



ÉCOLE POLYTECHNIQUE
FÉDÉRALE DE LAUSANNE

Méthodes et futures applications du WGS pour les bacilles de la lèpre

Charlotte Avanzi

Unité du Prof. S. Cole, EPFL

“RICAI 2017”

18/12/2017

LA LÈPRE

- **Maladie de Hansen**

- *M. leprae* (1893)
- *M. lepromatosis* (2008)

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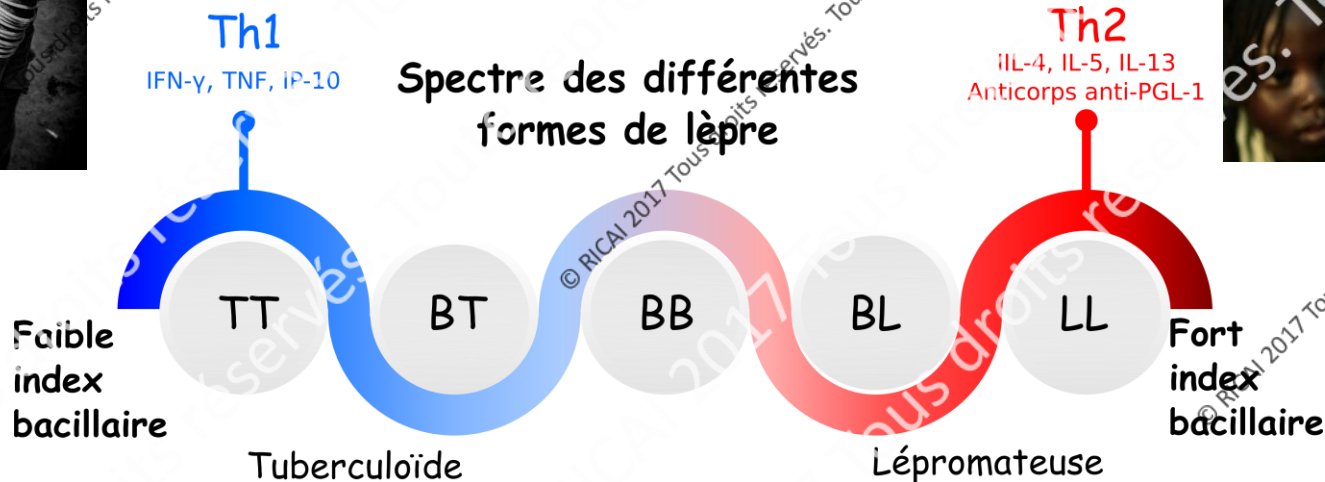
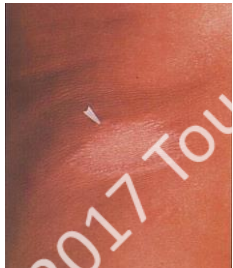
LA LÈPRE

- **Maladie de Hansen**

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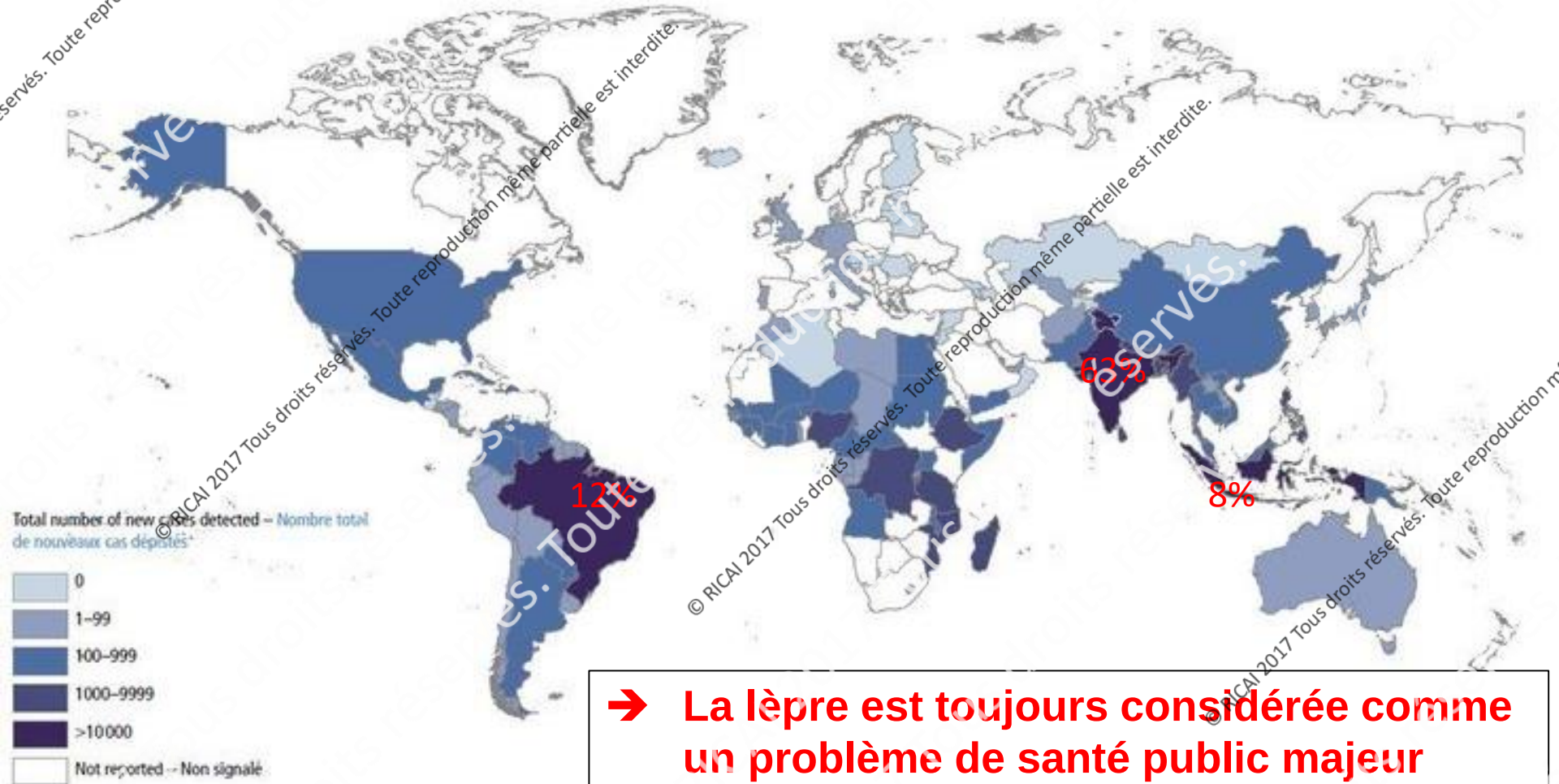
- **Multiforme, progressive et invalidante**

- Incubation de quelques mois à 20 ans



LA LÈPRE N'EST PAS ÉRADIQUÉE

200,000 nouveaux cas/an
≈ 8% d'enfants (<15 ans)



→ La lèpre est toujours considérée comme un problème de santé public majeur dans plus de 14 pays

CARACTÉRISTIQUES DES BACILLES

- Non cultivable *in vitro*
- Modèles *in vivo* (*M. leprae*)



- Temps de division: 12 jours
- Mode de transmission: inconnu

LA POLYCHIMIOTHERAPIE (PCT)

Paucibacillaire
(<5 lésions)
6 mois

DAPSONE

Cible : FolP1

Posologie: 100mg (j)

RIFAMPICINE

Cible : RpoB

Posologie: 600mg (m)

LA POLYCHIMIOThERAPIE (PCT)

Paucibacillaire
(<5 lésions)
6 mois

DAPSONE
Cible : FolP1
Posologie: 100mg (j)

RIFAMPICINE
Cible : RpoB
Posologie: 600mg (m)

CLOFAZIMINE
Cible: inconnue
Posologie: 50mg (j);
300mg (m)

Multibacillaire
(>5 lésions)
12 mois

LA POLYCHIMIOThERAPIE (PCT)

Paucibacillaire
(<5 lésions)
6 mois

DAPSONE

Cible : FolP1
Posologie: 100mg (j)

RIFAMPICINE

Cible : RpoB
Posologie: 600mg (m)

CLOFAZIMINE

Cible: inconnue
Posologie: 50mg (j);
300mg (m)

Multibacillaire
(>5 lésions)
12 mois

DEUXIÈME LIGNE

OFLOXACINE

Cible: GyrA/GyrB
Posologie: 400mg (j)

MINOCYCLINE

Cible: inconnue
Posologie: 100mg (j)

CLARITHROMYCINE

Cible: inconnue
Posologie: 500mg (j)

Identification of Primary Drug Resistance to Rifampin in *Mycobacterium leprae* Strains from Leprosy Patients in Amazonas State, Brazil

Matilde del Carmen Contreras Mejia,^a Maísa Porto Dos Santos,^{a,c} George Allan Villarouco da Silva,^{a,b} Isabella da Motta Passo Felipe Gomes Naveca,^b Maria da Graça Souza Cunha,^a Milton Ozório Moraes,^c Lucia de Paula^{a,g}

Clinical Infectious Diseases

BRIEF REPORT

Transmission of Drug-Resistant Leprosy in Guinea-Conakry Detected Using Molecular Epidemiological Approaches

Charlotte Avanzi,¹ Philippe Bussé,¹ Andrej Benjak,¹ Chloé Loiseau,¹ Abdoulaye Fomba,² Glodia Dombia,² Idrissa Camara,³ André Lamou,³ Gouressy Sock,³ Tiguidanké Drame,³ Mamadou Kodio,² Fatoumata Sakho,³ Samba O. Sow,² Stewart T. Cole,¹ and Roch Christian Johnson⁴

INTERNATIONAL JOURNAL OF LEPROSY

CASE REPORTS

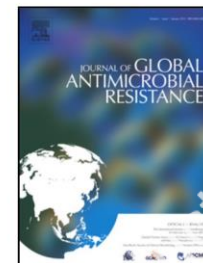
A Second Case of Multidrug-resistant *Mycobacterium leprae* Isolated from a Japanese Patient with Relapsed Lepromatous Leprosy¹

Masanori Matsuoka, Yoshiko Kashiwabara, Zhang Liangfen, Masamichi Goto, and Shin-ichi Kitajima²

Accepted Manuscript

Title: Molecular detection of multi drug resistant *Mycobacterium leprae* from Indian leprosy patients

Authors: Mallika Lavania, Itu Singh, Ravindra P Turankar, Madhvi Ahuja, Vinay Pathak, Utpal Sengupta, Loretta Das, Archana Kumar, Joydeepa Darlong, Rajeev Nathan, Asha Maseey



Primary Multidrug-Resistant Leprosy, United States



Drug and Multidrug Resistance among *Mycobacterium leprae* Isolates from Brazilian Relapsed Leprosy Patients

Adalgiza da Silva Rocha,^a Maria das Graças Cunha,^b Lucia Martins Diniz,^c Claudio Salgado,^d Maria Araújo P. Aires,^e José Augusto Nery,^f Eugénia Novick Gallo,^g Alice Miranda,^h Monica M. F. Magnanini,^g Masanori Matsuoka,^h Euzenir Nunes Sarno,ⁱ Philip Noel Suffys,^g and Maria Leide W. de Oliveira^g

ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, Dec. 2001, p. 3635–3639
0066-8040/01/\$04.00+0 DOI: 10.1128/AAC.45.12.3635-3639.2001
Copyright © 2001, American Society for Microbiology. All Rights Reserved.

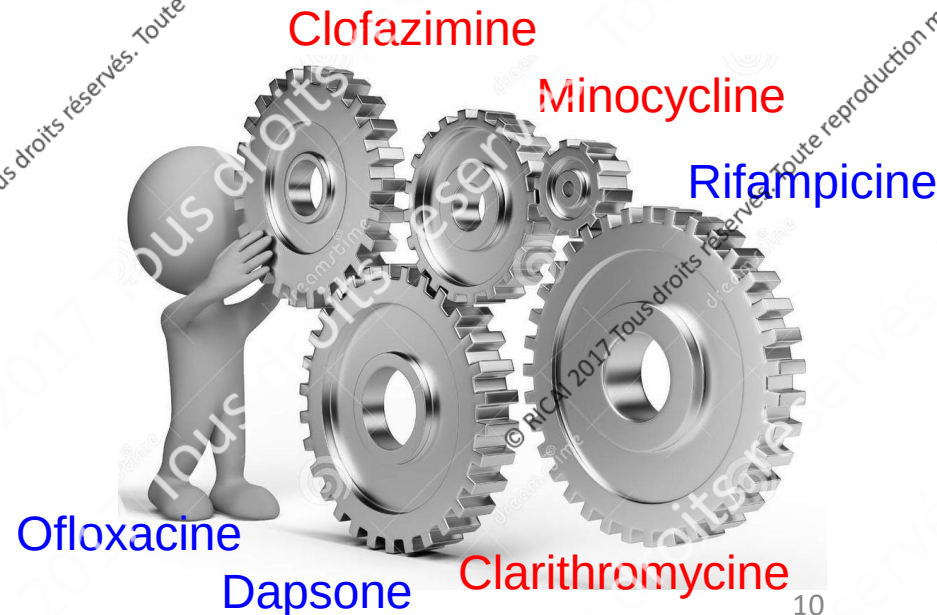
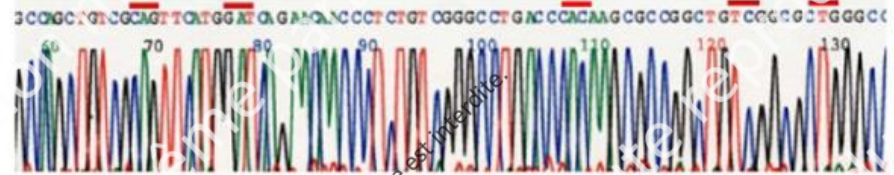
Multidrug Resistant *Mycobacterium leprae* from Patients with Leprosy

SHINJI MAEDA,^{1,2} MASANORI MATSUOKA,^{1*} NOBORU NAKATA,¹ MASANORI KAI,¹ YUMI MAEDA,¹ KEN HASHIMOTO,¹ HIROAKI KIMURA,¹ KAZUO KOBAYASHI,² AND YOSHIKO KASHIWABARA¹

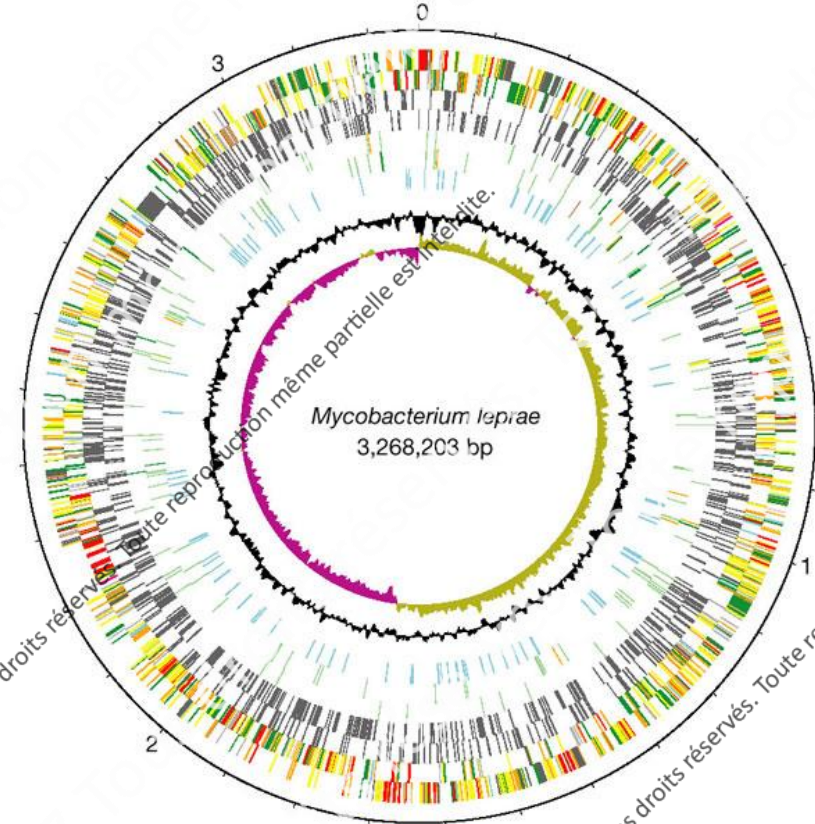
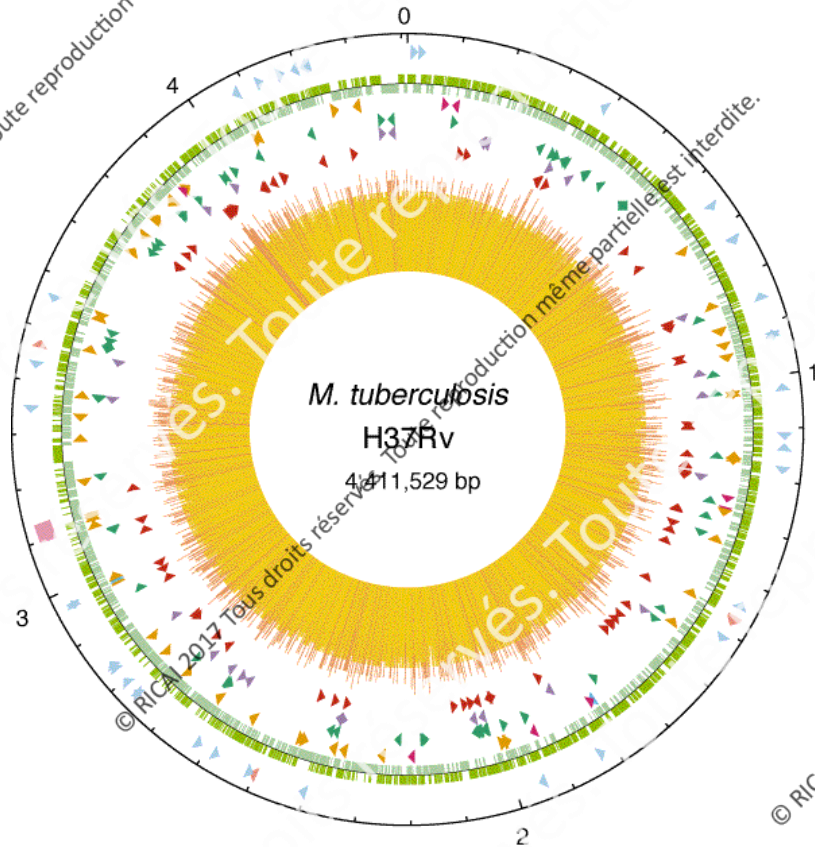
ENJEUX DE LA RÉSISTANCE

- Détection des résistances
 - *rpoB*
 - *folP1*
 - *gyrA*
- Mécanismes de résistance

Rifampicin (DRDR)



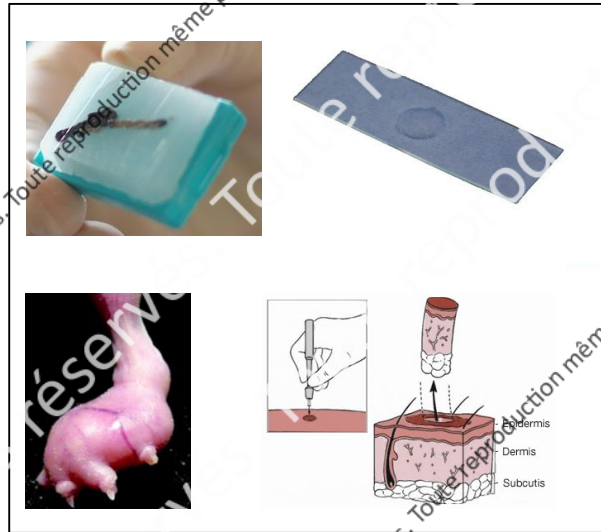
SOLUTION: LE WGS?



>22,000 génomes

~ 20 génomes

M. LEPRAE EST DIFFICILE À SÉQUENCER!



1- DNA extraction

3- DNA lib. preparation

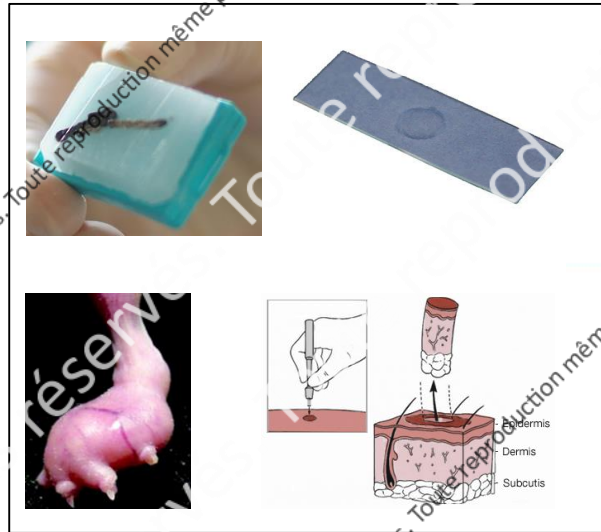
2- DNA shearing

4- DNA lib. sequencing

5- DNA sequence analysis

DNA Reads

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3- DNA lib. preparation

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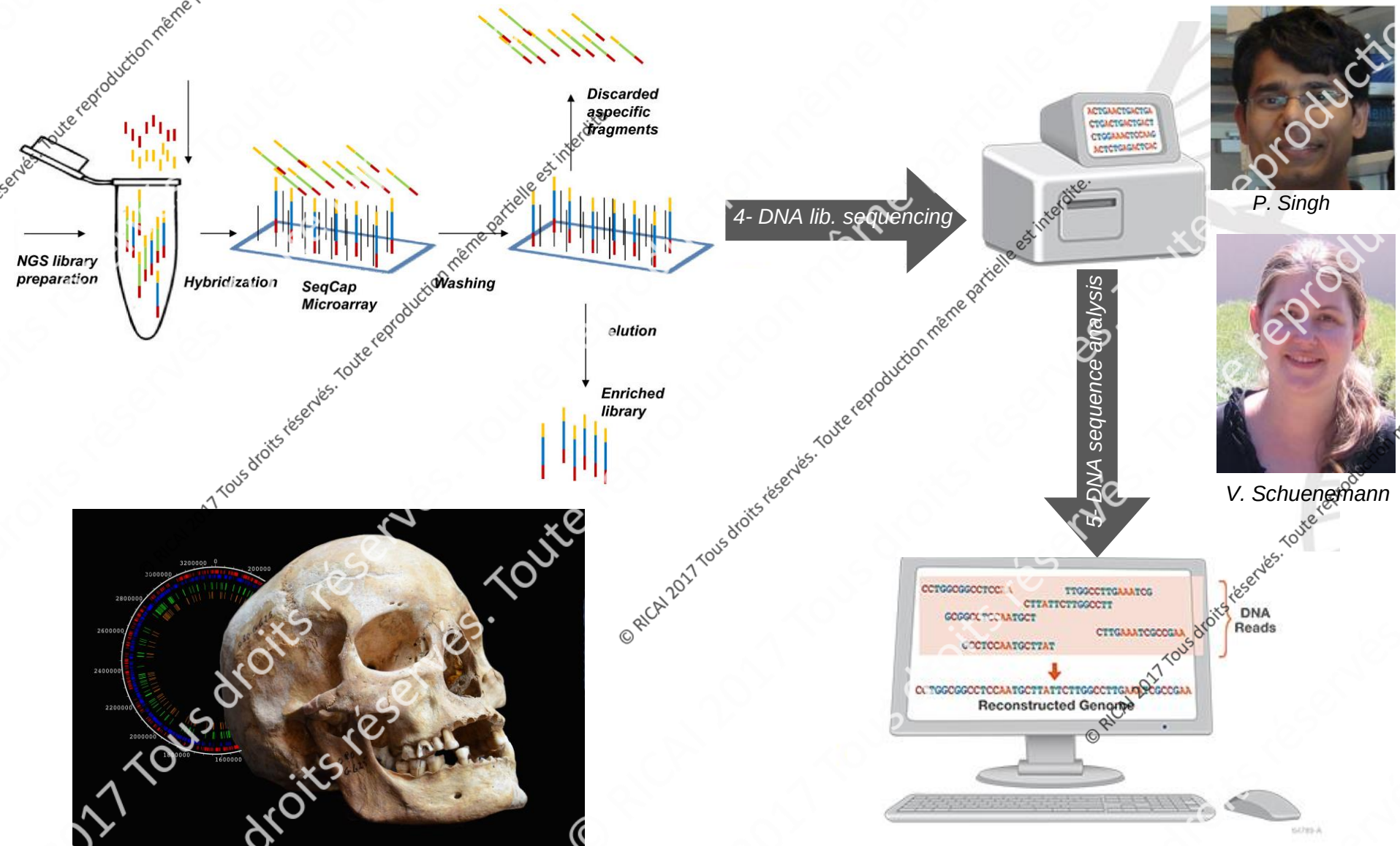
Fragmentation: Covaris
Kit Kapa Hyper prep
HiSeq (SE, 100, 200mo)

% d'alignement
- Humain: 99%
- *M. leprae*: 1%

DNA Reads

ADN de l'hôte

OUTILS N°1: ENRICHISSEMENT DES LIBRAIRIES!

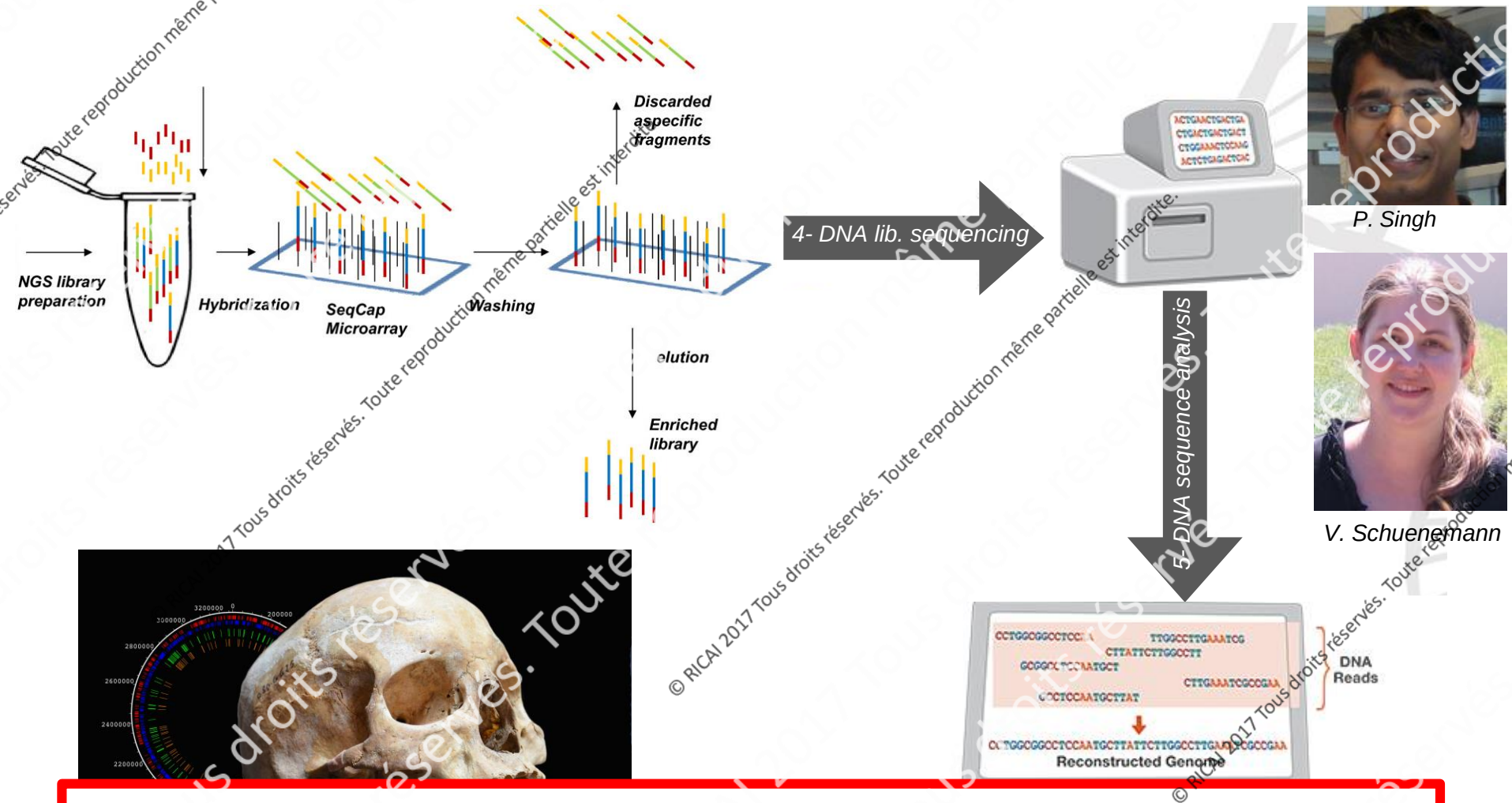


P. Singh



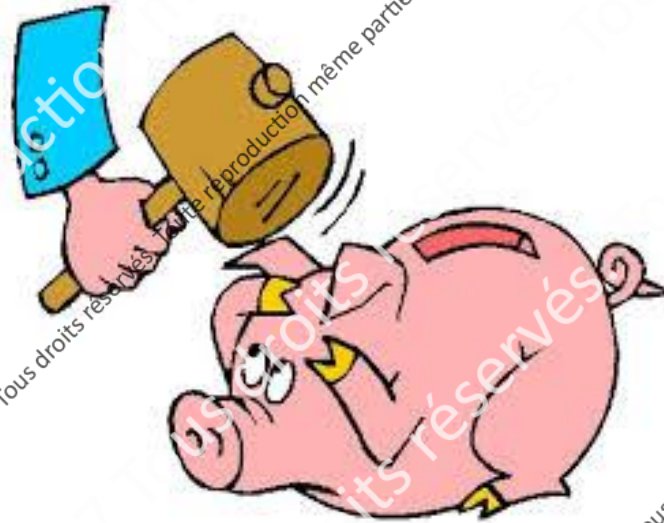
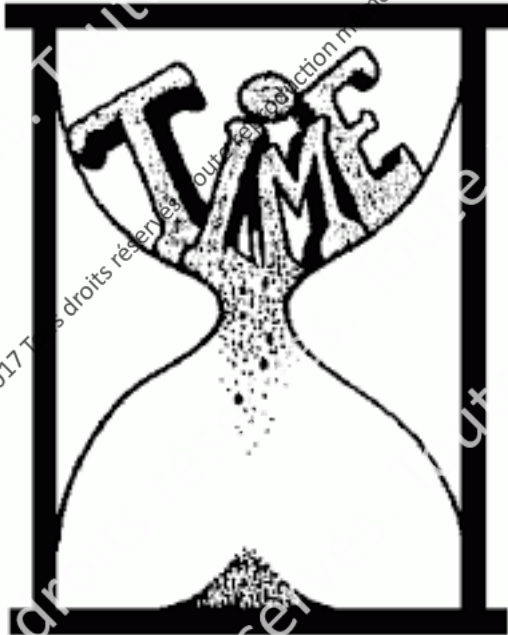
V. Schuenemann

OUTILS N°1: ENRICHISSEMENT DES LIBRAIRIES!



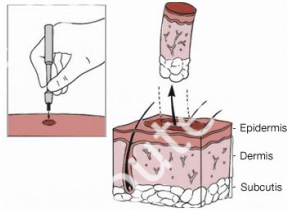
Echantillons avec peu de bacilles (ex: ADN ancien)
Multiplexage de 10 échantillons / ligne

OUTILS N°1: INCONVENIENTS!



OUTILS N°2: EVITONS LA CAPTURE !

... Sur des biopsies de peau



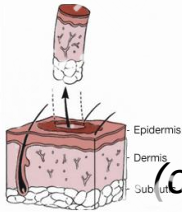
1- DNA extraction



ADN humain

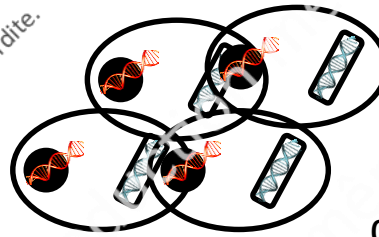
OUTILS N°2: DÉPLÉTION DE L'ADN DE L'HÔTE

... Sur des biopsies de peau



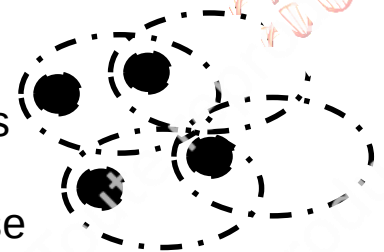
Digestion du tissu

(collagenase, trypsine, prot. K)



Cellules de l'hôte

Lyse des cellules
de l'hôte et DNase



QIAamp DNA Microbiome Kit



Shotgun sequencing
(ML Pipeline)

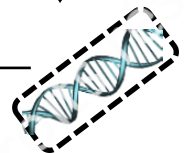
M. leprae %?

PCR & Lib. prep

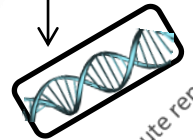


Purification de l'ADN

sur colonne

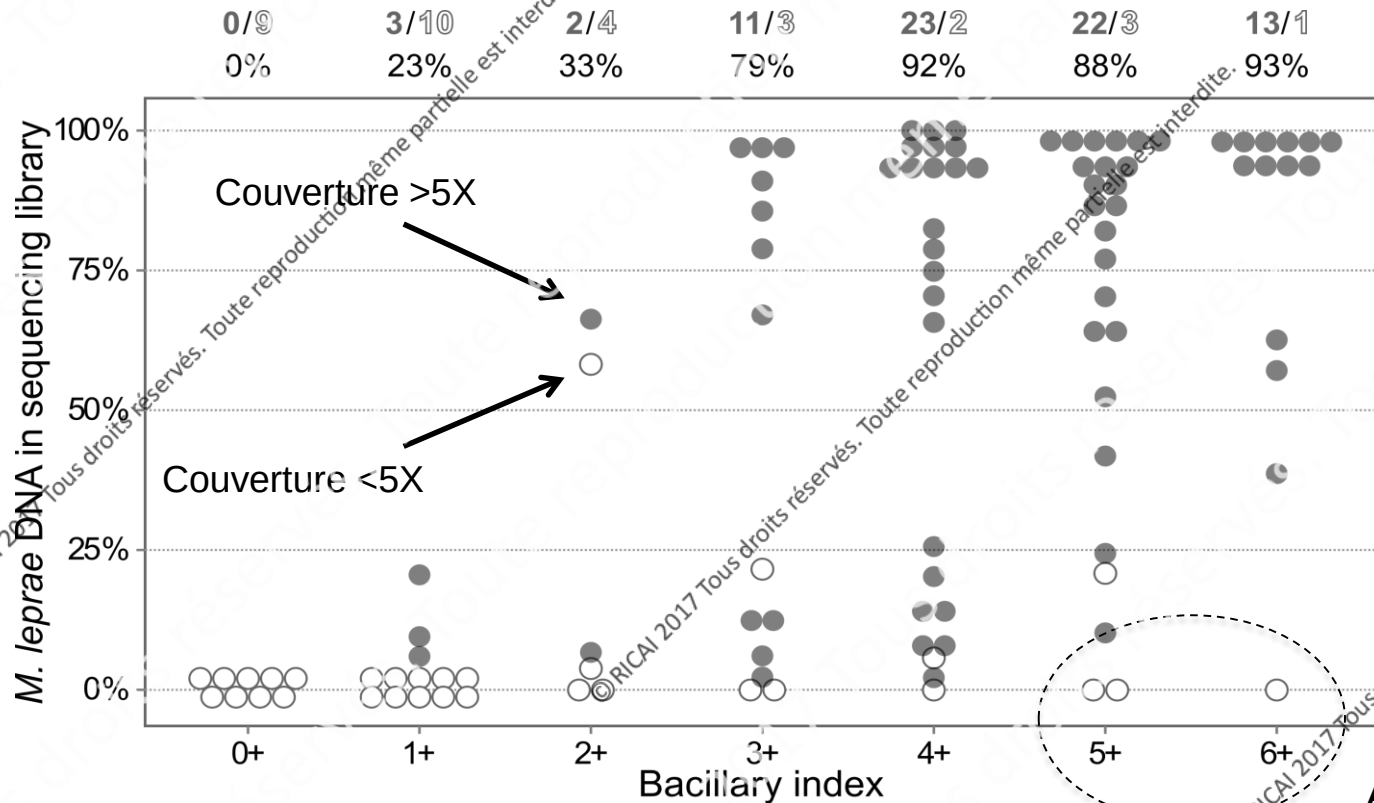


Lyse bactérienne
(chimique & mécanique)



EFFICACITÉ DE LA MÉTHODE

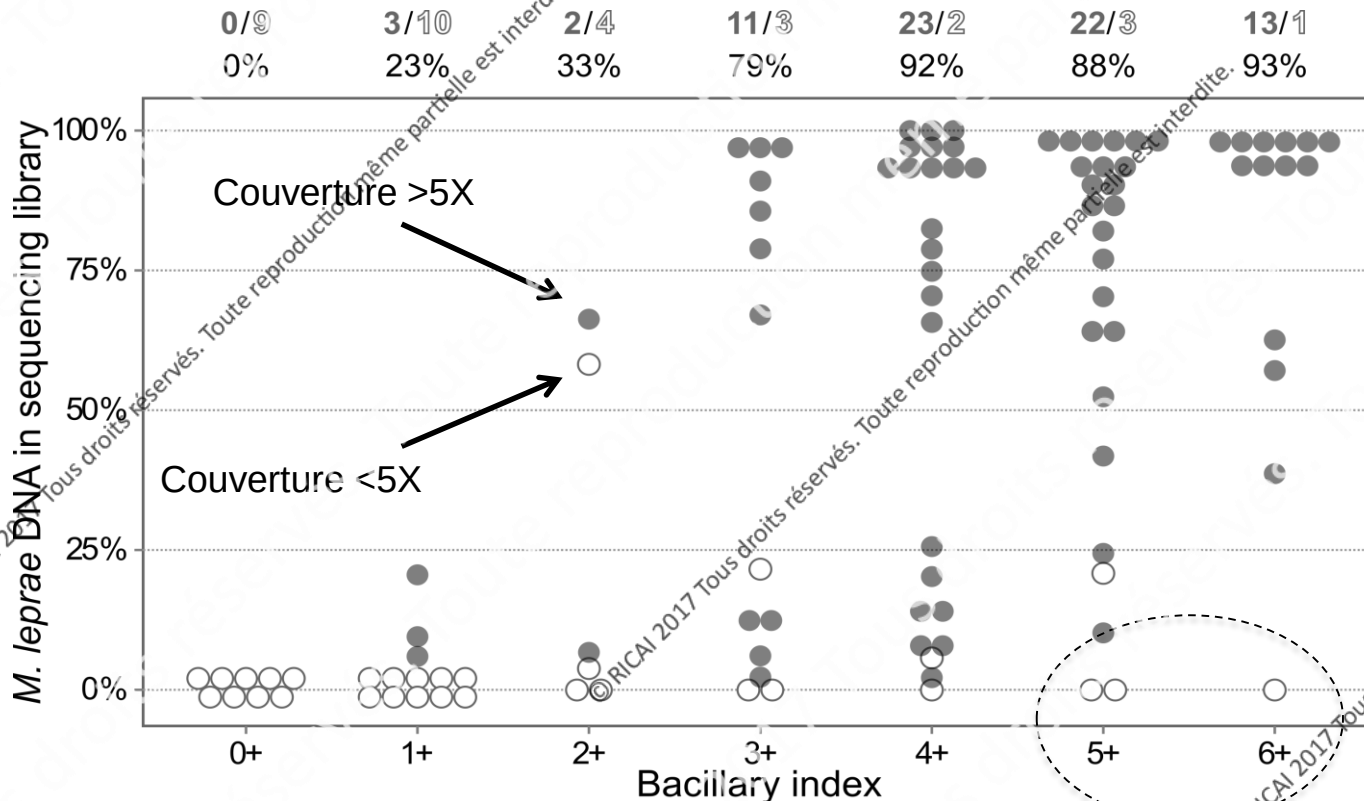
106 biopsies cutanées



Ancienne
méthode

EFFICACITÉ DE LA MÉTHODE

106 biopsies cutanées



Limitations: pour les faibles bacilloscopies (<3+)

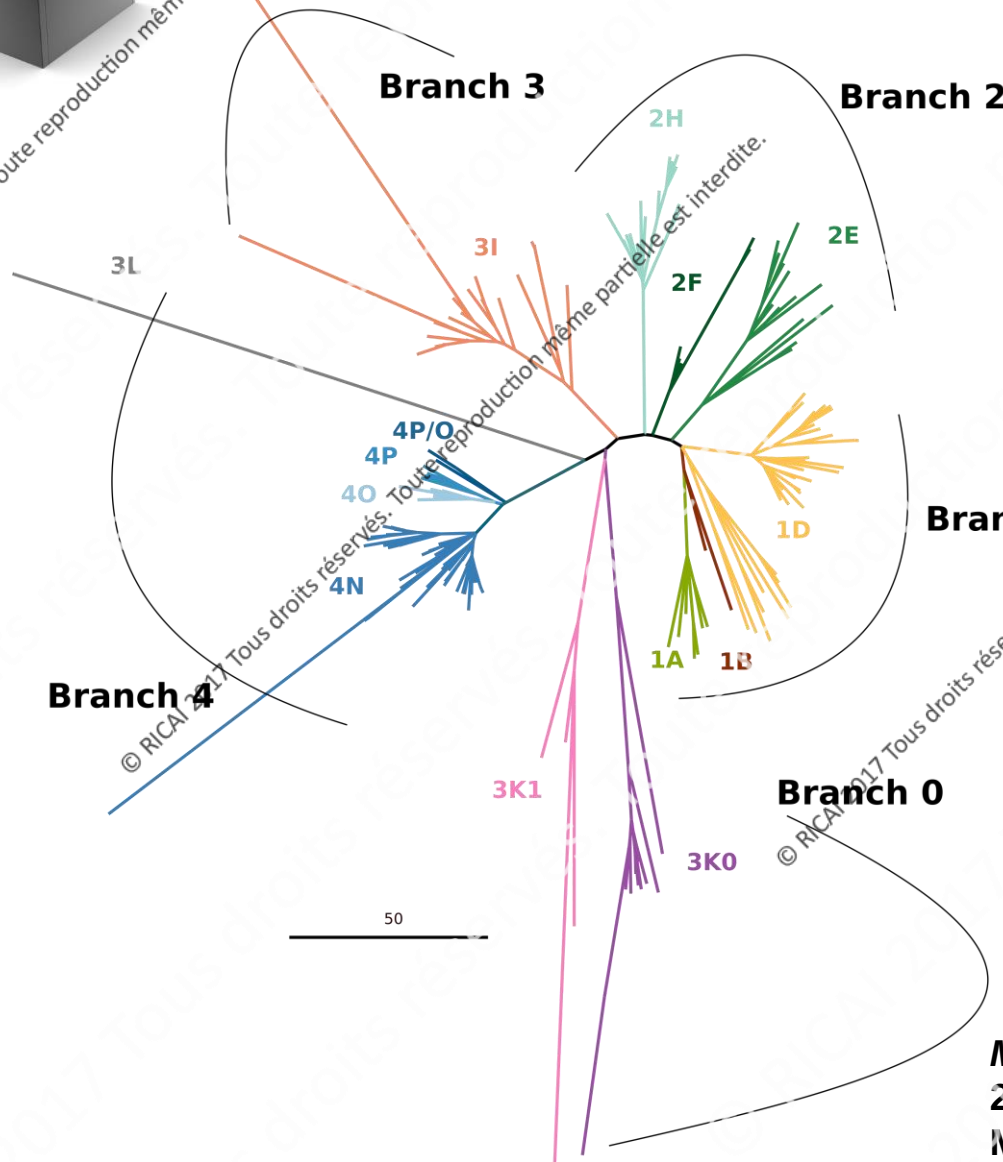
Solution: plus de profondeur ou capture sur puce

~ 20-30 échantillons/ligne

Ancienne
méthode

DE 20 À +100 GÉNOMES

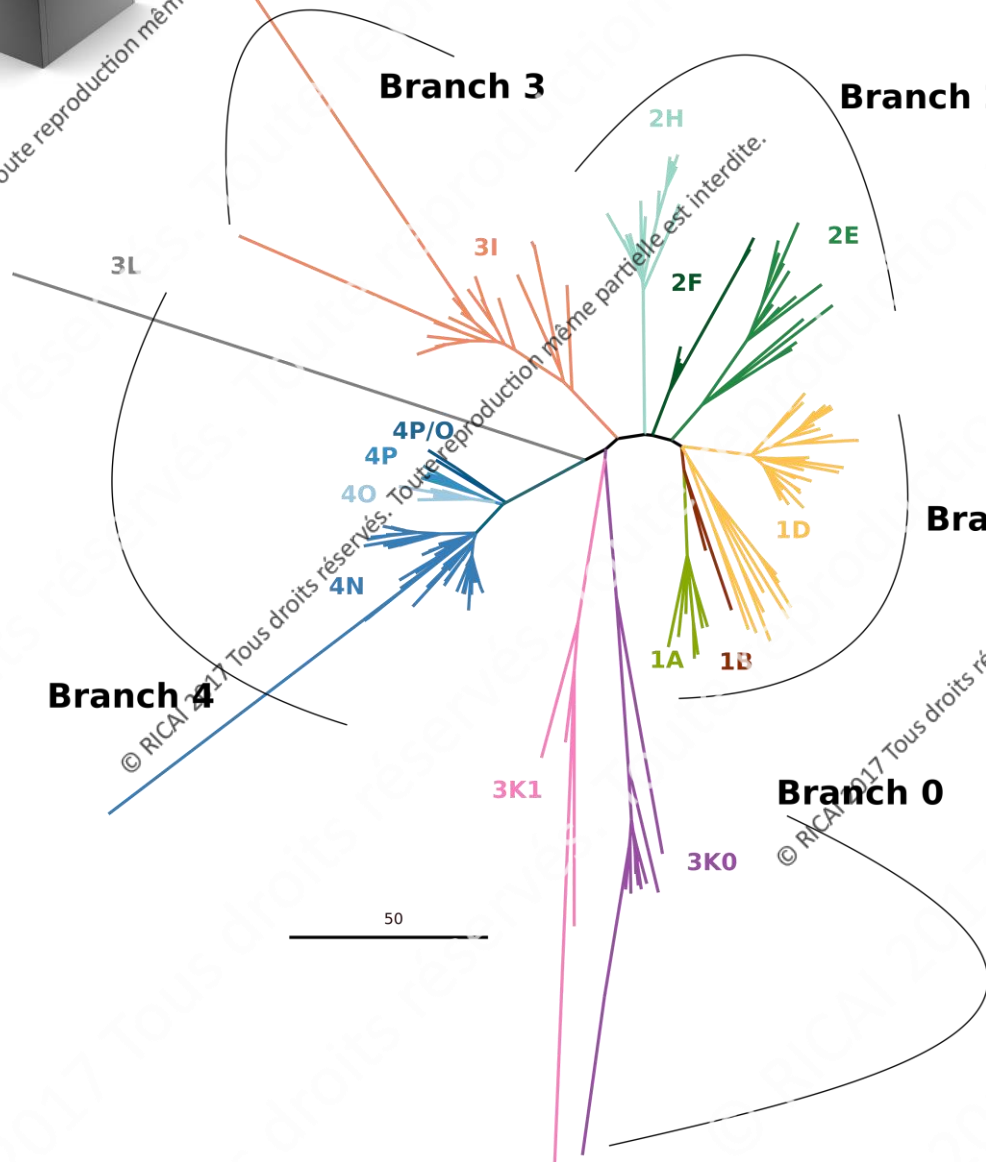
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M. leprae - 185 génomes (ACLP: *M. lepromatosis*)
20 pays
MP (500 bootstraps)

DE 20 À +100 GÉNOMES

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Phylogénie

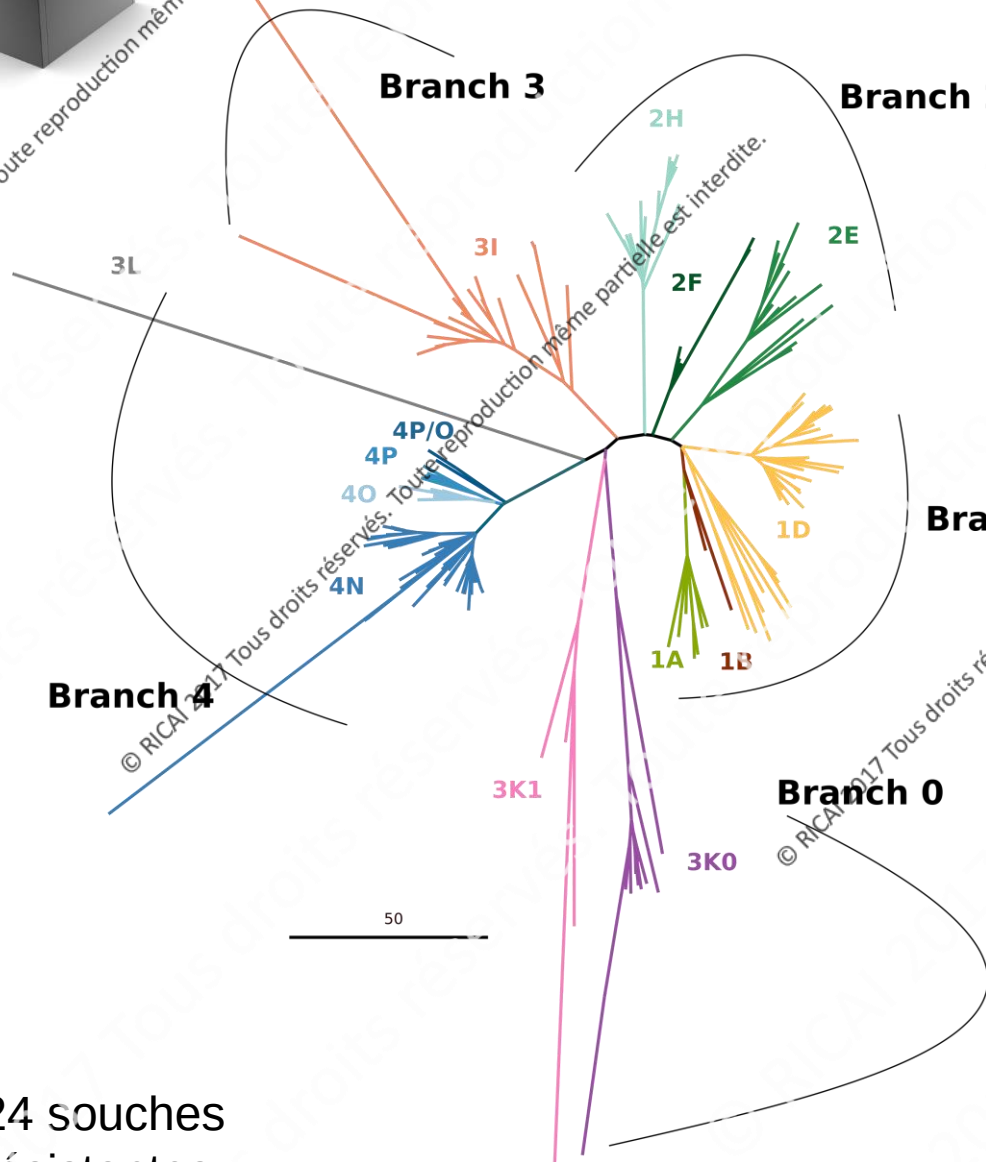
Transmission

Résistance

M. leprae - 185 génomes (ACLP: *M. lepromatosis*)
20 pays
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Phylogénie

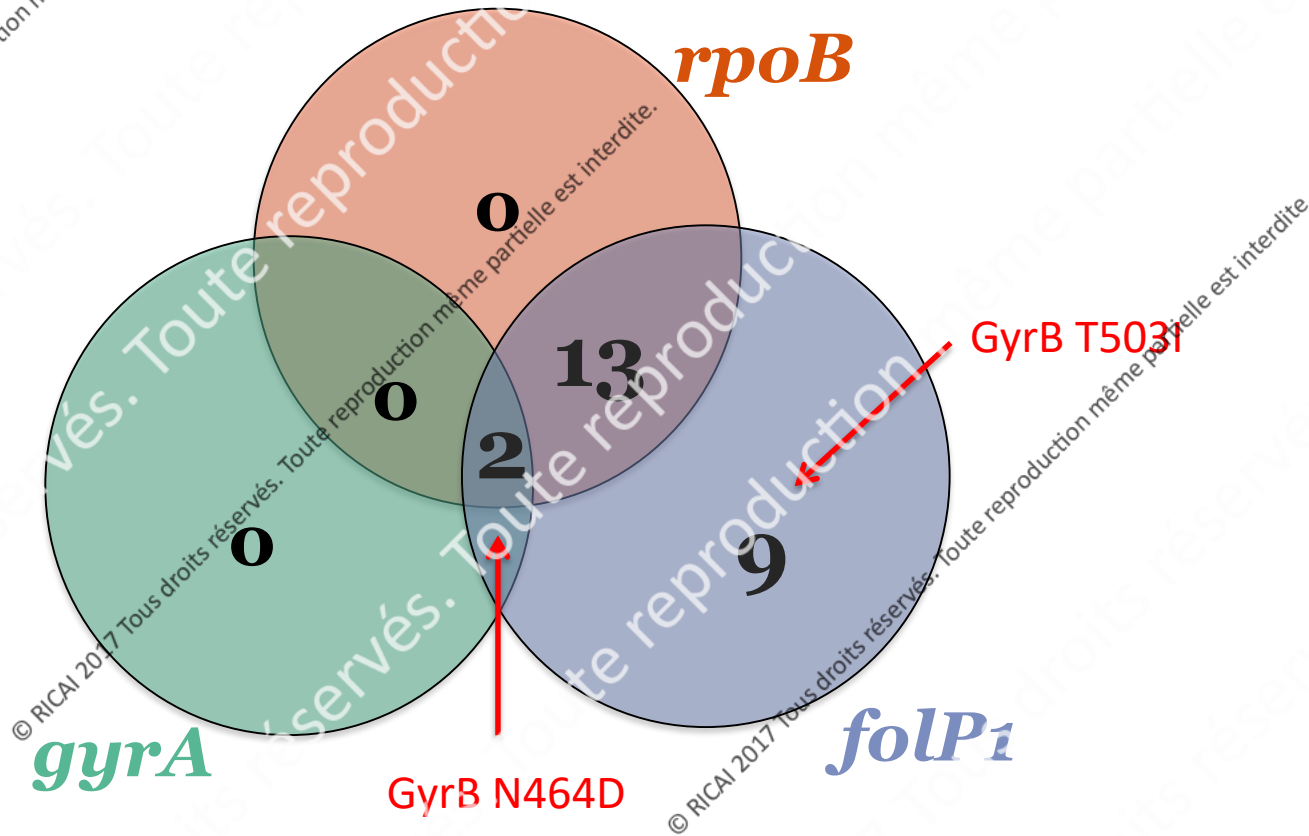
Transmission

Résistance

24 souches
résistantes

M. leprae - 185 génomes (ACLP: *M. lepromatosis*)
20 pays
MP (500 bootstraps)

24 SOUCHES RÉSISTANTES



Possibles mutations compensatrices dans *rpoB*, *rpoC* et *rpoA* (**T187P**)

GÈNES HYPERMUTÉS (TOP 10)

Gene or region	Description	Non-synonymous mutations (multi-allele loci)	Synonymous mutations	Homo-plasy	Frameshift	STOP
<i>ML0411</i>	Serine-rich antigen	28 (4)	1	4		
<i>ML1040c</i>	Putative ATP-dependent helicase	18 (1)	0	0		
<i>fadD9</i>	Probable fatty-acid-CoA ligase	9	1	1	6(1)	2
<i>ML1750c</i>	Putative nucleotide cyclase	17	1	0		
<i>ML1512c</i>	Putative ribonuclease I	17	0	0		
<i>ribD</i>	Bifunctional enzyme riboflavin biosynthesis protein	13 (1)	0	2	2	1
<i>rpoB</i>	DNA-directed RNA polymerase (beta chain)	12 (1)	0	3		
<i>ML1753c</i>	Probable transcriptional regulatory protein	9	0	0		
<i>gyrA</i>	DNA gyrase (subunit A)	8	8	1		
<i>ML1300</i>	Conserved hypothetical protein	8	0	0		

fadD9: 16/18 mutations dans des souches résisantes

ribD: 15/18 mutations dans des souches résistantes

GÈNES HYPERMUTÉS (TOP 10)

Gene or region	Description	Non-synonymous mutations (multi-allele loci)	Synonymous mutations	Homoplasy	Frameshift	STOP
<i>ML0411</i>	Serine-rich antigen	28 (4)	1	4		
<i>ML1040c</i>	Putative ATP-dependent helicase	18 (1)	0	0		
<i>fadD9</i>	Probable fatty acid-CoA ligase	9	1	1	6(1)	2
<i>ML1750c</i>	Putative nucleotide cyclase	17	1	0		
<i>ML1512c</i>	Putative ribonuclease J	17	0	0		
<i>ribD</i>	Bifunctional enzyme riboflavin biosynthesis protein	13 (1)	0	2	2	1
<i>rpoB</i>	DNA-directed RNA polymerase (beta chain)	12 (1)	0	3		
<i>ML1753c</i>	Probable transcriptional regulatory protein	9	0	0		
<i>gyrA</i>	DNA gyrase (subunit A)	8	8	1		
<i>ML1300</i>	Conserved hypothetical protein	8	0	0		

fadD9: 16/18 mutations dans des souches résisantes

ribD: 15/18 mutations dans des souches résistantes

ribD A DES ORTHOLOGUES CHEZ....

- *M. tb*: Rv2671 (*ribD*)
- *M. smegmatis*: MSMEG_2787

RiBD EST UN ANALOGUE DE DHFR

- *M. tb*: Rv2671 (ribD) – pas essentiel
- *M. smegmatis*: MSMEG_2787

Structural Insights into *Mycobacterium tuberculosis* Rv2671 Protein as a Dihydrofolate Reductase Functional Analogue Contributing to *para*-Aminosalicylic Acid Resistance

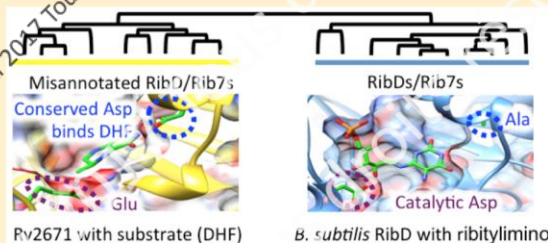
Yu-Shan Cheng[†] and James C. Sacchettini^{*,†,‡}

[†]Department of Chemistry, Texas A&M University, College Station, Texas 77842, United States

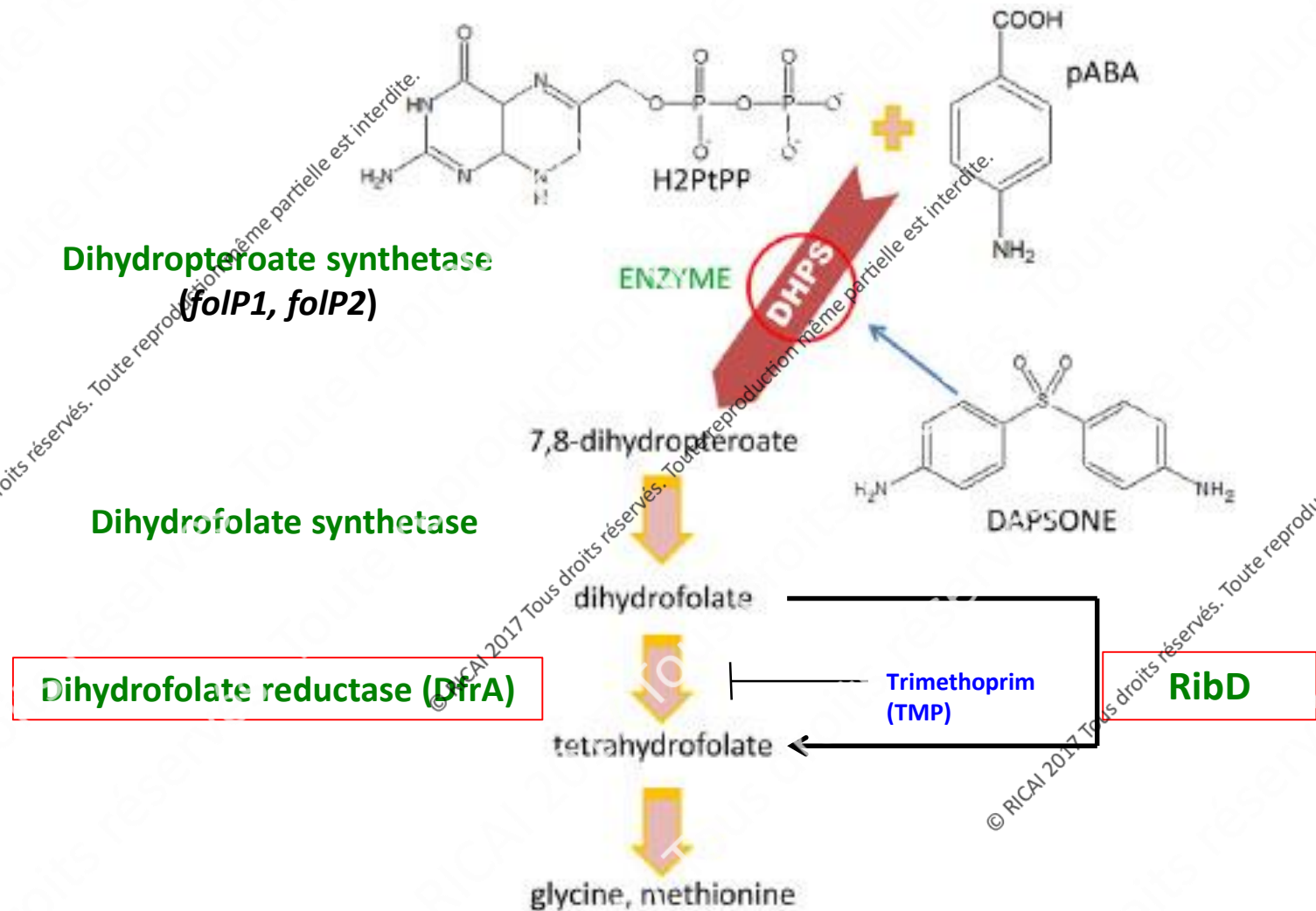
[‡]Department of Biochemistry and Biophysics, Texas A&M University, College Station, Texas 77843, United States

Supporting Information

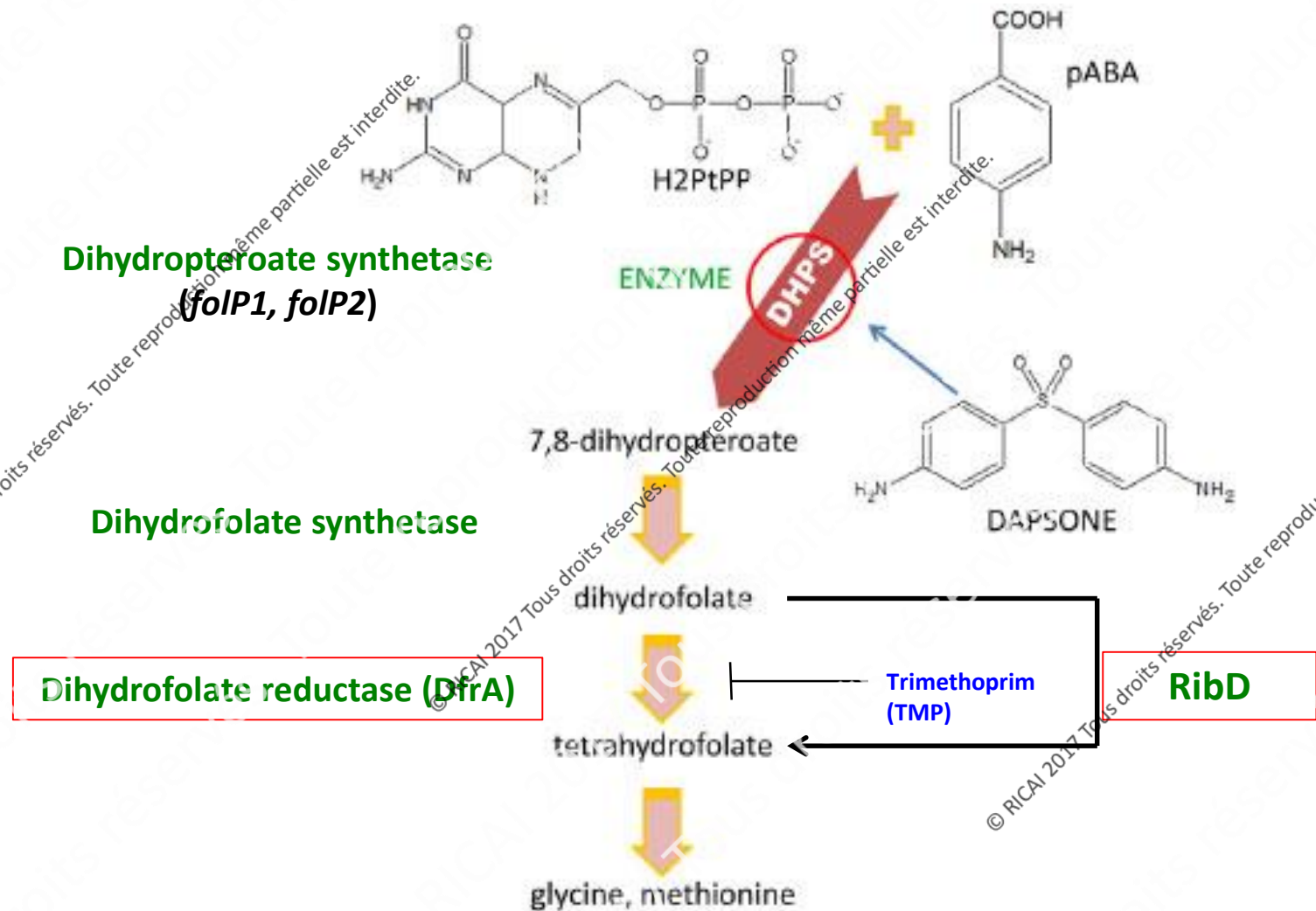
ABSTRACT: *Mycobacterium tuberculosis* (Mtb) Rv2671 is annotated as a 5-amino-6-ribitylamino-2,4(1H,3H)-pyrimidin-6-one 5'-phosphate (AROPP) reductase (RibD) in the riboflavin biosynthetic pathway. Recently, a strain of Mtb with a mutation in the 5' untranslated region of Rv2671, which resulted in its overexpression, was found to be resistant to dihydrofolate reductase (DHFR) inhibitors including the anti-Mtb drug *para*-aminosalicylic acid (PAS). In this study, a biochemical analysis of Rv2671 showed that it was able to catalyze the reduction of dihydrofolate (DHF) to tetrahydrofolate (THF), which explained why the overexpression of Rv2671 was sufficient to confer PAS resistance. We solved the structure of Rv2671 in complex with the NADP⁺ and tetrahydrofolate (THF), which revealed the structural basis for the DHFR activity. The structures of Rv2671 complexed with two DHFR inhibitors, trimethoprim and trimetrexate, provided additional details of the substrate binding pocket and elucidated the differences between their inhibitory activities. Finally, Rv2671 was unable to catalyze the reduction of AROPP, which indicated that Rv2671 and its closely related orthologues are not involved in riboflavin biosynthesis.



VOIE DES FOLATES ET INHIBITEURS

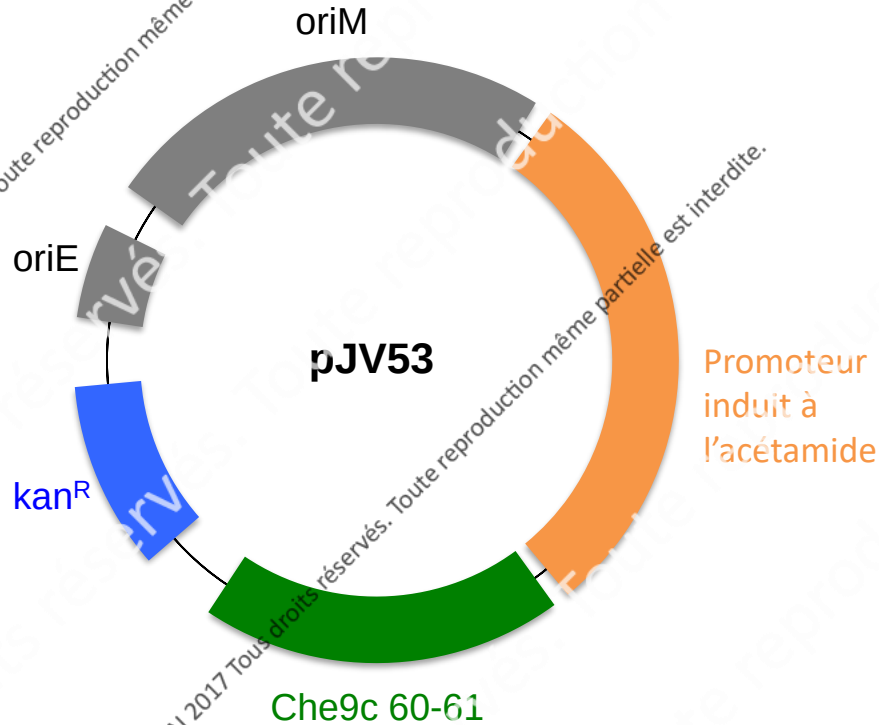


VOIE DES FOLATES ET INHIBITEURS

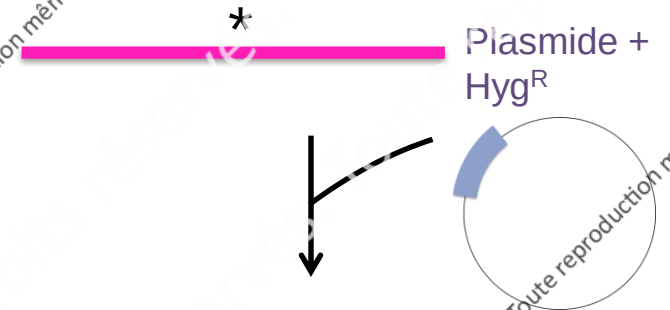


Hypothèse 1: autre mécanisme de résistance à la dapsone

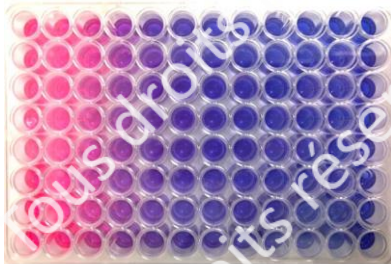
RECOMBINAISON CHEZ *M. SMEGMATIS*



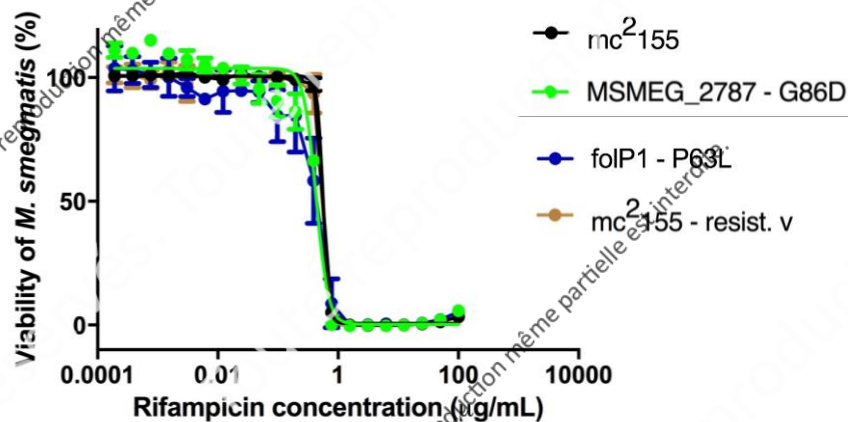
***Mutation ponctuelle**
Synthétique sbADN



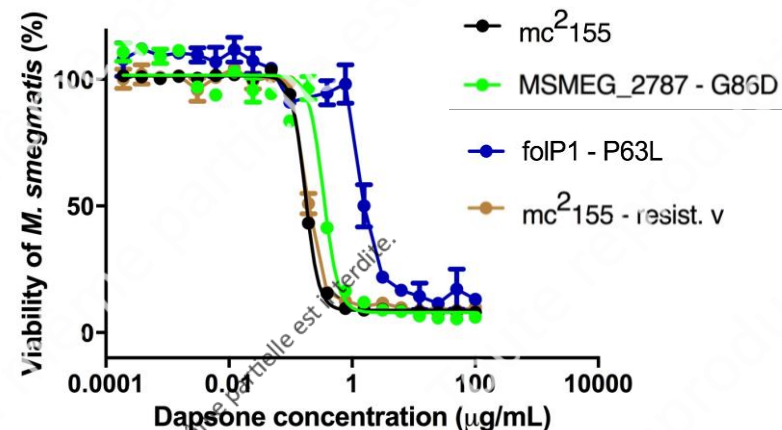
sbADN recombiné dans le chromosome



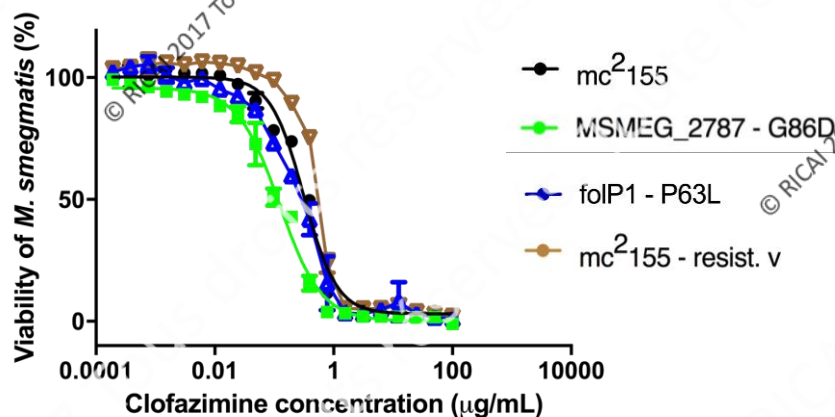
RÉSULTATS PRÉLIMINAIRES



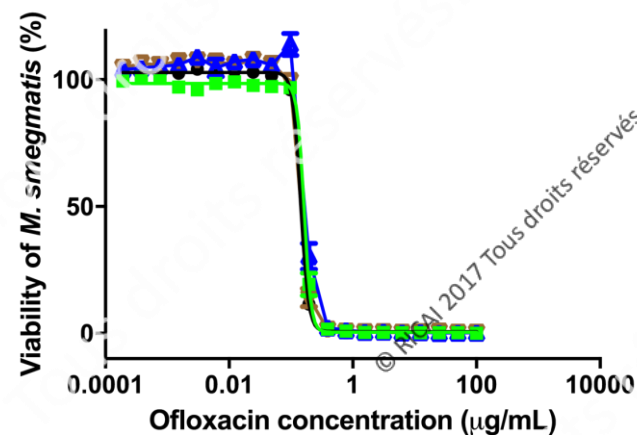
	mc ² ₁₅₅	MSMEG_2787 - G86D	folP1-P63L	mc ² ₁₅₅ - resist.
MIC	0.7652	0.7999	0.8656	0.6576



	mc ² ₁₅₅	MSMEG_2787 - G86D	folP1-P63L	mc ² ₁₅₅ - resist.
MIC	0.2561	0.7523	2.499	0.2437

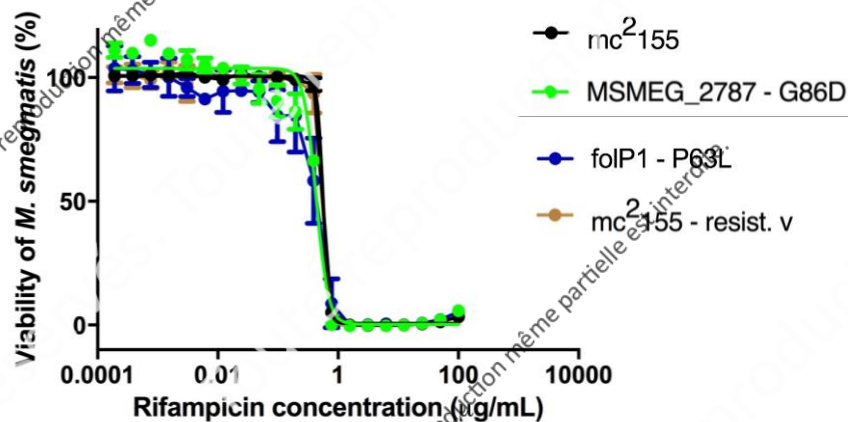


	mc ² ₁₅₅	MSMEG_2787 - G86D	folP1-P63L	mc ² ₁₅₅ - resist.
MIC	1.076	0.6453	1.204	1.052

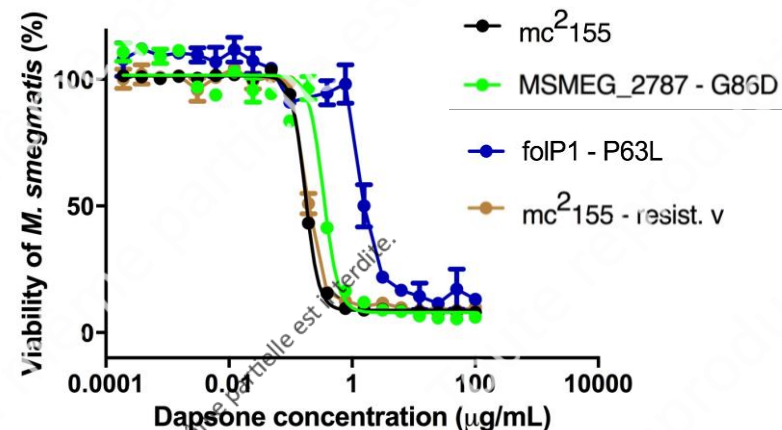


	mc ² ₁₅₅	MSMEG_2787 - G86D	folP1-P63L	mc ² ₁₅₅ - resist.
MIC	0.2029	0.2109	~ 0.2025	0.2067

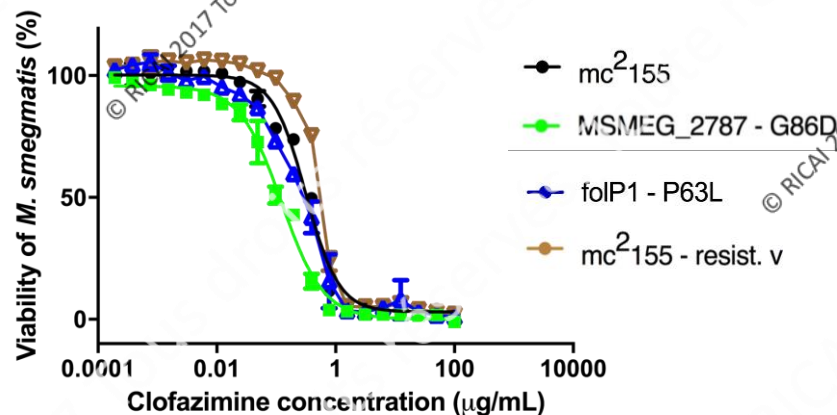
RÉSULTATS PRÉLIMINAIRES



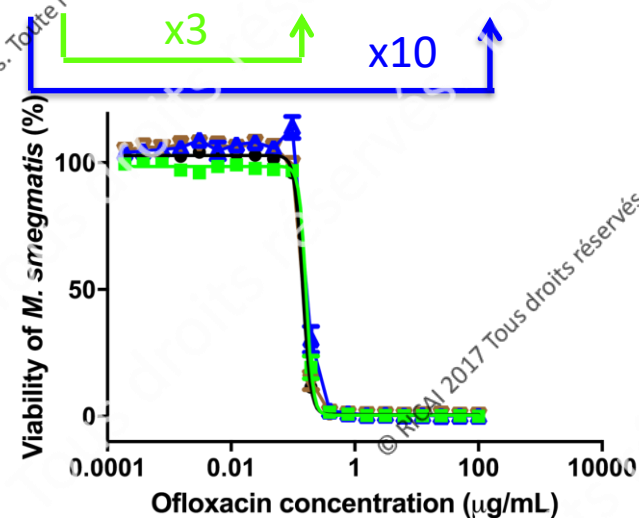
	mc ² ₁₅₅	MSMEG_2787 - G86D	folP1-P63L	mc ² ₁₅₅ - resist.
MIC	0.7652	0.7999	0.8656	0.6576



	mc ² ₁₅₅	MSMEG_2787 - G86D	folP1-P63L	mc ² ₁₅₅ - resist.
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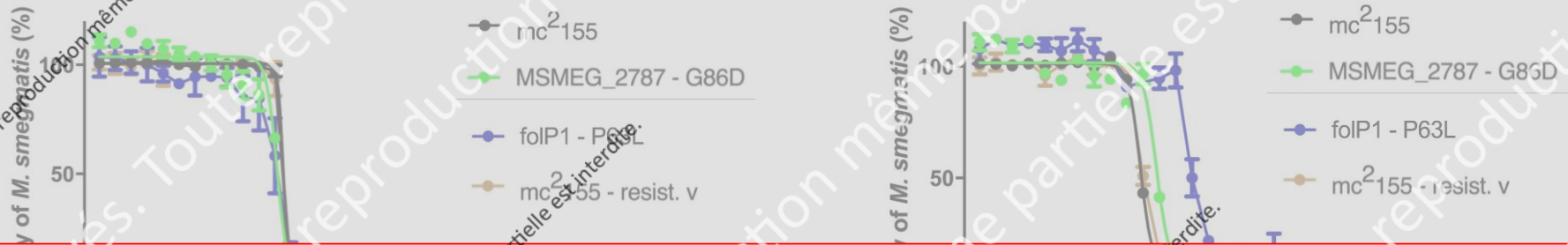


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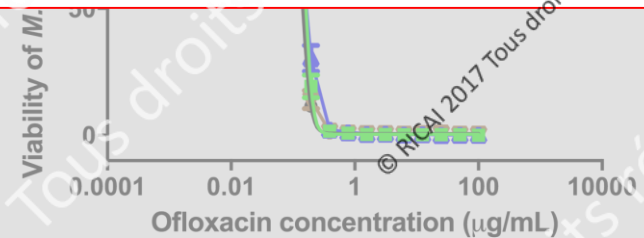
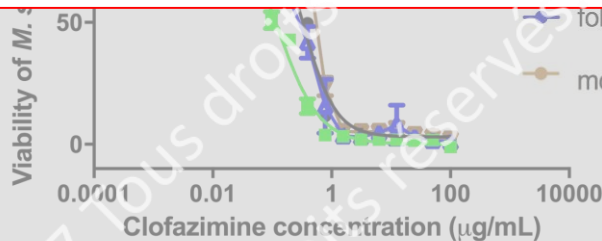


	mc ² ₁₅₅	MSMEG_2787 - G86D	folP1-P63L	mc ² ₁₅₅ - resist.
MIC	0.2029	0.2109	~ 0.2025	0.2067

RÉSULTATS PRÉLIMINAIRES



- Faible résistance pour *folP1*
- Résultats non concluants pour le mutant *ribD* (dapsone)
- Autres mutations?
- Résistance à un autre médicament?
- Mécanismes de compensation?
- *M. smegmatis* n'est pas le bon modèle?



	mc ² 155	MSMEG_2787 - G86D	folP1-P63L	mc ² 155 - resist.
MIC	1.076	0.6453	1.204	1.052

	mc ² 155	MSMEG_2787 - G86D	folP1-P63L	mc ² 155 - resist.
MIC	0.2029	0.2109	~0.2025	0.2067

CONCLUSIONS & FUTURES APPLICATIONS



- Outils performant pour le séquençage des génomes de *M. leprae* à partir des échantillons cliniques
- Le WGS est une approche performante pour l'étude des résistances:
 - Identification de nouveaux mécanismes
 - Autres mutations à tester: *fadD9* par exemple
 - Mais... pas facile à démontrer ensuite!
- Futures applications
 - Augmenter le nombre de souches résistantes séquencées
 - Accès à l'historique des patients est primordial!
 - Etude avec plus de souches résistantes provenant de patients ayant rechutés ou ré-infectés: résistance & persistance vs. virulence

REMERCIEMENTS

