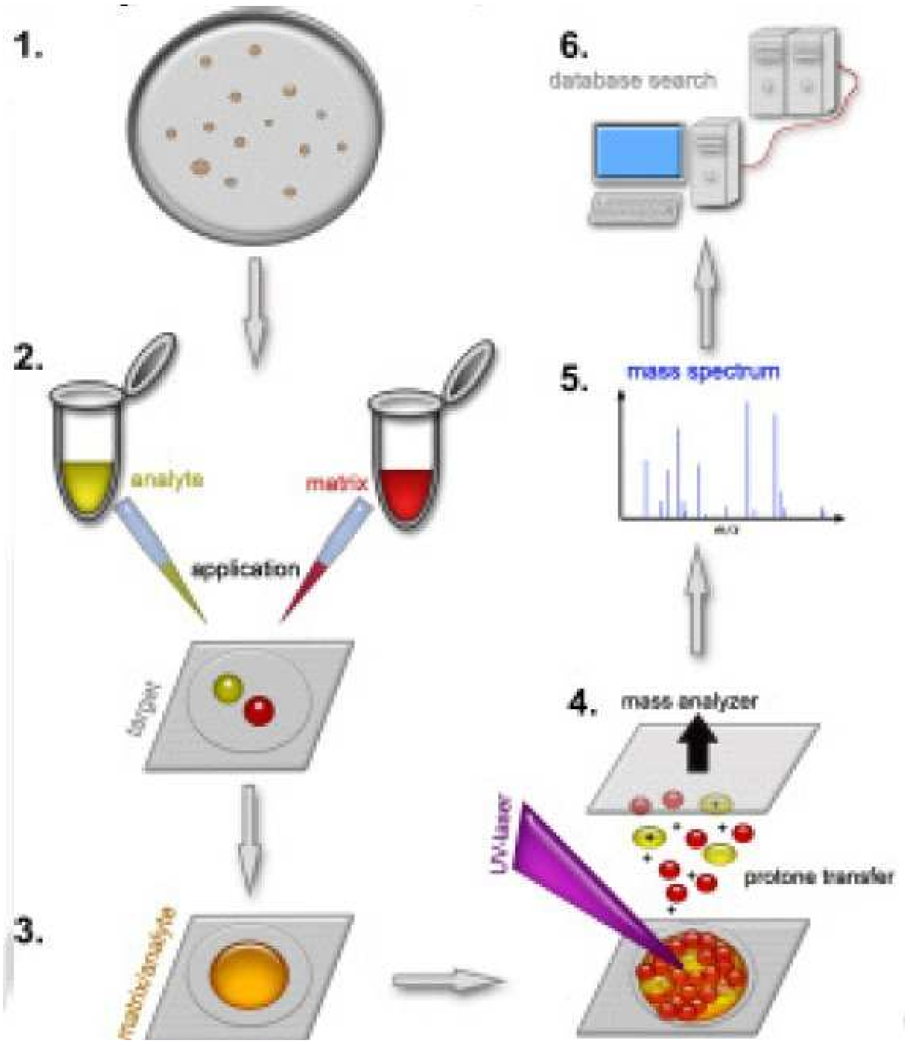
# The principle of MS…

This was
a car!

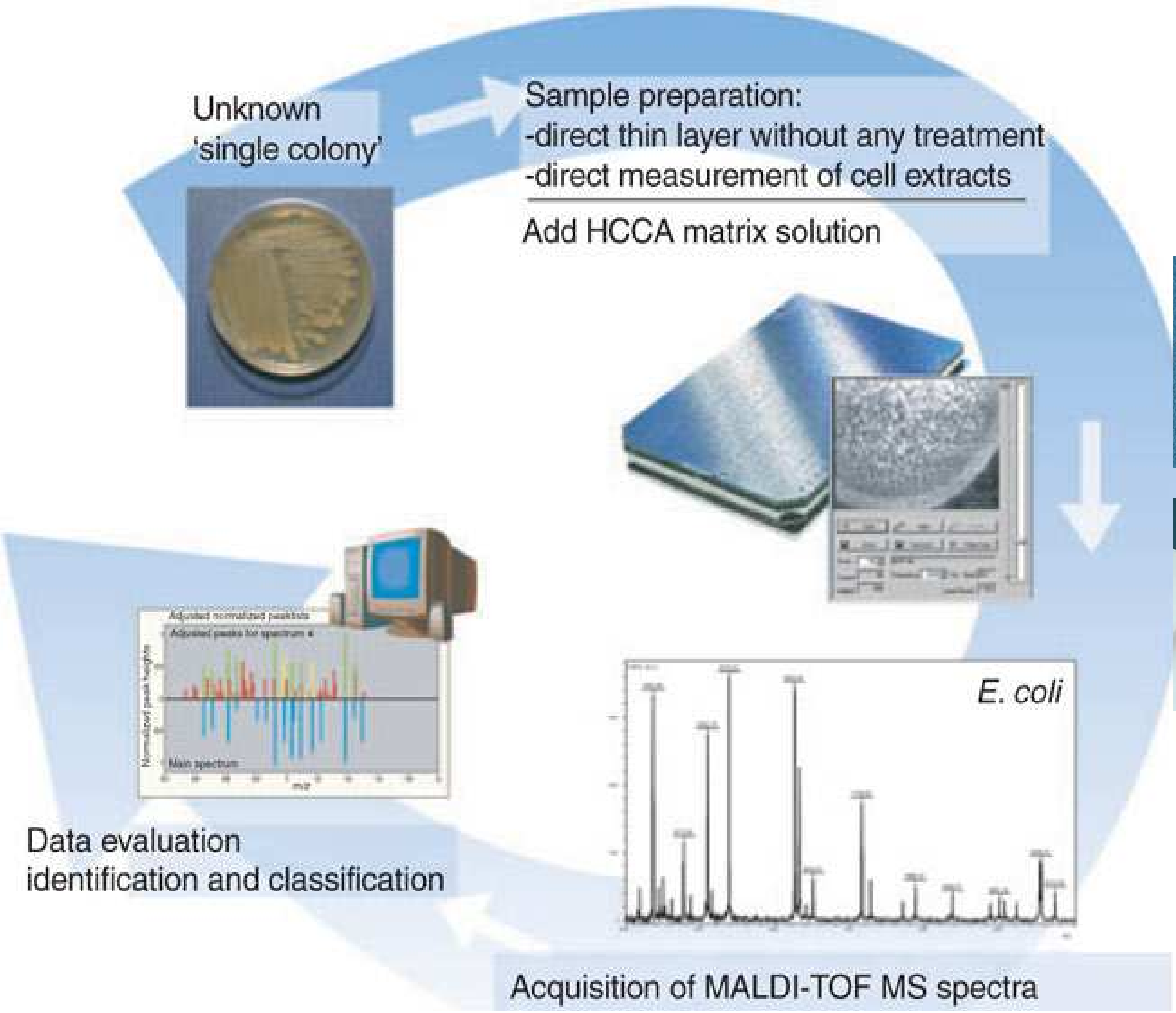
# The principle of MS…



# Workflow of MALDI-TOF MS-based bacterial identification



α-cyano-4-hydroxy-cinnamic acid in 50% acetonitrile-2.5% trifluoroacetic acid



Unknown
'single colony'

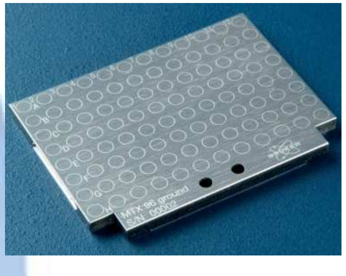
Sample preparation:
-direct thin layer without any treatment
-direct measurement of cell extracts

Add HCCA matrix solution

Acquisition of MALDI-TOF MS spectra

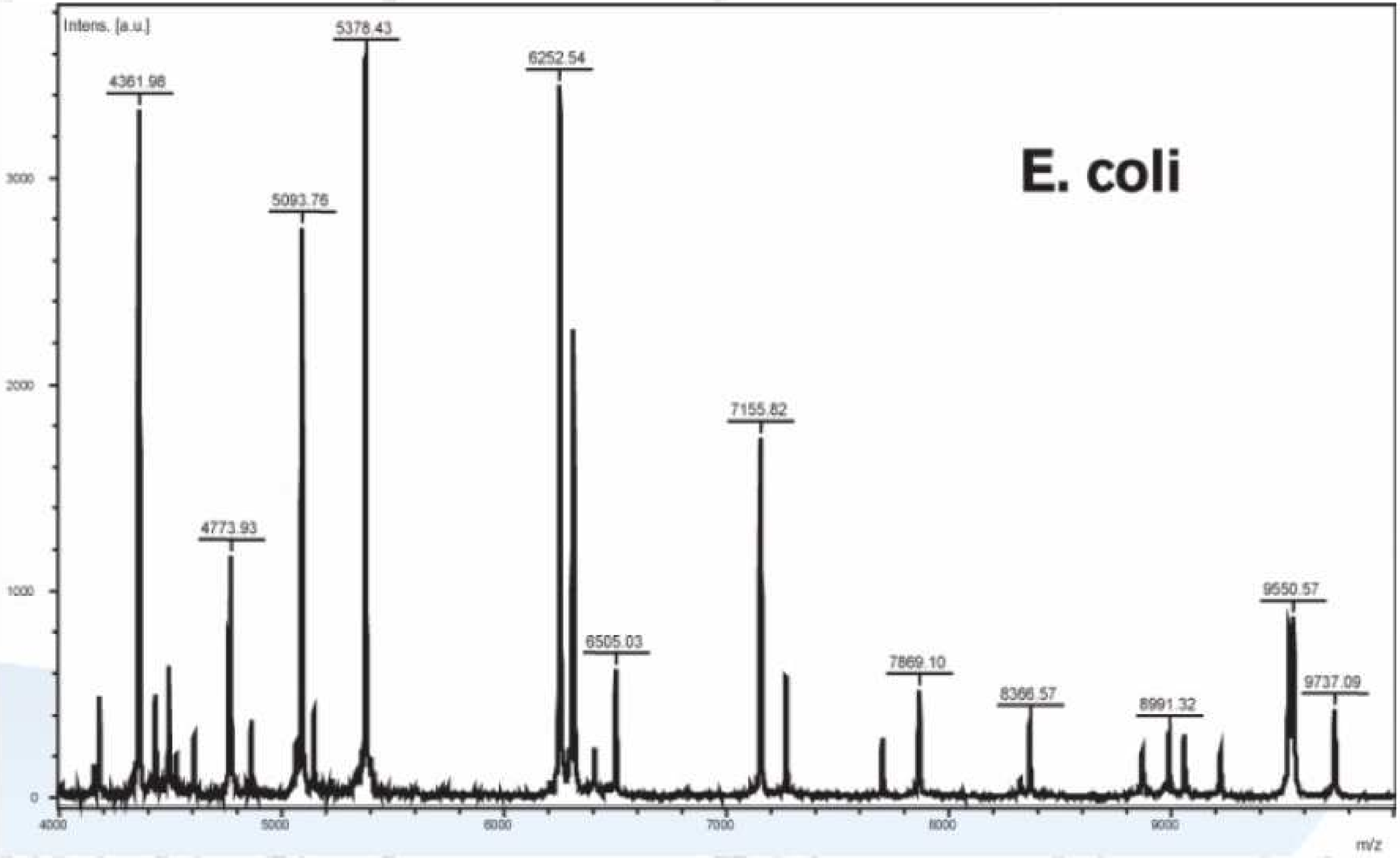
Data evaluation
identification and classification

Put one colony
on the target
And add a matrix

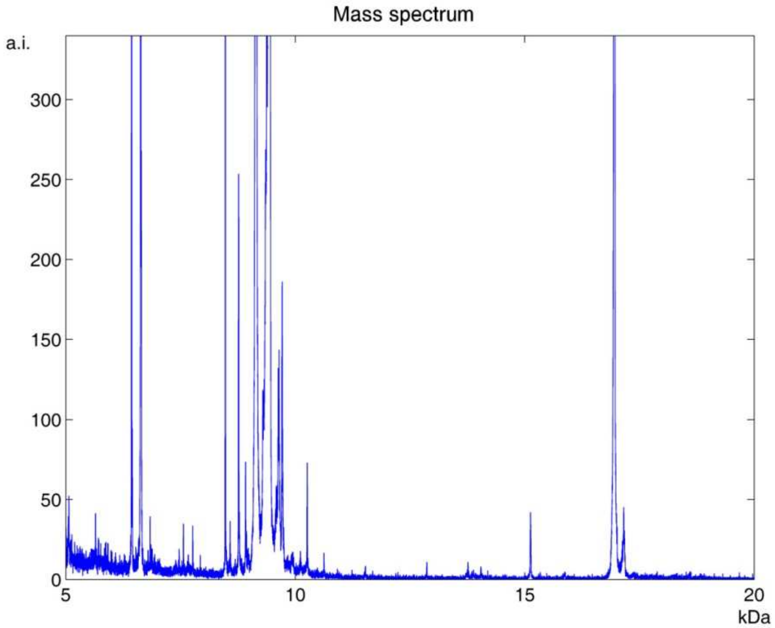


Insert the target
and start shooting

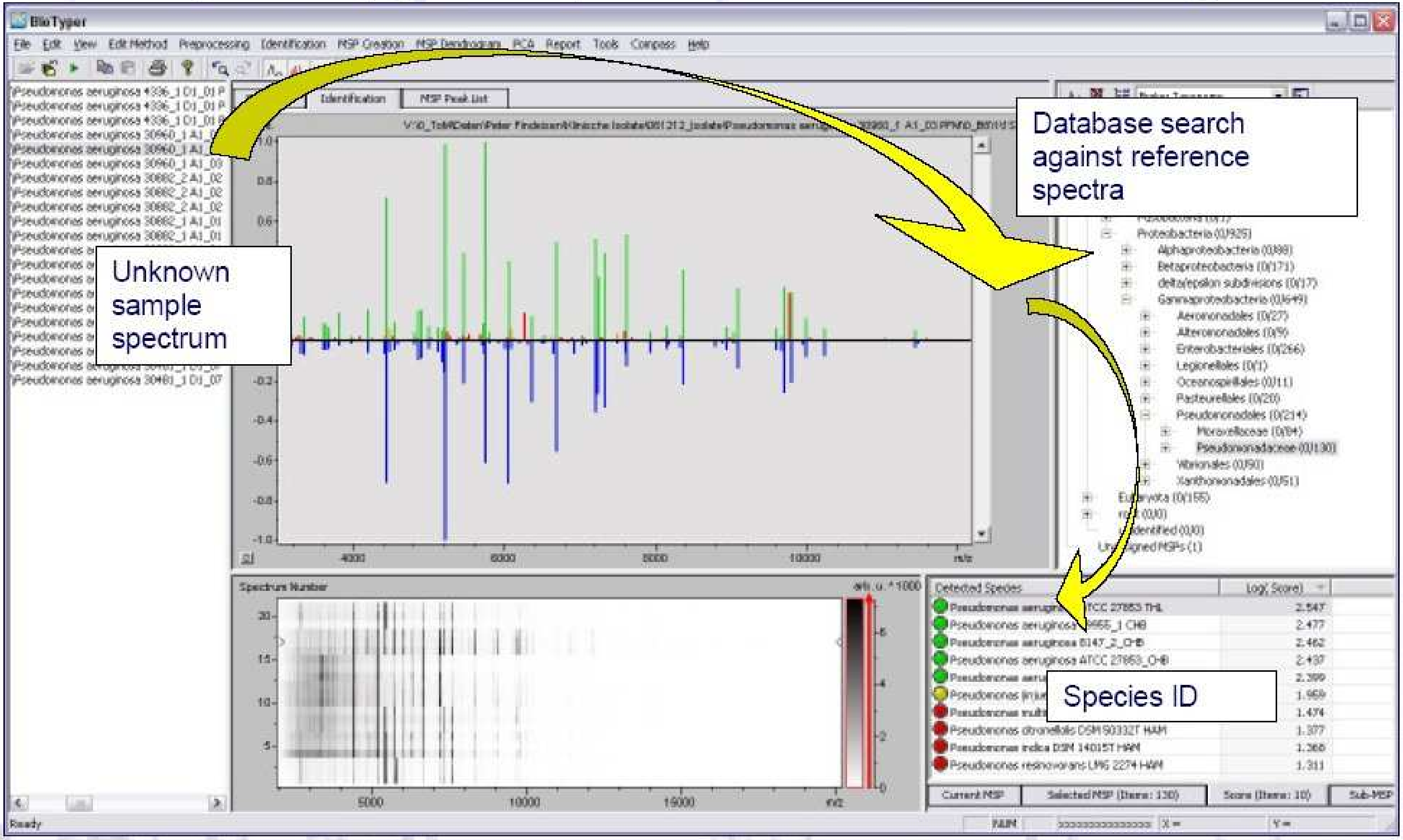
# Example of a MALDI-TOF MS Spectrum



# Data are then interpreted



# MALDI-TOF MS Analysis Software (BioTyper$^{TM}$) – Pattern Matching



| Detected Species | Log(Score) |
|---|---|
| Pseudomonas aerugin[illegible]TCC 27853 THL | 2.547 |
| Pseudomonas aeruginosa [illegible]9955_1 CHB | 2.477 |
| Pseudomonas aeruginosa 8147_2_CHB | 2.462 |
| Pseudomonas aeruginosa ATCC 27853_CHB | 2.437 |
| Pseudomonas aeru | 2.399 |
| Pseudomonas [illegible] | 1.959 |
| Pseudomonas multi | 1.474 |
| Pseudomonas citronellolis DSM 50332T HAM | 1.377 |
| Pseudomonas indica DSM 14015T HAM | 1.366 |
| Pseudomonas resinovorans LMG 2274 HAM | 1.311 |

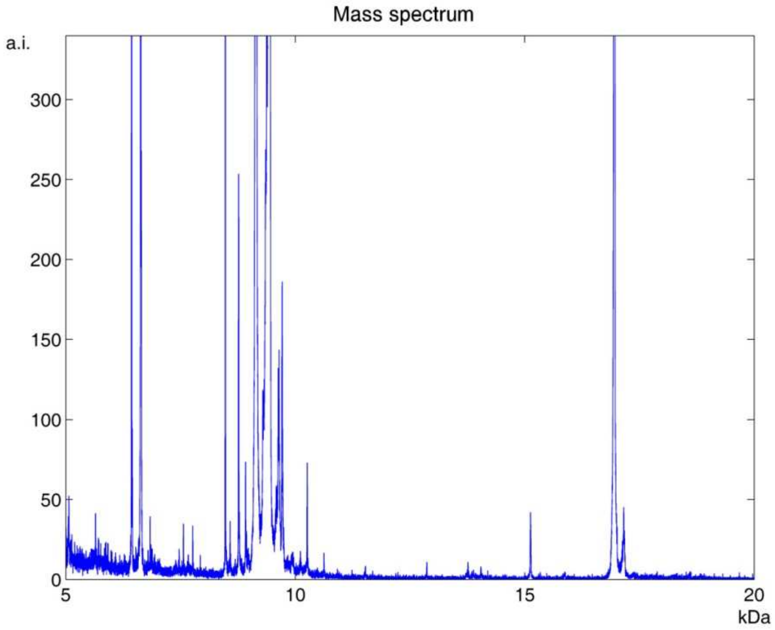
Unknown sample spectrum

Database search against reference spectra

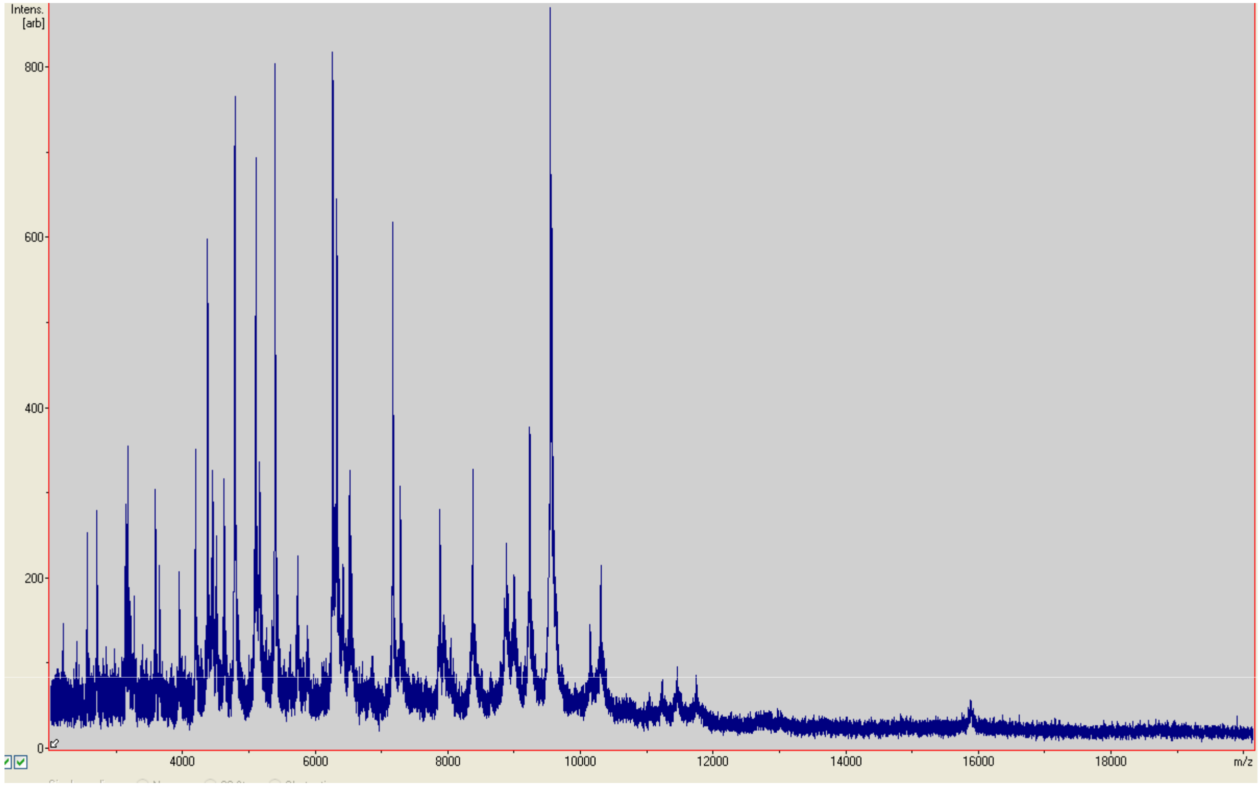
Species ID

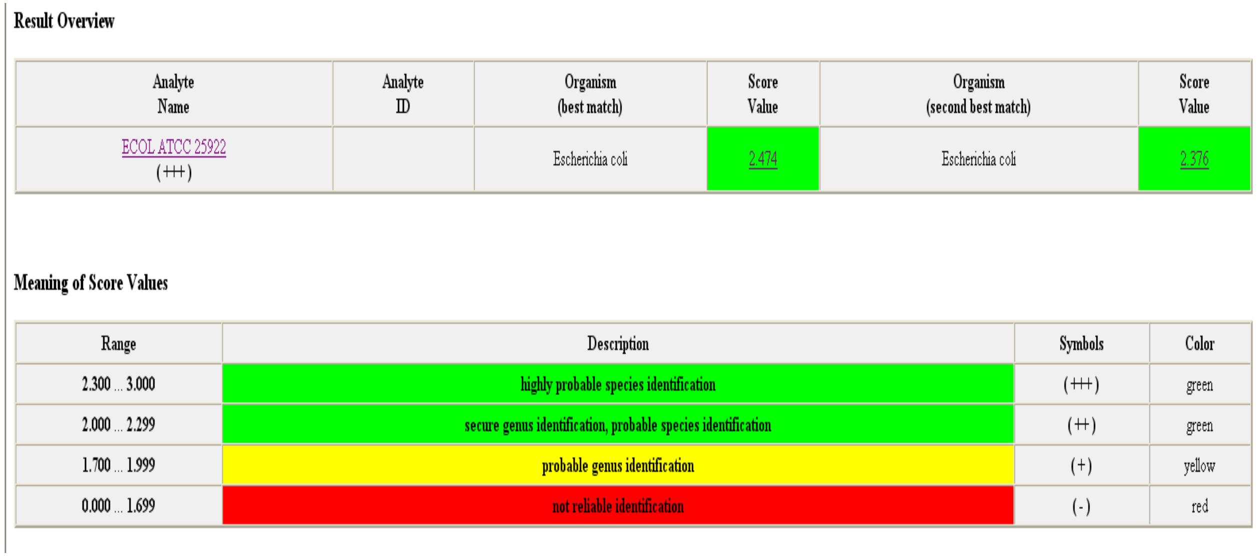
Bruker Daltonik GmbH, Germany

# Data are then interpreted



| Range | Description | Symbols | Color |
|---|---|---|---|
| 2.300 … 3.000 | highly probable species identification | ( +++ ) | green |
| 2.000 … 2.299 | secure genus identification, probable species identification | ( ++ ) | green |
| 1.700 … 1.999 | probable genus identification | ( + ) | yellow |
| 0.000 … 1.699 | no reliable identification | ( - ) | red |





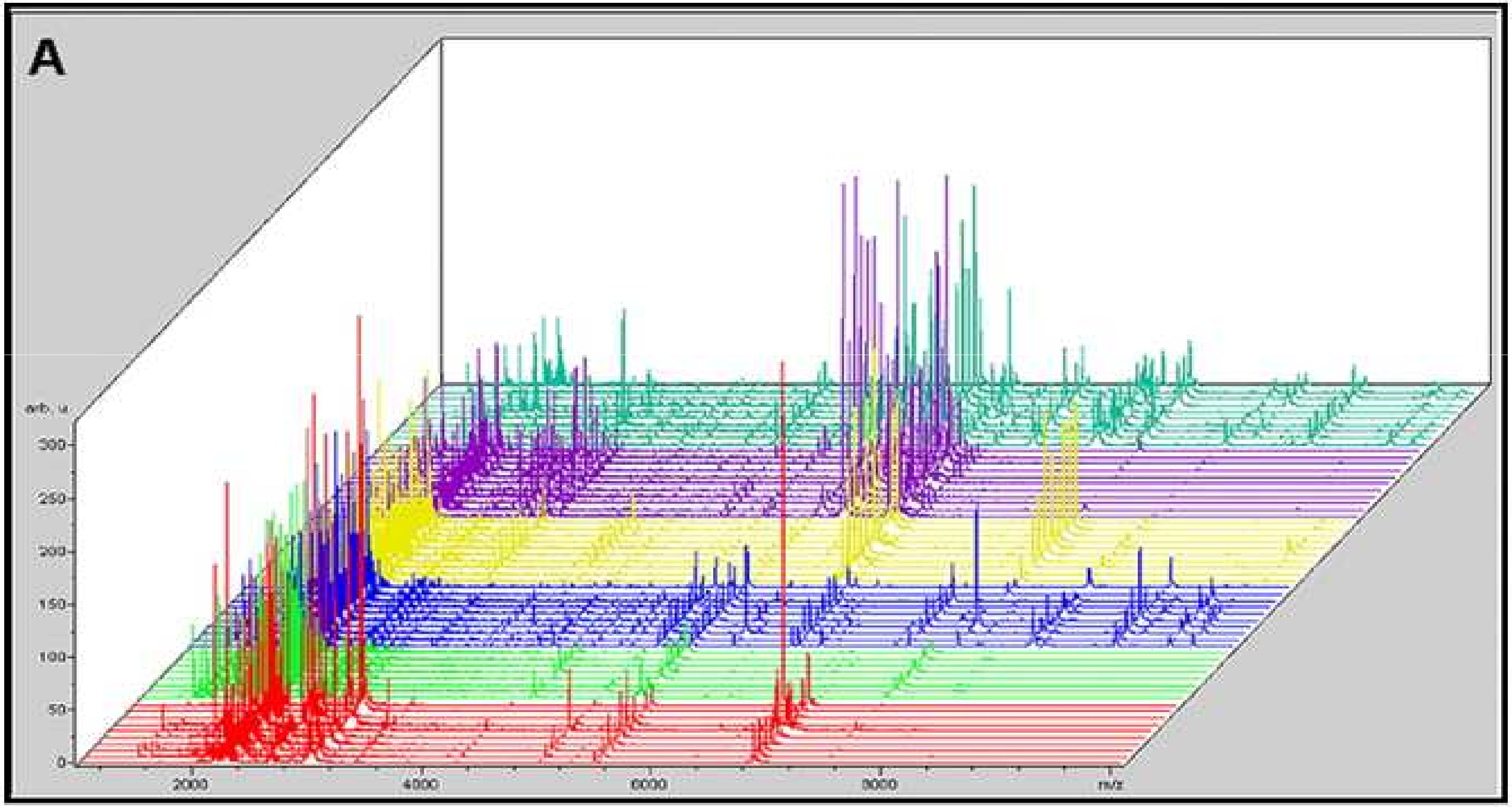
**Result Overview**

| Analyte Name | Analyte ID | Organism (best match) | Score Value | Organism (second best match) | Score Value |
|---|---|---|---|---|---|
| ECOL ATCC 25922<br>(+++) | | Escherichia coli | 2.474 | Escherichia coli | 2.376 |

**Meaning of Score Values**

| Range | Description | Symbols | Color |
|---|---|---|---|
| 2.300 ... 3.000 | highly probable species identification | (+++) | green |
| 2.000 ... 2.299 | secure genus identification, probable species identification | (++) | green |
| 1.700 ... 1.999 | probable genus identification | (+) | yellow |
| 0.000 ... 1.699 | not reliable identification | (-) | red |

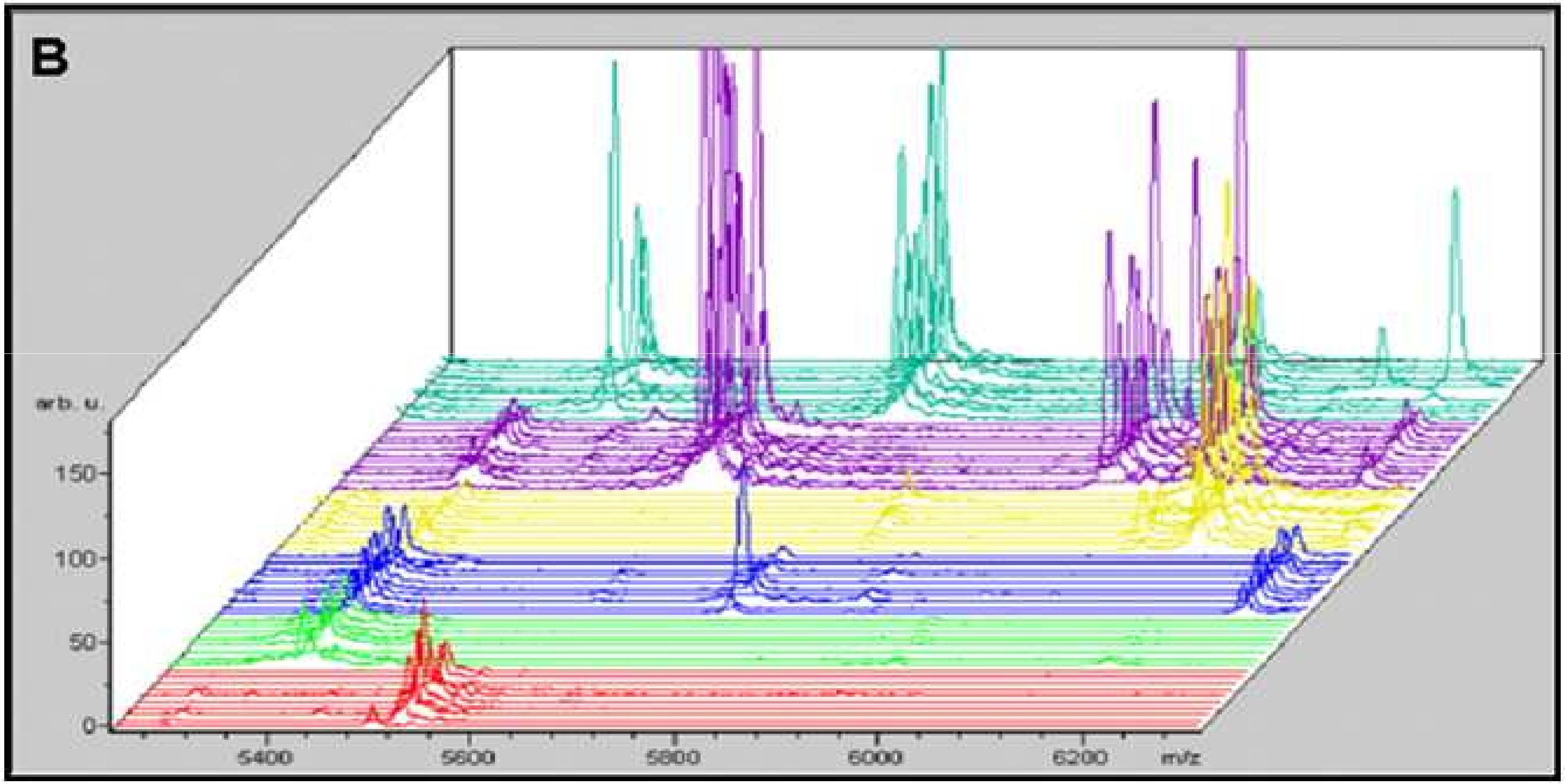
# The principle of MS…



*S. aureus*; *Streptococcus* group B; *E. coli*; *K. pneumoniae*; *Salmonella* serotype B; and, *P. aeruginosa* over *m*/*z* 1800–9000

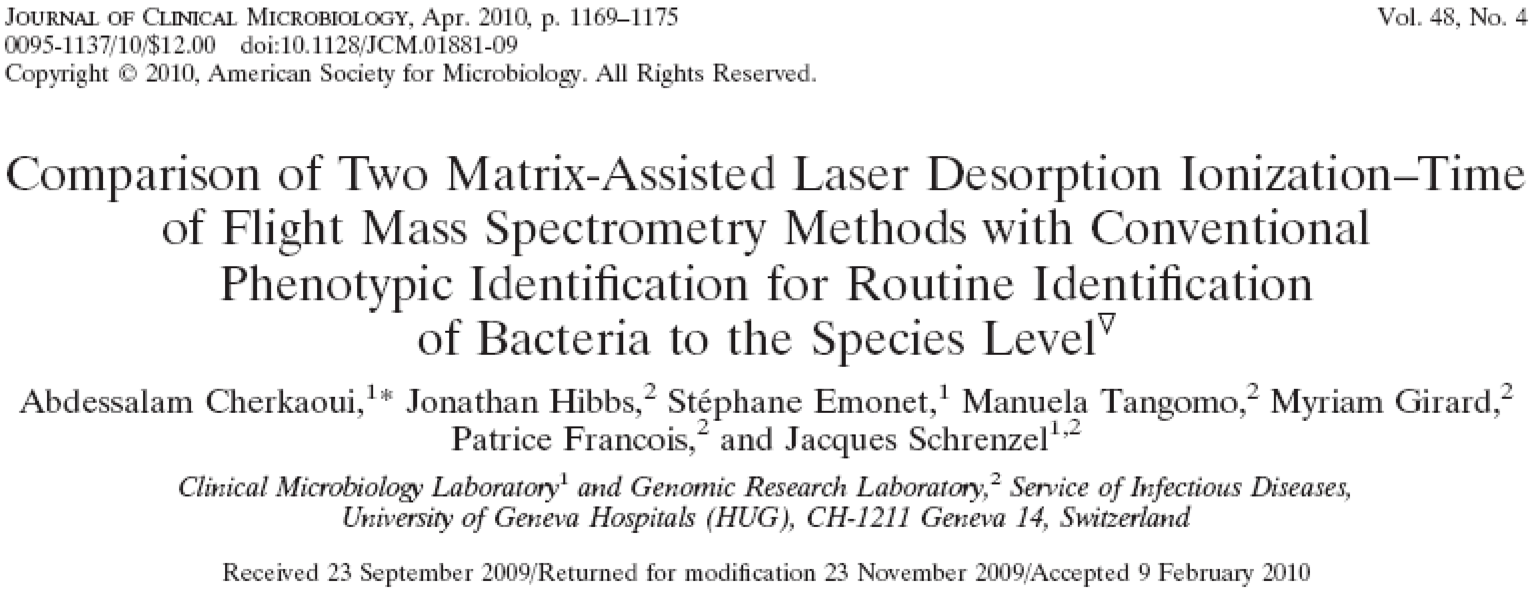
Sen-Yung Hsieh et al November, 2007

# The spectra are enlarged in the region of 5000–8500 Da/*z*



*S. aureus*; *Streptococcus* group B; *E. coli*; *K. pneumoniae*; *Salmonella* serotype B; and, *P. aeruginosa* over *m*/*z* 1800–9000

Sen-Yung Hsieh et al November, 2007



JOURNAL OF CLINICAL MICROBIOLOGY, Apr. 2010, p. 1169–1175 Vol. 48, No. 4
0095-1137/10/$12.00 doi:10.1128/JCM.01881-09

# Comparison of Two Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry Methods with Conventional Phenotypic Identification for Routine Identification of Bacteria to the Species Level[∇]

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Patrice Francois,[2] and Jacques Schrenzel[1,2]

*Clinical Microbiology Laboratory[1] and Genomic Research Laboratory,[2] Service of Infectious Diseases,
University of Geneva Hospitals (HUG), CH-1211 Geneva 14, Switzerland*

Received 23 September 2009/Returned for modification 23 November 2009/Accepted 9 February 2010

Cherkaoui A *et al*, JCM 2010

# Study design

- 720 clinical isolates
- Collected during 21 consecutive working days
- Various swabs (n=261), urine (n=197), blood cultures (n=120), respiratory tract (n=120), and stools (n=12)

# Study design

- 720 clinical isolates
- Collected during 21 consecutive working days
- Various swabs (n=261), urine (n=197), blood cultures (n=120), respiratory tract (n=120), and stools (n=12)
- Two rotating laboratory technologists processed in parallel freshly isolated colonies on two MS systems
- Results were first compared to our phenotypic routine (API and Vitek2)
- Any discordant result led to 16S rDNA sequencing (gold standard)

# Interpretation of the results

1- high score value ≥2.0 for Bruker and ≥90 for Shimadzu
=> isolates rated as identified to the species level

2- intermediate score value ≥1.7 for B and ≥70 for S
=> isolates rated as identified to the genus level

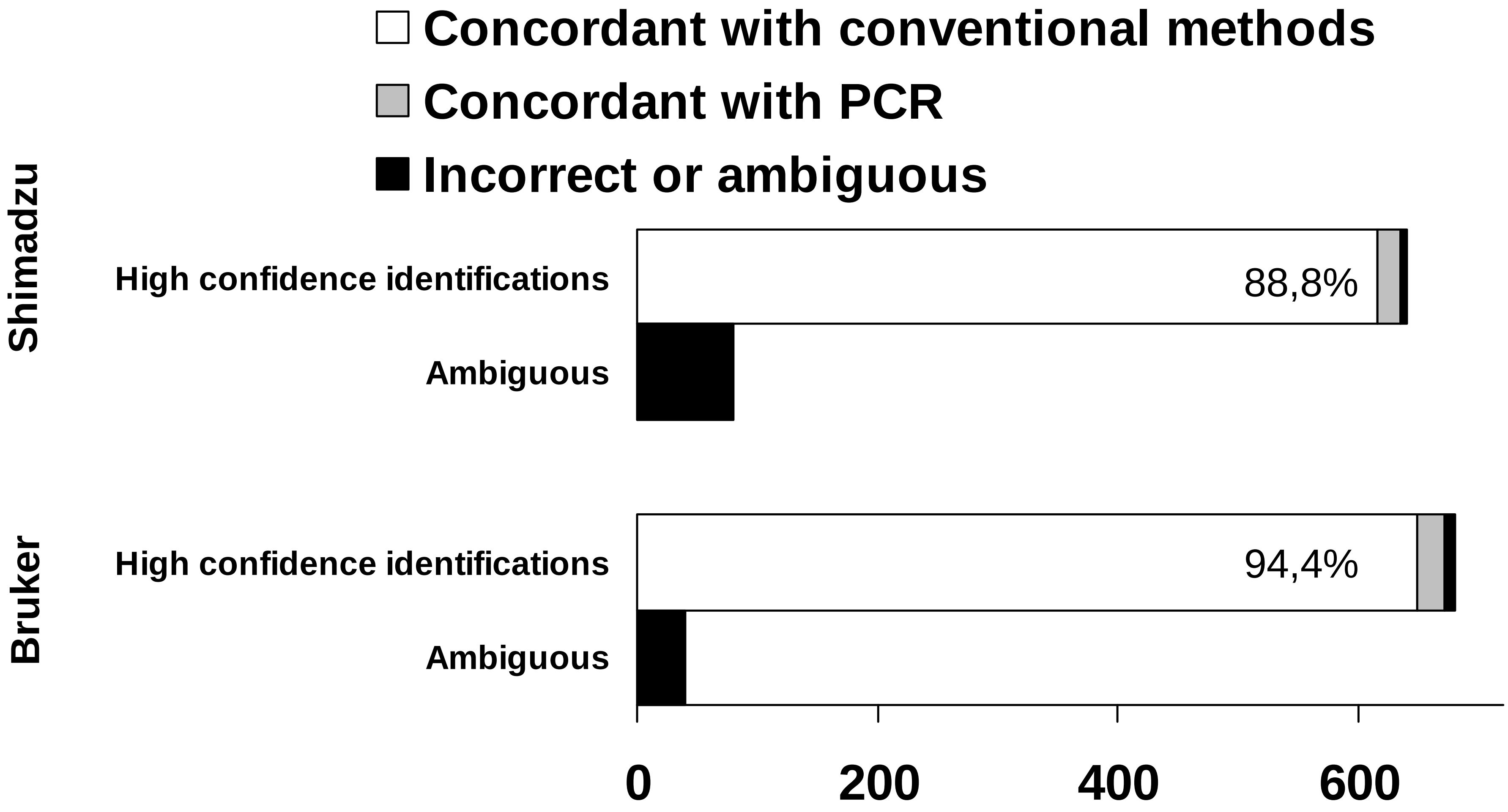
3- low score value <1.7 for B and <70 for S
=> isolates rated as ambiguous, thus not reported

# Study design (2)

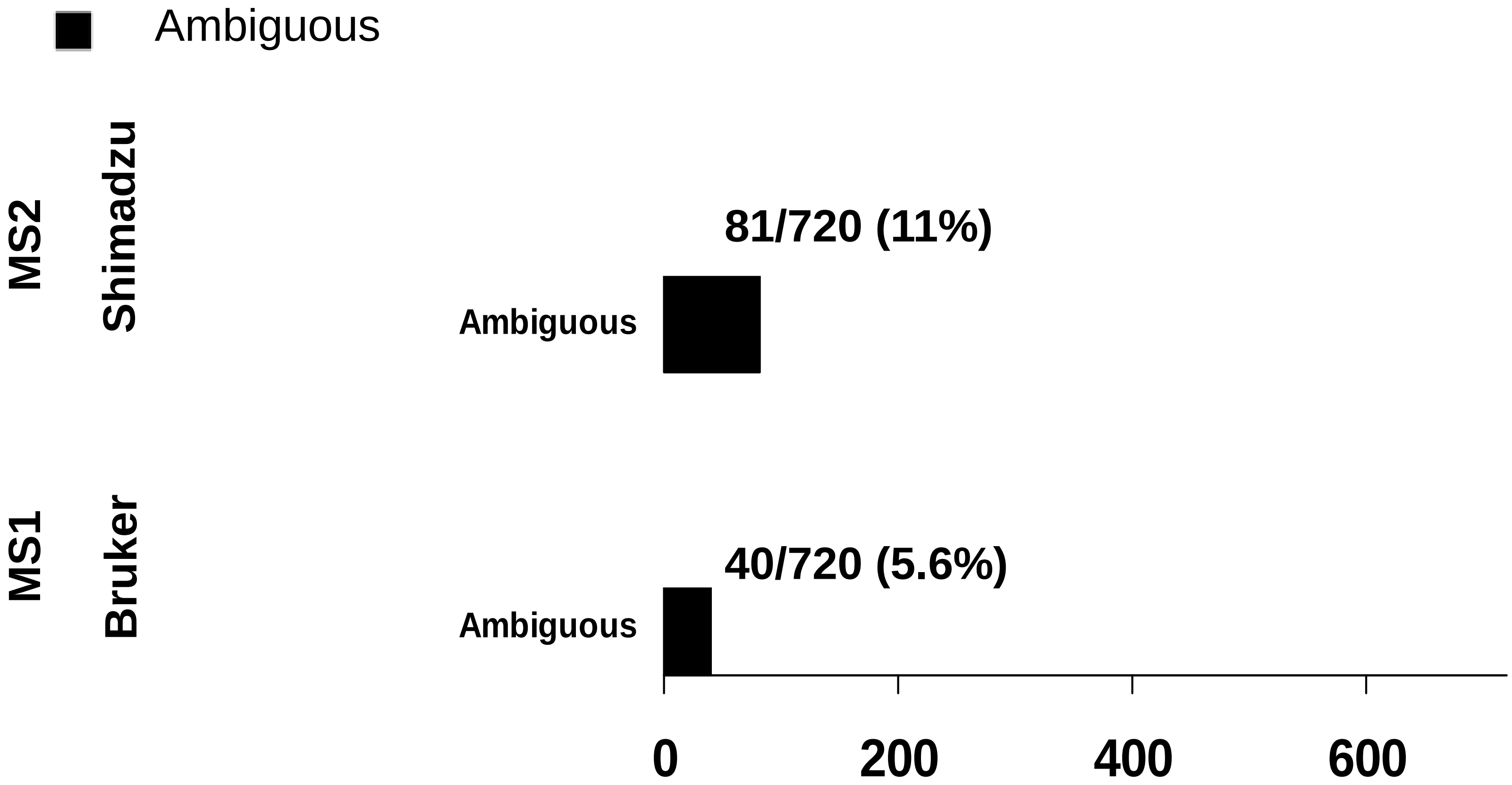
- Whenever the quality of MS scores revealed ambiguous, a second experiment was performed on a fresh bacterial culture.
  - Additional identification was performed on 54/720 (7.5%) and 39/720 (5.4 %) isolates, on MS 1 and 2

- No attempt was made to employ the specific extraction procedures recommended by the manufacturers, e.g. for streptococcal speciation.

# Accuracy of MALDI-TOF MS identifications of 720 clinical isolates



# Accuracy of MALDI-TOF MS id of 720 clinical isolates



# Analysis of all incorrect cases

| Cases | Phenotypic | 16S rDNA | MALDI-MS | System |
|---|---|---|---|---|
| 1 | No ID | Achromobacter xylosoxidans | A. denitrificans | Bruker |
| 1 | S. epid | No ID | S. capitis | Bruker |
| 1 | S. mitis | Streptococcus sp | S. pneumoniae | Bruker |
| 2 | No ID | Streptococcus bovis | S. lutiensis | Bruker |
| 1 | No ID | Clostridium boltei | C. casei | Bruker |
| | | | | |
| 1 | S. epid | Staphylococcus sp | S. capitis/caprae | Shimadzu |
| 1 | S. mitis | Streptococcus sp | S. pneumoniae | Shimadzu |
| 1 | S. mitis | Streptococcus sp | S. oralis | Shimadzu |

# Analysis of all incorrect cases

| Cases | Phenotypic | 16S rDNA | MALDI-MS | System |
|---|---|---|---|---|
| 1 | No ID | Achromobacter xylosoxidans | A. denitrificans | Bruker |
| 1 | S. epid | No ID | S. ca | Bruker |
| 1 | S. mitis | Streptococcus sp | | Bruker |
| 2 | No ID | Streptococcus bo | | ker |
| 1 | No ID | Clostridium boltei | | ruker |
| | | | | |
| 1 | S. epid | Staphylococcus sp | | Shimadzu |
| 1 | S. mitis | Streptococcus sp | S. pneumoniae | Shimadzu |
| 1 | S. mitis | Streptococcus sp | S. oralis | Shimadzu |

Establish rules considering these cases

# Results: based on species

- Outstanding identification of Enterobacteriaceae, *Staphylococcus aureus* and *Pseudomonas aeruginosa*.

- Lower yields (but no false-positive identification) when analyzing enterococci (75-56%) or streptococci (37-26%) to the species level.

- Latter results could certainly be improved by using dedicated matrix.

# Results: four categories

1- correct identification (same as biochemical tests) with a high score value ≥2.0 for Bruker and ≥90 for Shimadzu;

=> isolates rated as identified to the species level

2- correct identification (same as biochemical tests) with an intermediate score value ≥1.7 for B and ≥70 for S;

=> isolates rated as identified to the genus level

3- MS results inferior to the biochemical identification

4- MS results superior to the biochemical identification

# Results: four categories

1- correct identification - identified to the species level:

620/720 (86%) and 559/720 isolates (78%)

2- correct identification - identified to the genus level:

46/720 (6%) and 95/720 isolates (13%)

3- MS results inferior to the biochemical identification:

18/49 (37%) and 28/49 (57%), **but none wrong!**

4- MS results superior to the biochemical identification:

15/49 (30%) and 11/49 (23%) to the species level

16/49 (33%) and 10/49 (20%) to the genus level

# Cost and timeliness estimates of conventional identification

| | Cost per isolate ($US) | | Turnaround time (hr) | |
|---|---|---|---|---|
| | **Avg.** | **Total** | **Avg.** | **Total** |
| ***E. coli* (n=216)** | $0.20 | $43 | 1 | 216 |
| ***S. aureus* (n=55)** | $1.50 | $83 | 1 | 55 |
| **Other (n=449)** | $10.00 | $4,490 | 24 | 10,776 |
| **All isolates (n=720)** | **Total cost:** | **$4,616** | **Average time: 15 hrs** | |

# Cost and timeliness estimates of Bruker-based identification

| | Cost per isolate ($US) | | Turnaround time (hr) | |
|---|---|---|---|---|
| | **Avg.** | **Total** | **Avg.** | **Total** |
| **High confidence MALDI-TOF MS (n=636)** | $0.50 | $318 | 0.08 | 53 |
| **Lower-confidence and Ambiguous MALDI-TOF MS (n=84)** | $10.50 | $882 | 24 | 2,016 |
| | **Total cost:** | **$1,200** | **Average time: 3 hrs** | |

# Cost and timeliness estimates of identification methods

| | Cost per isolate ($US)<br>Total | Turnaround time (hr)<br>Average |
|---|---|---|
| **Conventional ID (n=720)** | $4,616 | 15 |
| **MALDI-TOF MS (n=720)** | $1,200 | 3 |

# Cost and timeliness estimates of identification methods

| | **Cost per isolate ($US)** | **Turnaround time (hr)** |
|---|---|---|
| | **Total** | **Average** |
| **Conventional ID (n=720)** | $4,616 | 15 |
| **MALDI-TOF MS (n=720)** | | |

MALDI saves time and cost

# Evaluation of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for the rapid identification of beta-hemolytic *streptococci*

- ❑ MALDI-TOF/MS analysis of 386 sub-cultured beta-hemolytic *streptococci* isolates resulted in high-confidence identifications to the species level for all 386 isolates, with 100% concordance with the Lancefield group classification as determined by the latex agglutination kit.

- ❑ The Vitek2 gave high-confidence identification to the species level for 269/306 isolates of group B streptococci (88%), 48/52 isolates of group A streptococci (92%) and 11/28 isolates of group C and G streptococci (39%).

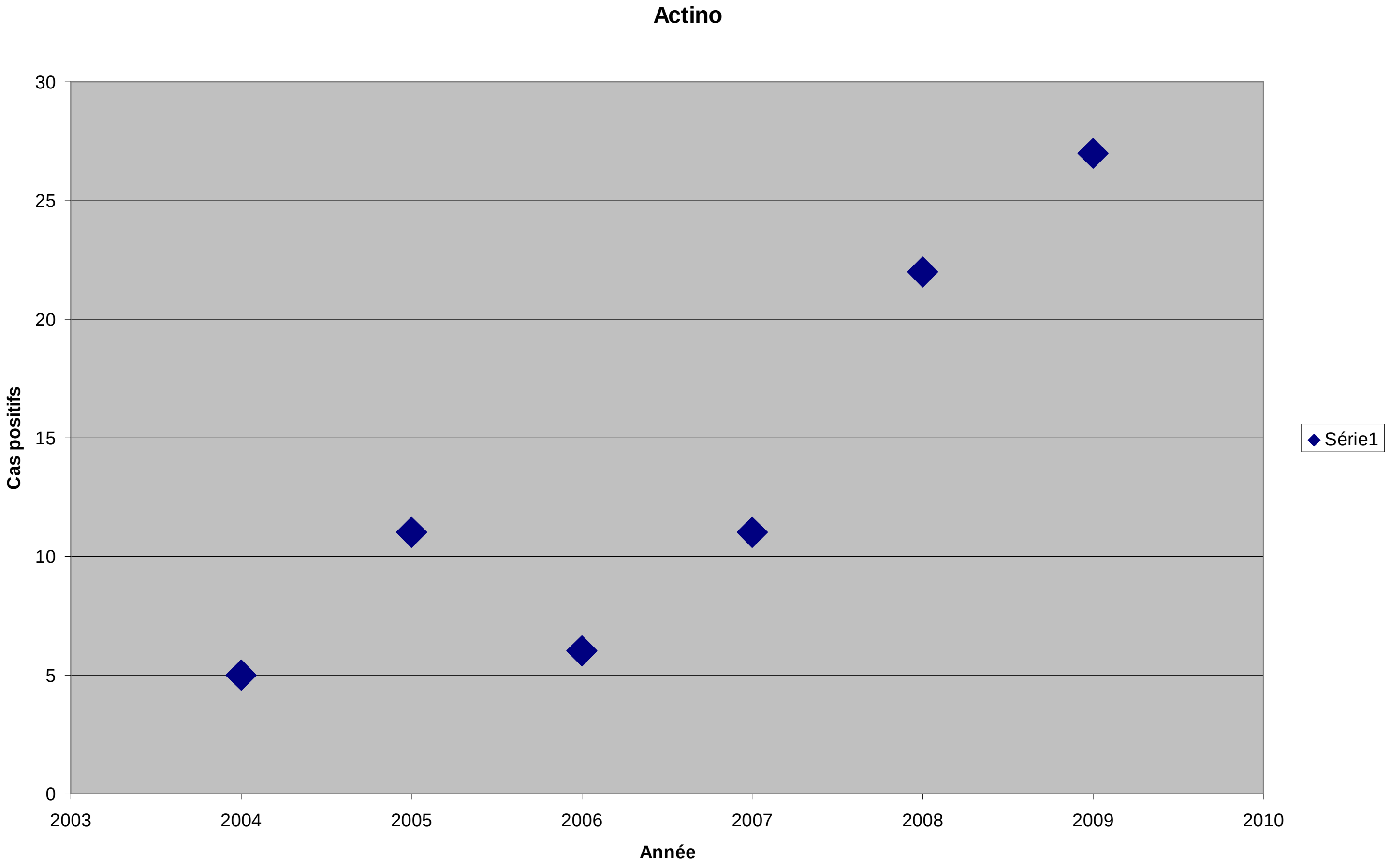
- ❑ Fourteen isolates were not identified by Vitek2, 12 were incorrectly identified and 32 isolates were identified ambiguously (%ID=50) as *Streptococcus agalactiae* or *Streptococcus dysgalactiae.*

- ❑ Whenever high-confidence MS identifications disagreed with Vitek2 results, 16S sequencing resolved identifications in favor of the MS system.

- ❑ The 12 incorrect Vitek2 results (%ID>90) were as follows: six isolates identified as *Gemella haemolysans*, two isolates identified as *Kocuria rosea*, one isolate identified as *Lactobacillus gravieae*, one isolate identified as *Streptococcus pluranimalium* and one isolate identified as *Kocuria varians*.

Cherkaoui A *et al*, 2011

# *Actinomyces* spp. Identifiés au LCB: l'effet « MALDI-TOF/MS »…



# Implementation: a few steps

| **Organismes** | **Gram/autres** | **Tests** |
|---|---|---|
| *S. aureus* | Cg+ amas | Catalase, Pastorex, DNase, Coagulase<br>mec A et femA, |
| *S. pneumoniae* | Cg+ diplocuqes | Optochine , Agglut. Pneumokit |
| *S. pyogenes*<br>*S. agalactiae*<br>*S. dysgalactiae* | Cg+ chaînes | Bacitracine , Bactrim<br>Slidex Streptokit |
| Enterococcus spp. | Cg+ chaînes | Bile esculine, NaCl 6.5%, Tellurite<br>Galerie AP / Vitek2 |
| *H. influenzae* | Petits bg- | Porphyrine , Galerie AP |
| *M. catarrhalis* | Coccobacilles Gram - | Oxidase,Tributyrine |
| Entérobactéries | Fermentation du Lactose, Oxidase | Vitek2 / Galerie AP |
| Germes non fermentatifs | Fermentation du Lactose, Oxidase | Vitek2 / Galerie AP |
| *B. cepacia* | Fermentation du Lactose | Oxidase variable<br>Vitek2 / Galerie AP |

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| *S. pyogenes*<br>*S. agalactiae*<br>*S. dysgalactiae* | Cg+ chaînes | Bacit<br>Bactr<br>Slide |
| Enterococcus spp. | Cg+ chaînes | Bile e Cl<br>6.5%<br>Galer 2 |
| *H. influenzae* | Petits bg- | Porp rie<br>AP |
| *M. catarrhalis* | Coccobacilles Gram - | Oxida ine |
| Entérobactéries | Fermentation du Lactose, Oxidase | Vitek AP |
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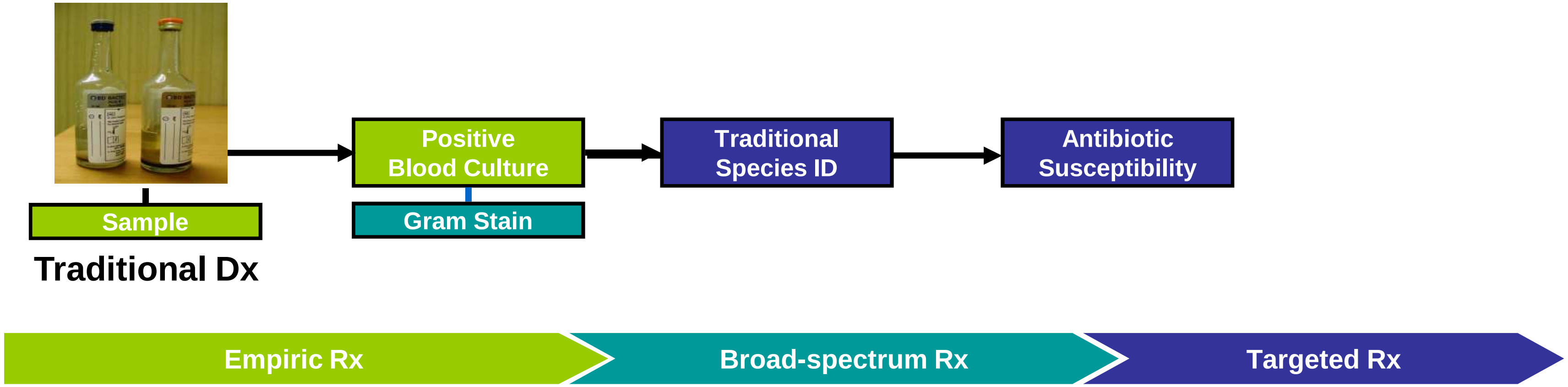
MALDI/MS

# New microbiology workflows



**Traditional Dx**

Sample

Positive Blood Culture

Gram Stain

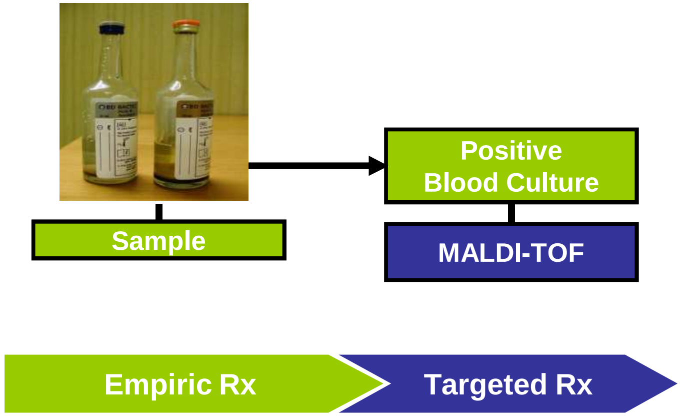
Traditional Species ID

Antibiotic Susceptibility

Empiric Rx

Broad-spectrum Rx

Targeted Rx



Sample

Positive Blood Culture

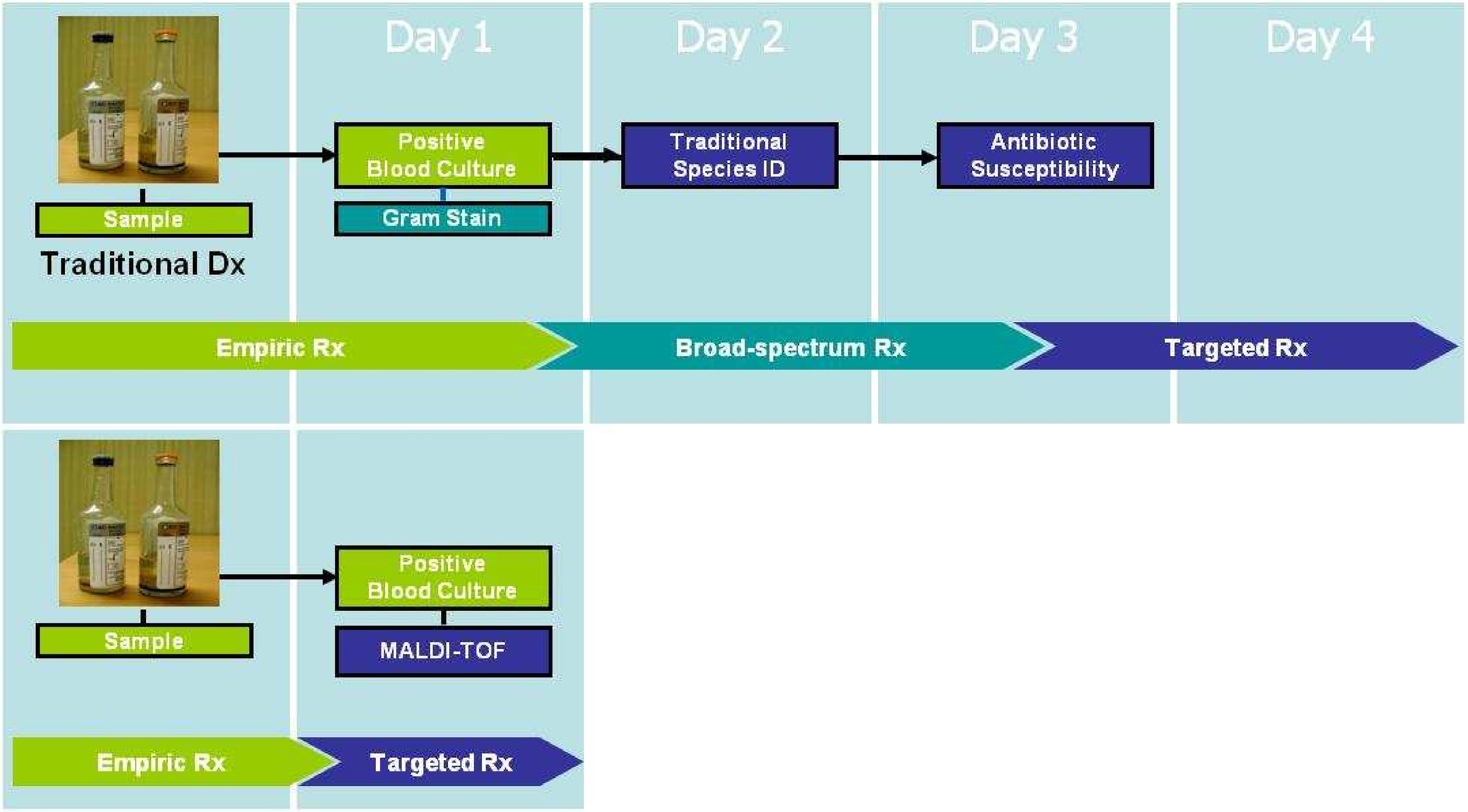
MALDI-TOF

Empiric Rx

Targeted Rx

***Graph adapted from AdvanDx***

# New microbiology workflows



***Graph adapted from AdvanDx***

# Conclusions

- MS fournit une ID rapide (8h de moins en moyenne), moins cher (environ $5 US/échantillon) et au moins aussi bons résultats que les approches phénotypique classiques

- L'absence de fausses ID est très rassurant mais une validation minutieuse des nouveaux flux de travail est obligatoire

- Intégration de MS dans le flux de routine et le contrôle de la mise à niveau de la base de données sont les défis actuels

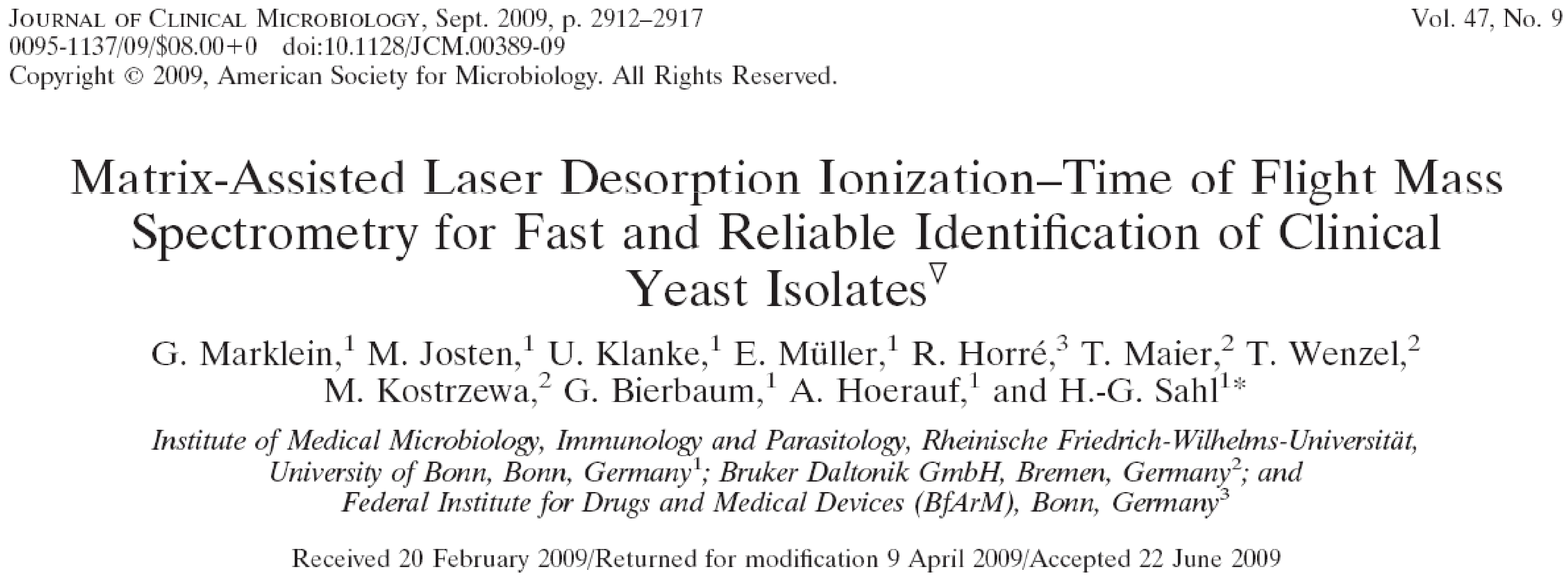
- Des schémas plus élaborés (d'autres matrices, typage de souches par homologie de la signature, etc) devraient être explorées


Var-matin

# MS IN THE FUTURE?

- **ID of an increasing number of pathogens (improvement of database)**
- **ID of yeasts**
- **ID of virulence factors (PVL)**
- **ID of resistance (β-lactamase? MRSA?)**
- **ID of anaerobes (Actino)**

# MALDI-TOF MS FOR YEASTS?



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0095-1137/09/$08.00+0 doi:10.1128/JCM.00389-09

## Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry for Fast and Reliable Identification of Clinical Yeast Isolates▽

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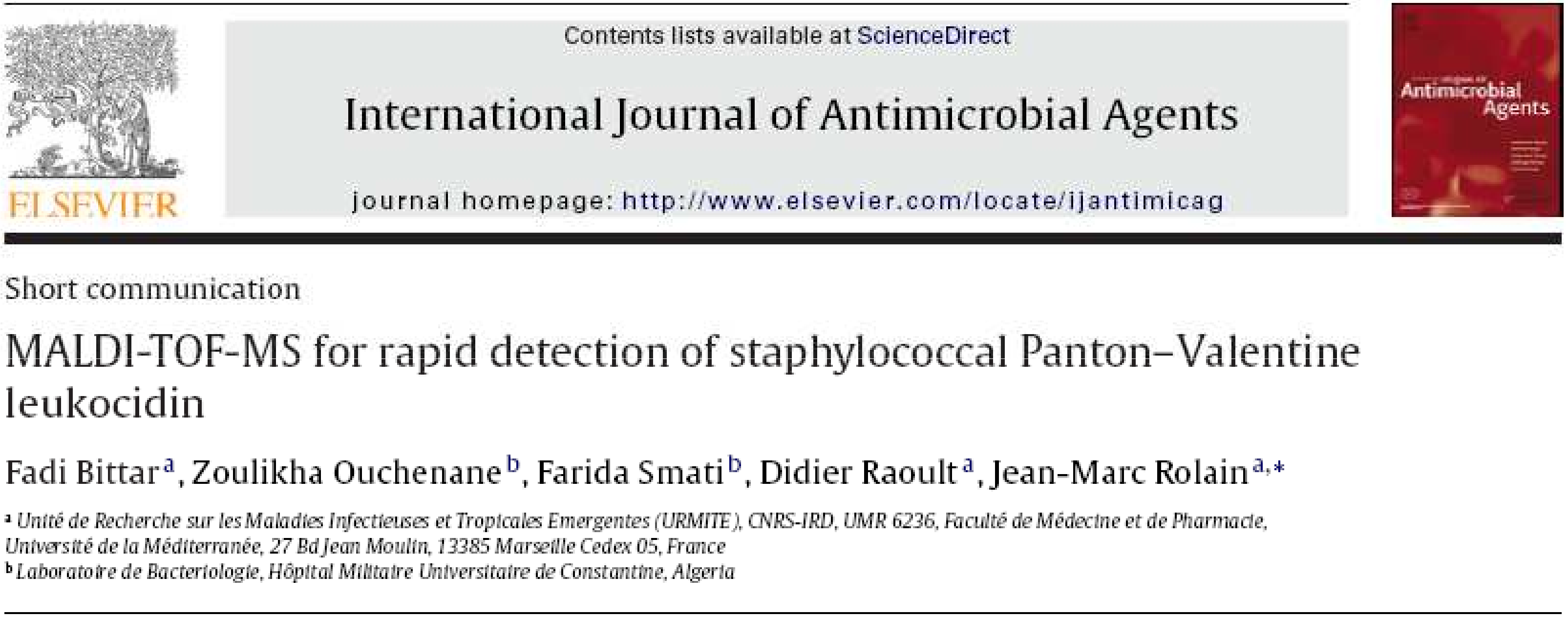
# MALDI TOF MS FOR VIRULENCE



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Short communication

## MALDI-TOF-MS for rapid detection of staphylococcal Panton–Valentine leukocidin

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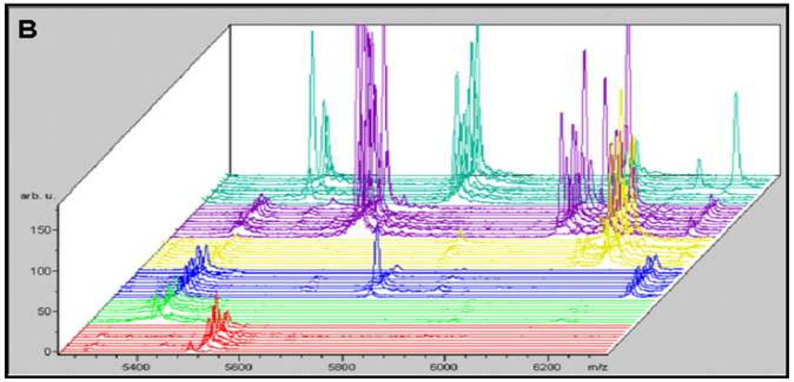


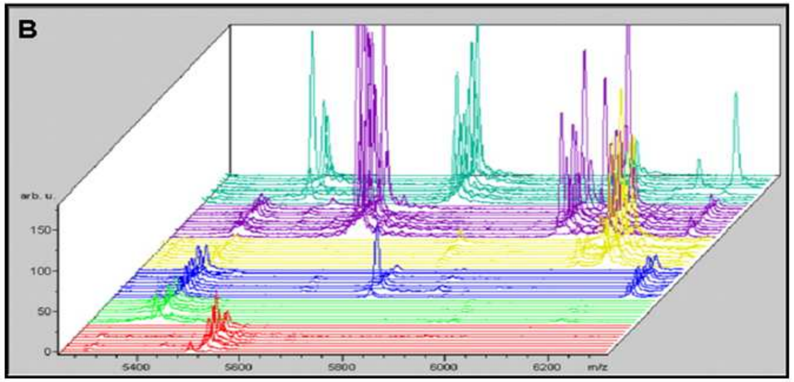
# MALDI-TOF MS FOR AB RESISTANCE?

Anal Bioanal Chem (2007) 389:1633–1638
DOI 10.1007/s00216-007-1558-7

TECHNICAL NOTE

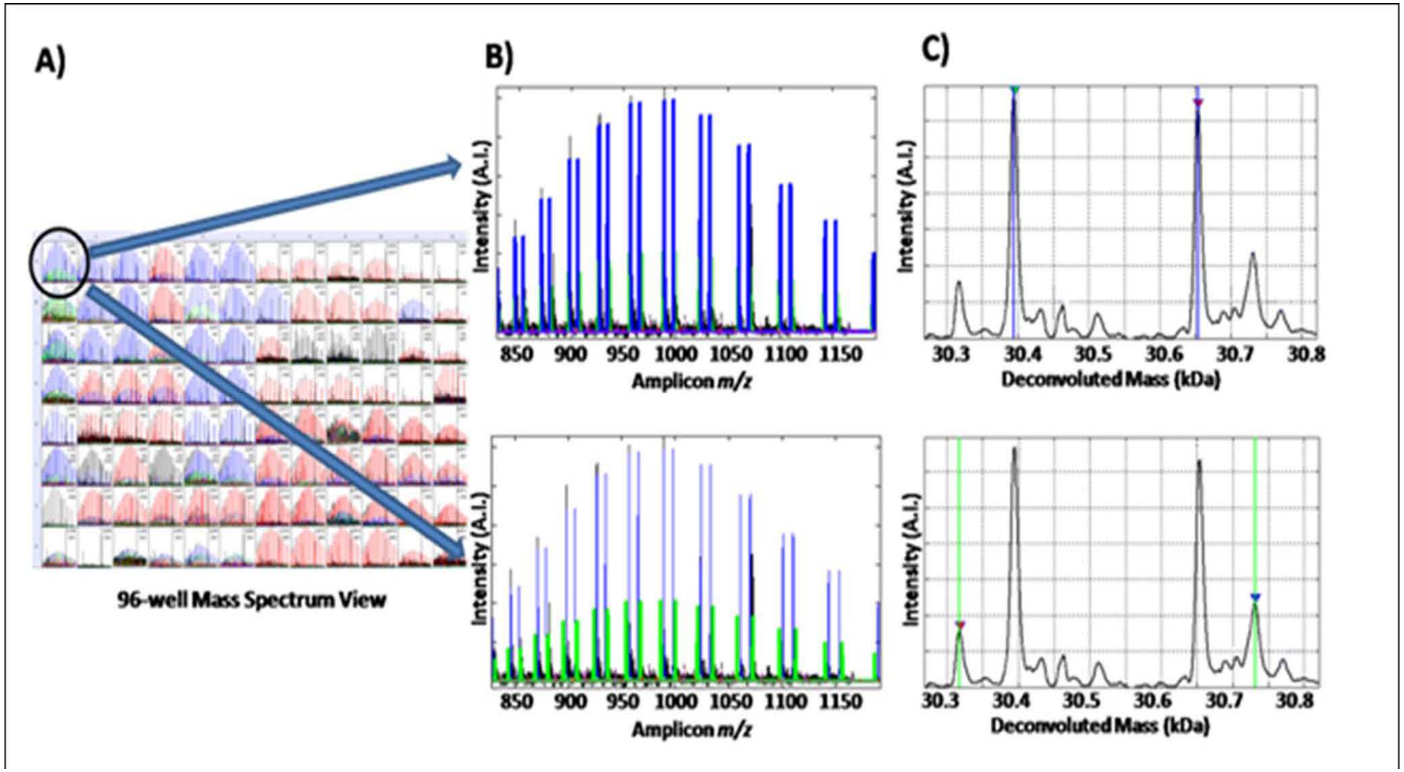
## Discrimination between wild-type and ampicillin-resistant *Escherichia coli* by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry

**Johanna E. Camara • Faith A. Hays**



# PCR/ESI-MS

## (Electrospray Ionization Mass Spectrometry)



Erin J. Kaleta *et al*, JCM 2010

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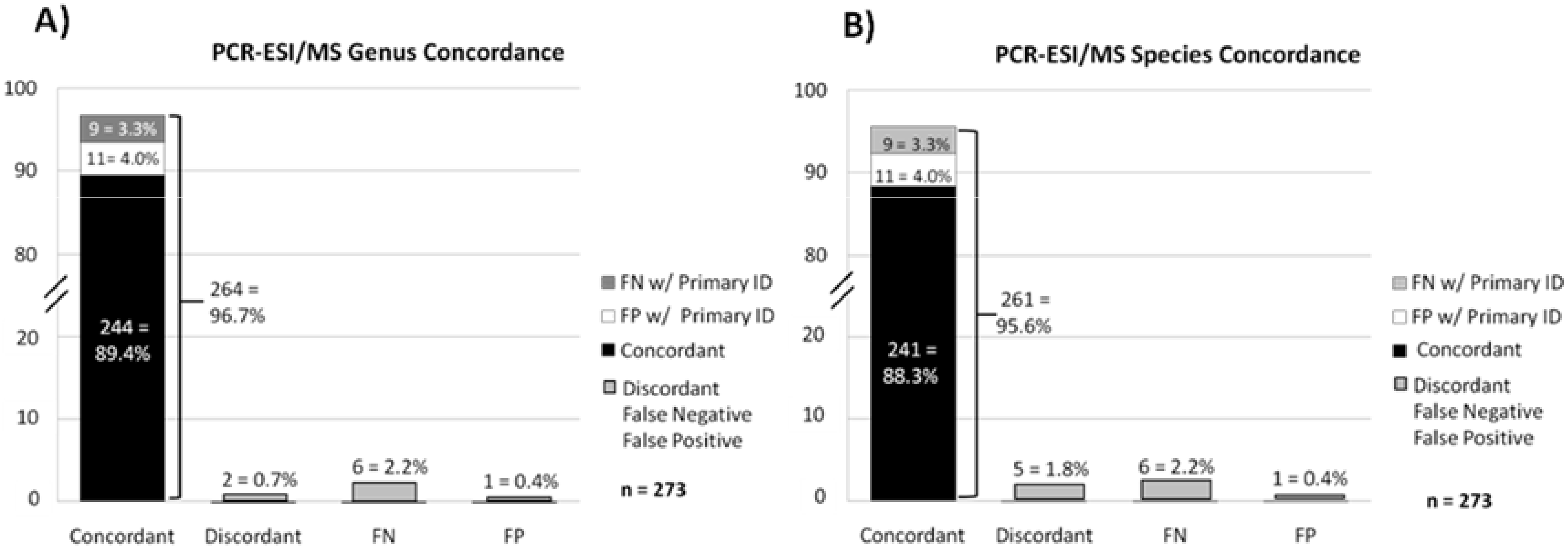

Erin J. Kaleta *et al*, 2011

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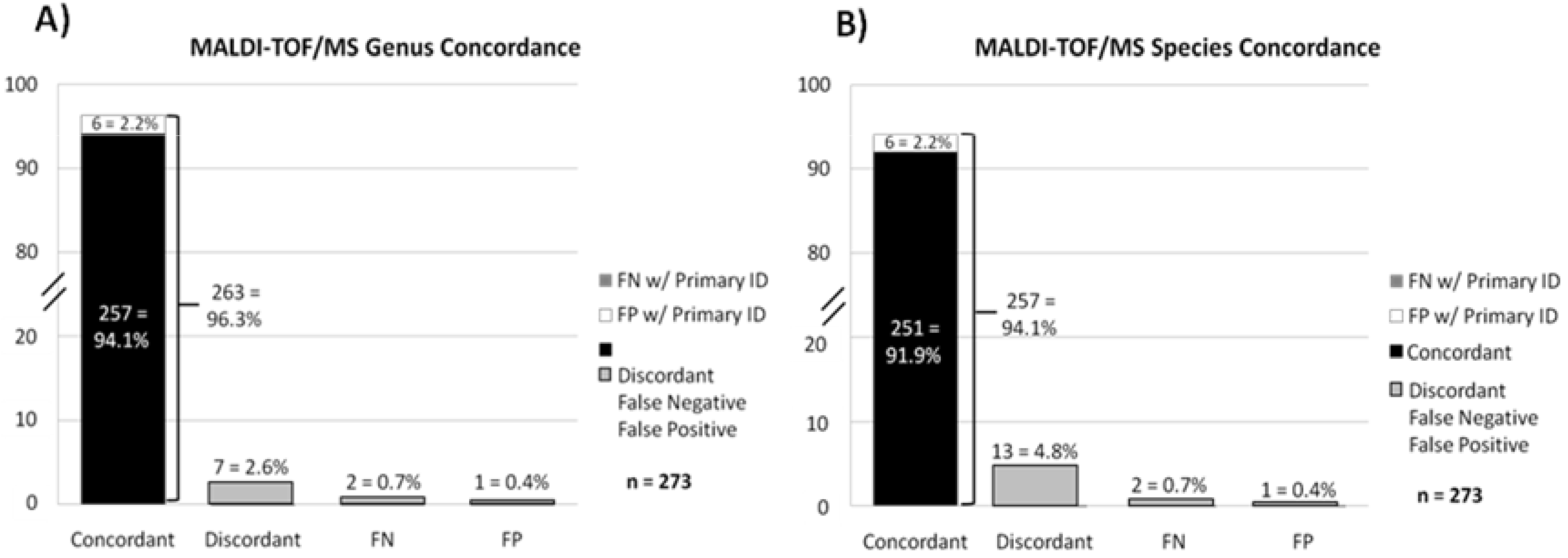

Erin J. Kaleta *et al*, 2011

Merci