

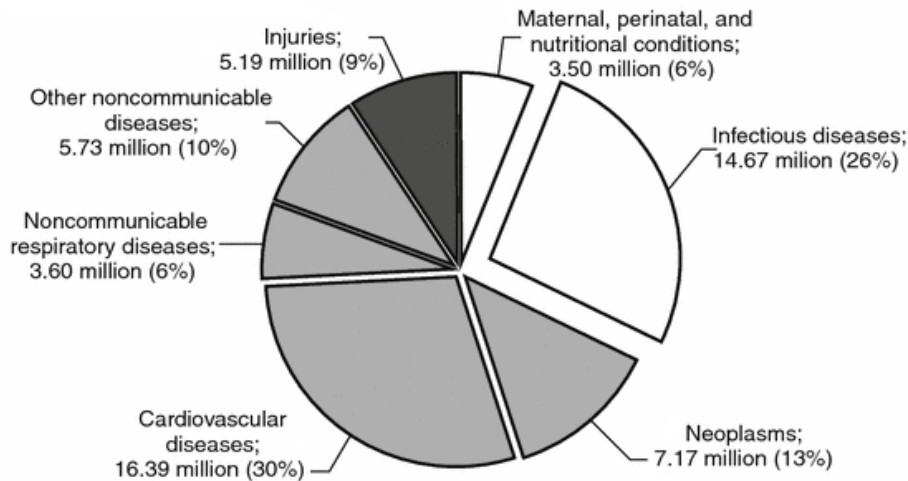
Nucleic Acid Modifications in Bacterial Pathogens – Impact on Pathogenesis, Diagnosis, & Therapy

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Doctoral Thesis Defense
Department of Biological Engineering
Massachusetts Institute of Technology
13 May 2014

Bacteria are killing us

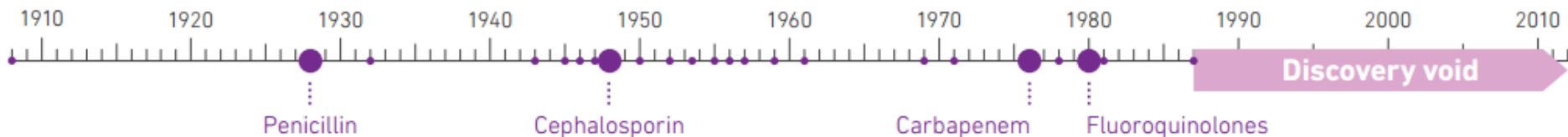
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Estimated minimum number of illnesses and deaths caused by antibiotic resistance:

At least  **2,049,442** illnesses,
 **23,000** deaths

Over the last 30 years, no major new types of antibiotics have been developed





EXPERT VOICES
Epidemiology/Health Services Research
ORIGINAL ARTICLE
THE LANCET Infectious Diseases
Evidence for infectious agents in cardiovascular disease and atherosclerosis

Pinheiro, Mathers, Kramer 2010 *Modern Infectious Disease Epidemiology* | CDC 2013 | WHO 2014

Introduction

Pathogenesis

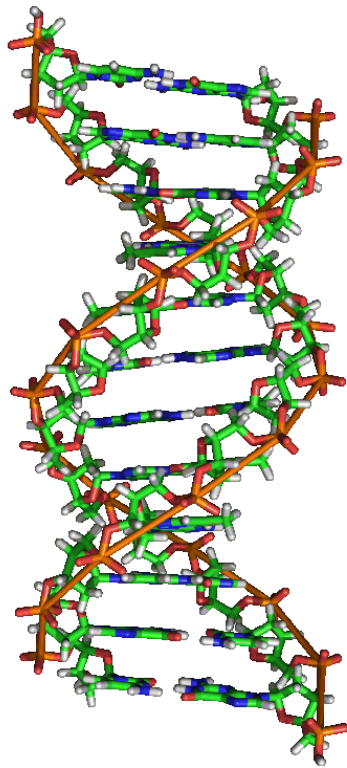
Diagnosis

Therapy

Contributions

Bacterial DNA and RNA are complicated

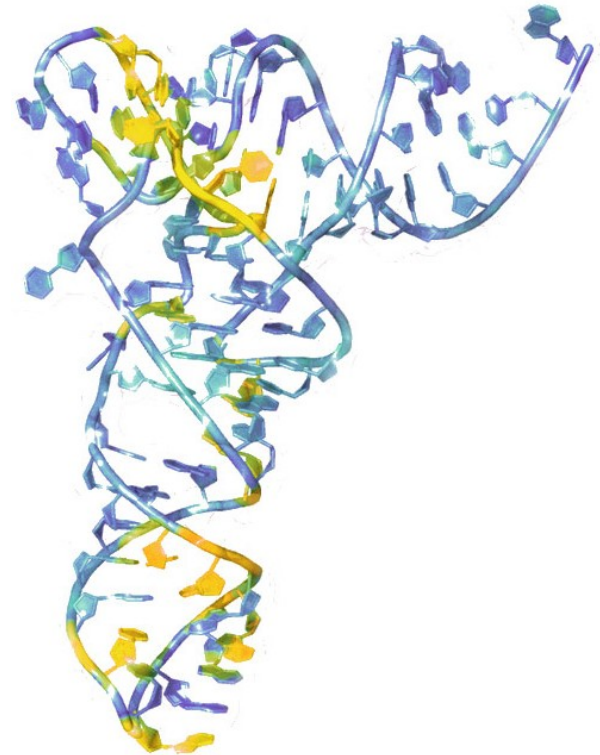
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DNA

A, C, G, T, U...

Why?



RNA

...m1A, m2A, m6A, Am, ms2m6A, i6A, ms2i6A, io6A, ms2io6A, g6A, t6A, ms2t6A, m6t6A, hn6A, ms2hn6A, Ar(p), I, m1I, m1Im, m3C, m5C, Cm, s2C, ac4C, f5C, m5Cm, ac4Cm, k2C, m1G, m2G, m7G, Gm, m22G, m2Gm, m22Gm, Gr(p), yW, o2yW, OHyW, OHyW*, imG, mimG, Q, oQ, galQ, manQ, preQ0, preQ1, G+, Y, D, m5U, Um, m5Um, m1Y, Ym, s2U, s4U, m5s2U, s2Um, acp3U, ho5U, mo5U, cmo5U, mcmo5U, chm5U, mchm5U, mcm5U, mcm5Um, mcm5s2U, nm5s2U, mnm5U, mnm5s2U, mnm5se2U, ncm5U, ncm5Um, cmnm5U, cmnm5Um, cmnm5s2U, m62A, Im, m4C, m4Cm, hm5C, m3U, m1acp3Y, cm5U, m6Am, m62Am, m2,7G, m2,2,7G, m3Um, m5D, m3Y, f5Cm, m1Gm, m1Am, tm5U, tm5s2U, imG-14, imG2, ac6A, inm5U, inm5s2U, inm5Um, m2,7Gm, m42Cm, C+, m8A

Central question for this research

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What role are DNA and RNA modifications playing in bacterial pathogens, and do these modifications have utility as therapeutic targets?

Outline for today's talk

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The role of tRNA modifications in *Helicobacter pylori* stress response and pathogenesis

- Epidemiology and burden of disease
- RNA modifications as drivers of pathogenesis

Development of a novel BSL-2 animal model of mycobacterial lung infection and assessment of RNA modifications as urinary biomarkers

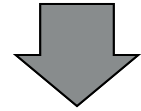
- Epidemiology and burden of disease
- RNA modifications as biomarkers

The role of bacterial DNA phosphorothioation in resistance to oxidative and antibiotic stresses

- DNA modifications as resistance determinants
- Relationship between oxidative and antibiotic stresses

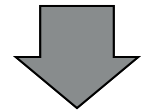
Pathogenesis

- Establish infection
- Target: stop disease



Diagnosis

- Confirm infection
- Target: faster therapy



Therapy

- Clear infection
- Target: cure disease

The role of tRNA modifications in *Helicobacter pylori* stress response and pathogenesis

In collaboration with Kok Seong Lim and Sebastian Smick

Helicobacter pylori is a major health concern

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Pervasive human pathogen

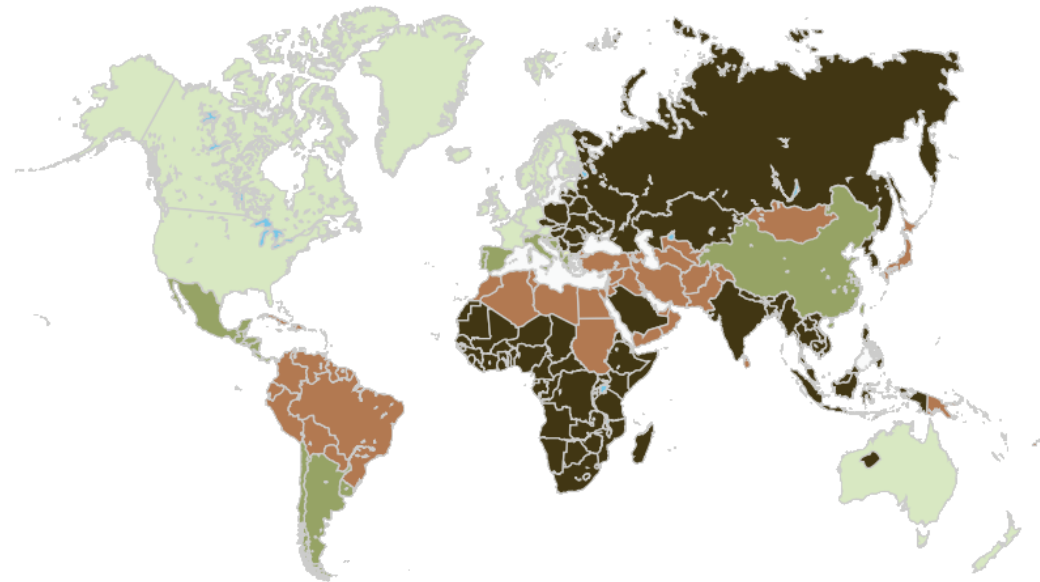
- Infects stomach, causes ulcers
- Undiagnosed in 90% of cases
- Usually persists for life

Huge public health burden

- 50% of the world infected
- Disproportionately affects underdeveloped regions
- Group 1 carcinogen for gastric cancer: 4th most deadly

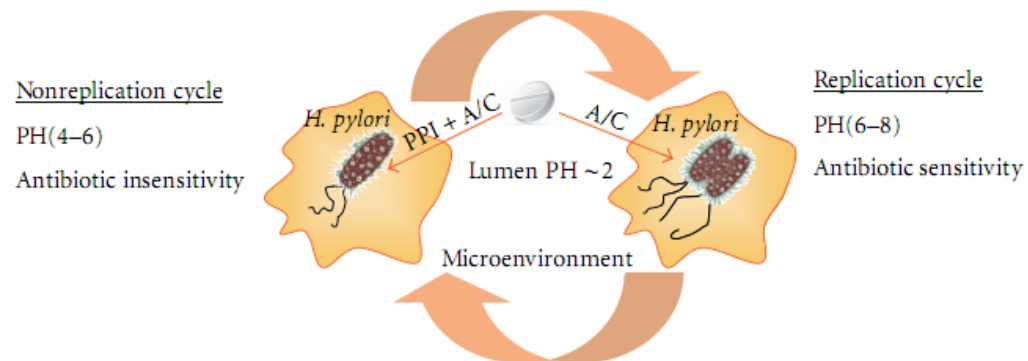
Difficult to eradicate

- Therapy synergizes resistance
- Extremely adapted to gut niche
- Need new drug targets



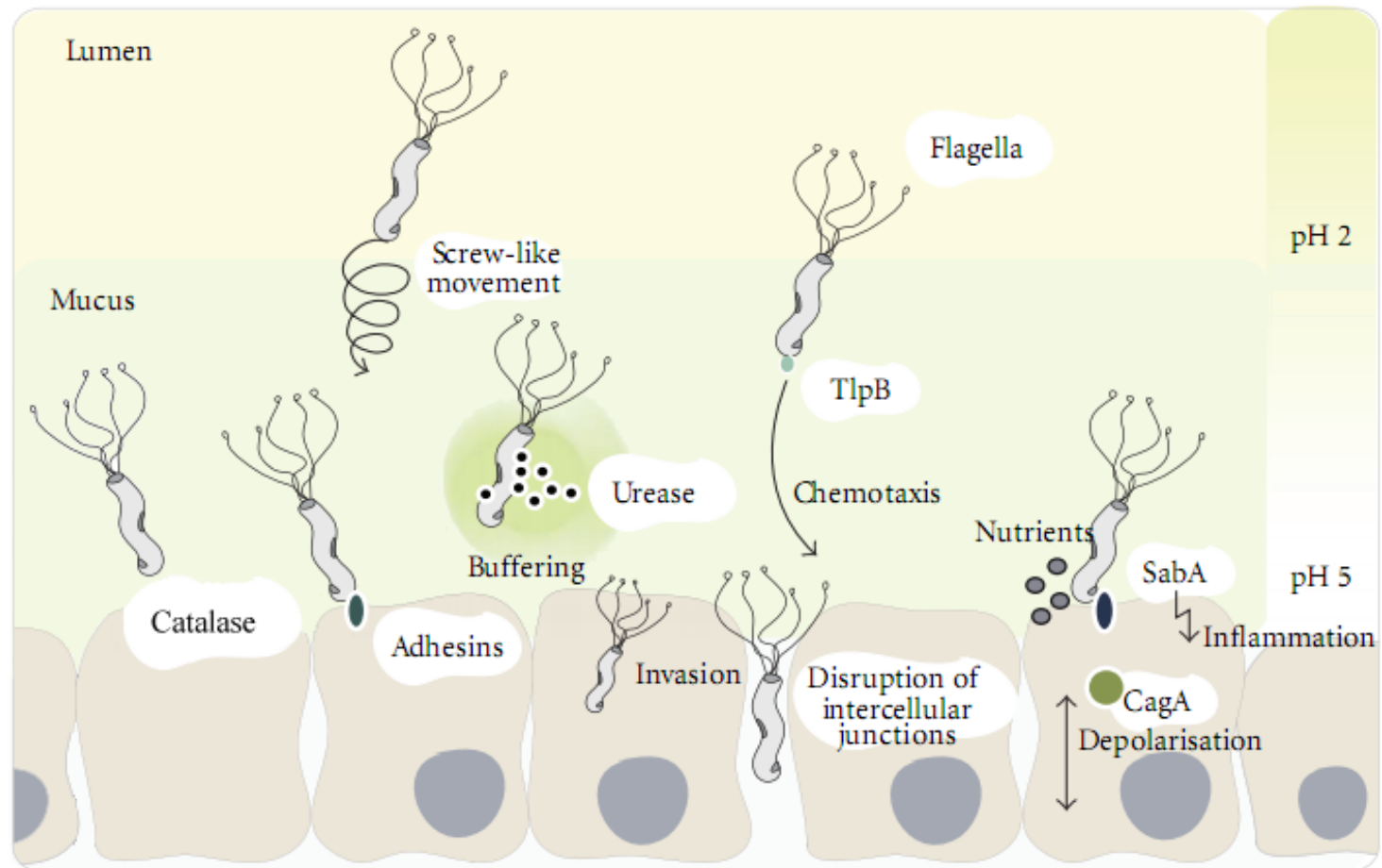
Prevalence of *H. pylori* infection (%)

<55% 55–64% 65–74% >75%



H. pylori is well adapted to its niche

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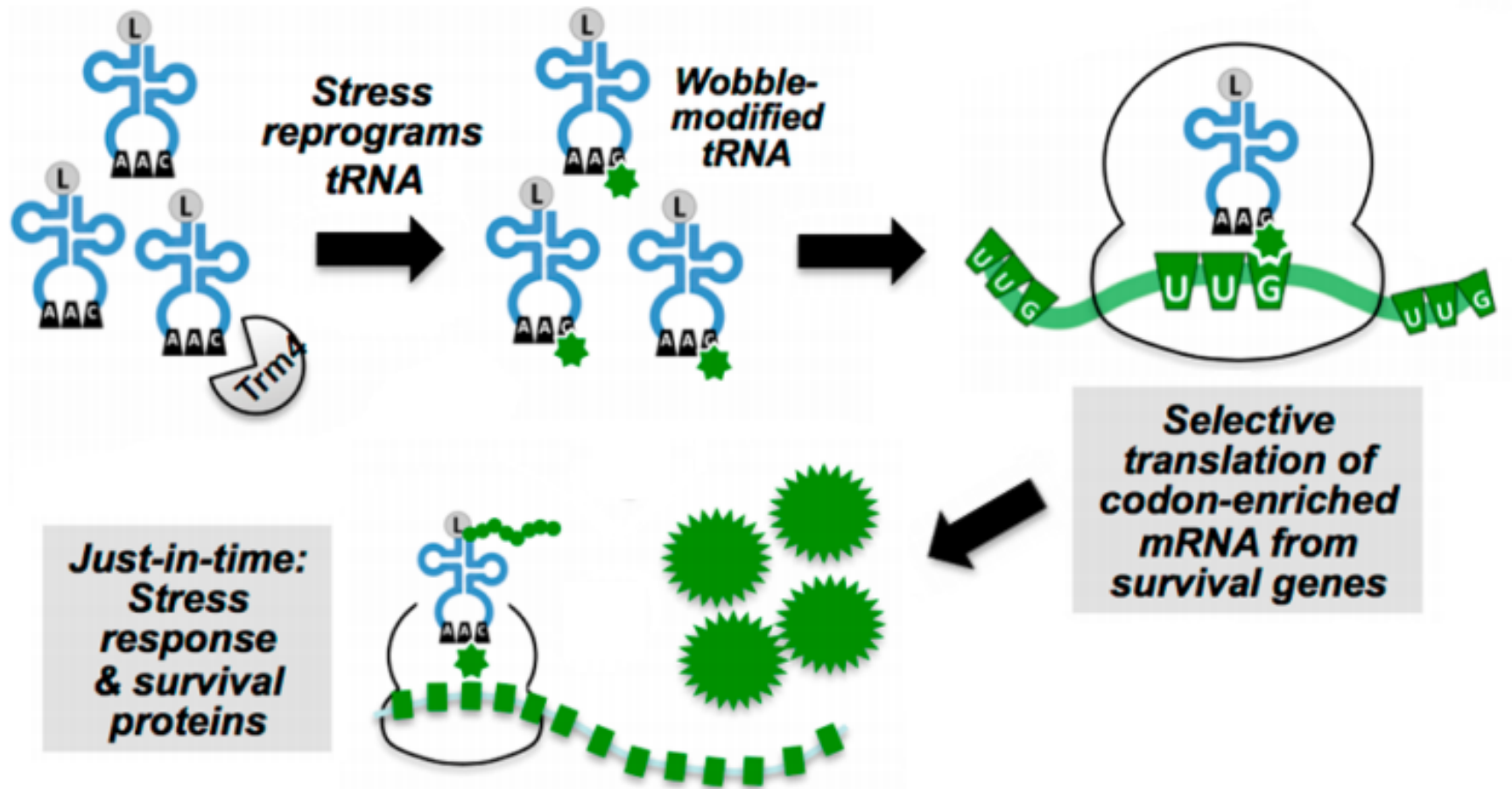
Molecular Microbiology (2004) 51(1), 15–32
doi:10.1046/j.1365-2958.2003.03788.x

Faye M. Barnard, Michael F. Loughlin, Hernan P. Fainberg, Michael P. Messenger, David W. Ussery, Paul Williams and Peter J. Jenks

Although successful and persistent colonization of the gastric mucosa depends on the ability to respond to changing environmental conditions and co-ordinate the expression of virulence factors during the course of infection, *Helicobacter pylori* possesses relatively few transcriptional regulators.

Translational control by tRNA modifications

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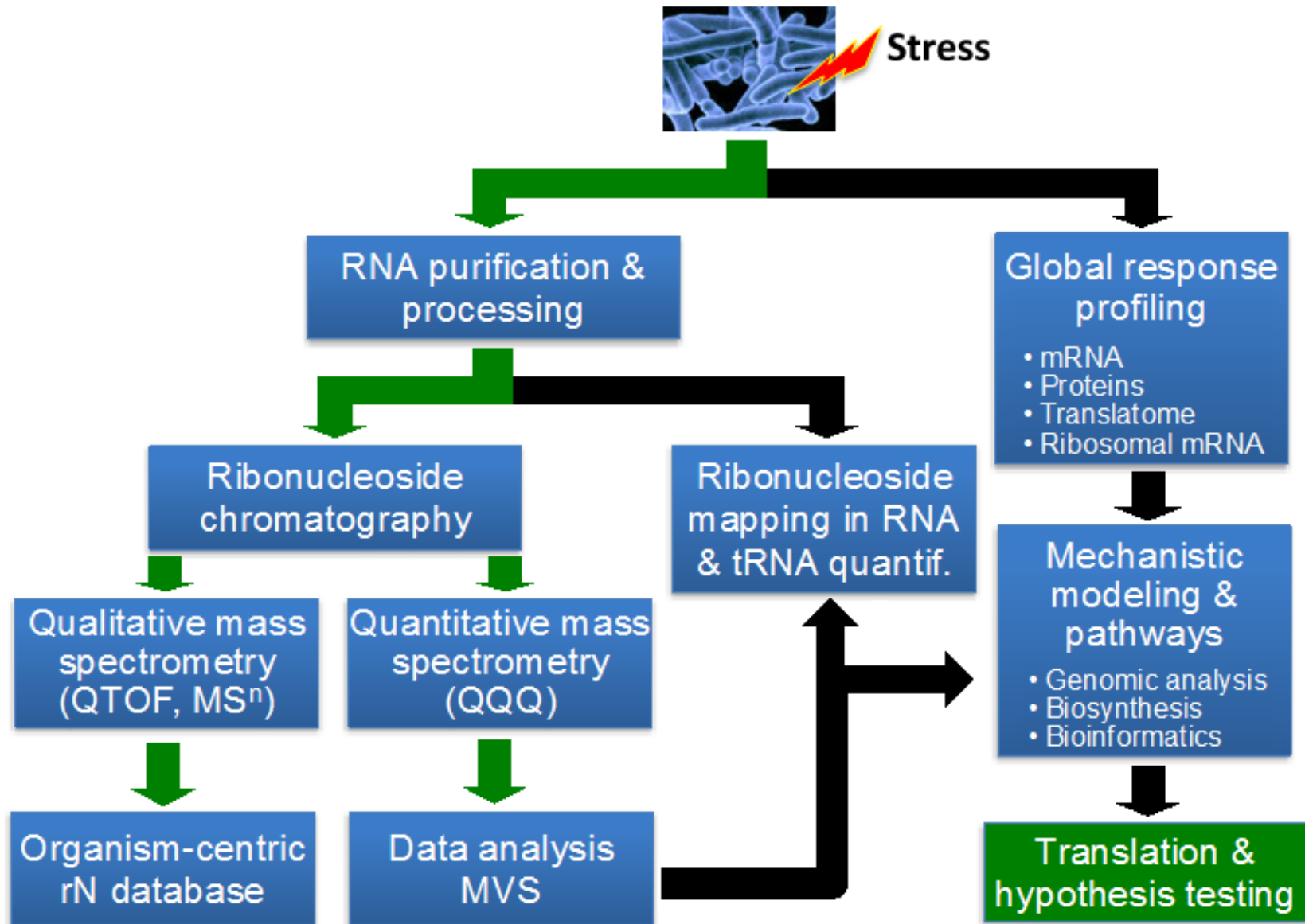


Well established in yeast and humans, but never shown in bacteria
H. pylori is a candidate due to its lack of transcriptional regulation

Dedon, Begley 2014 *Chem Res Toxicol*

Workflow for identifying critical modifications

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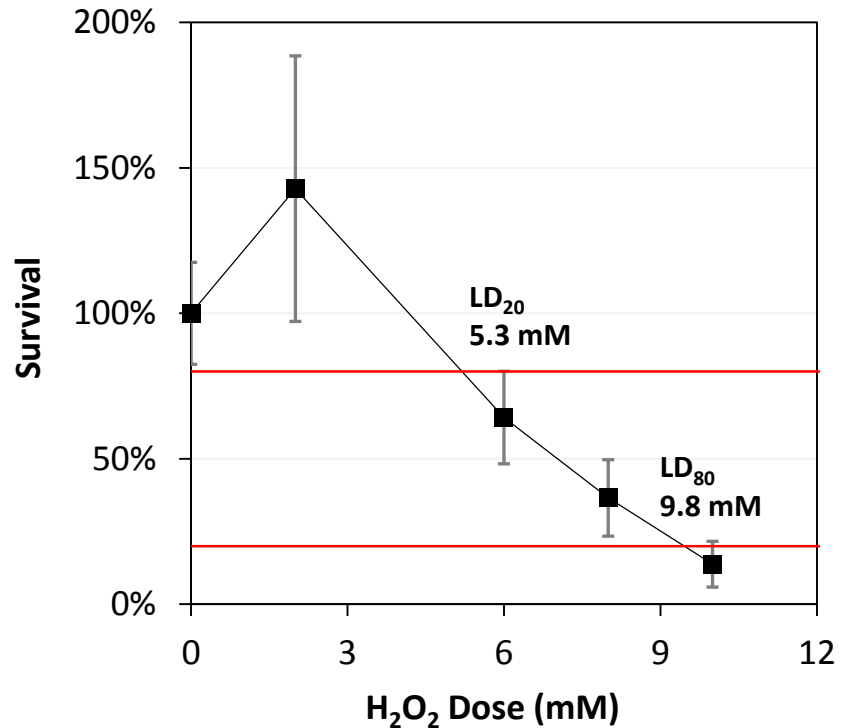
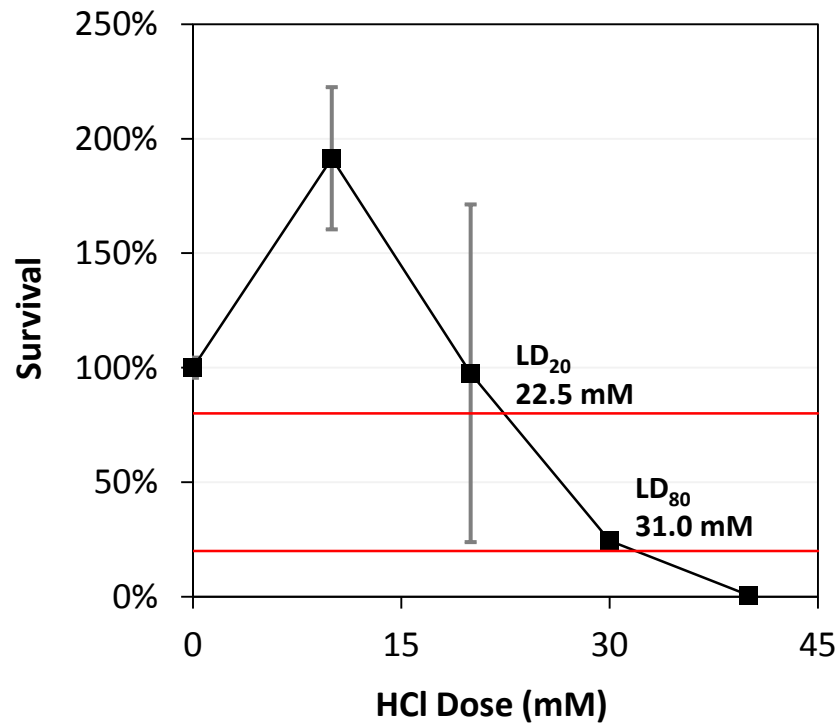
Dose-response curves standardize the stresses

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H. pylori strain 26695 (virulent, sequenced) exposed to key stresses

- HCl is the first barrier to infection, synergizes with antibiotic resistance
- H_2O_2 is a key feature of the innate immune response

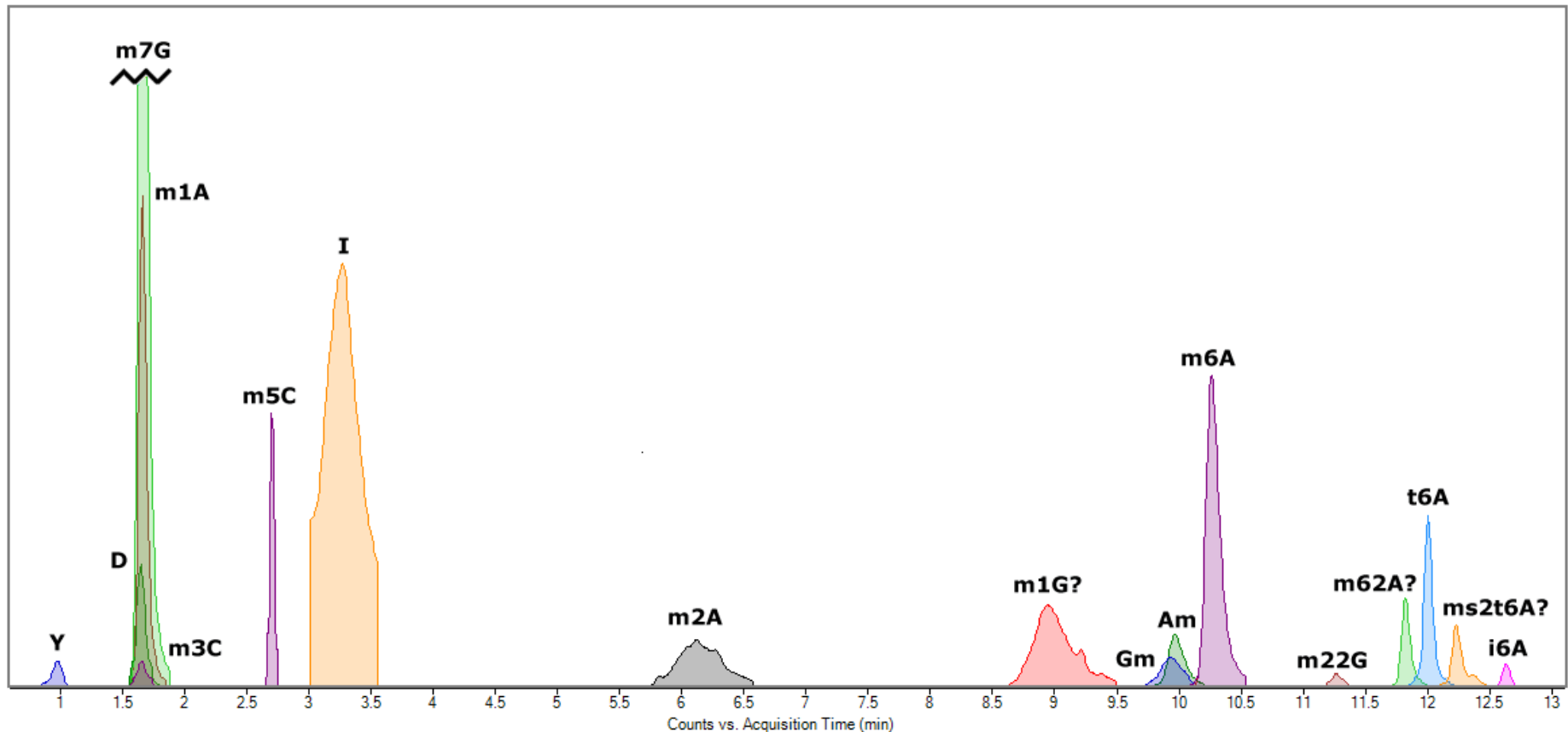
Hormesis seen at low toxicity doses for both stresses



H. pylori modified nucleoside spectrum

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LC-MS/MS method to resolve and quantify 17 ribonucleoside species
14 species confirmed with standards; 3 (?) tentatively identified
Incomplete list, but sufficient to identify stress-induced patterns



Introduction

Pathogenesis

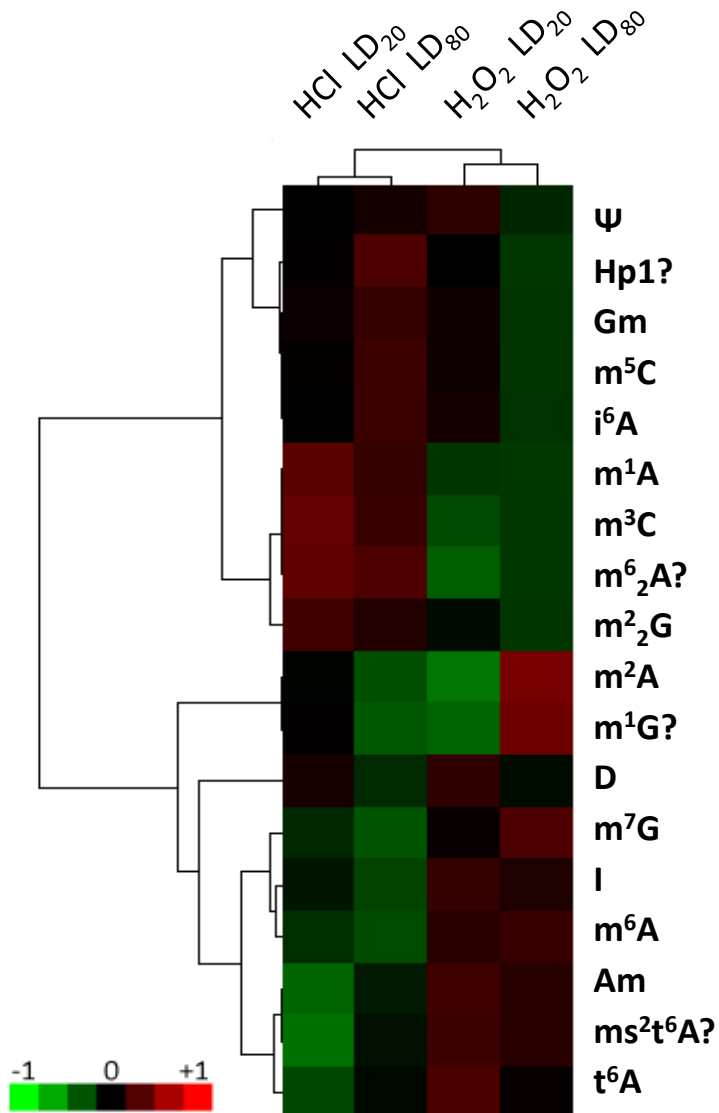
Diagnosis

Therapy

Contributions

Stress induces large changes in nucleoside pattern

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Three biological replicates run in technical triplicate at each dose

Normalized for sample loading by UV signal against a calibration curve

Normalized signals log transformed, mean centered, plotted as a heatmap

First report of stress-induced tRNA modification reprogramming in a human pathogen

Are any of these modifications essential?

Key nucleosides distinguish stresses

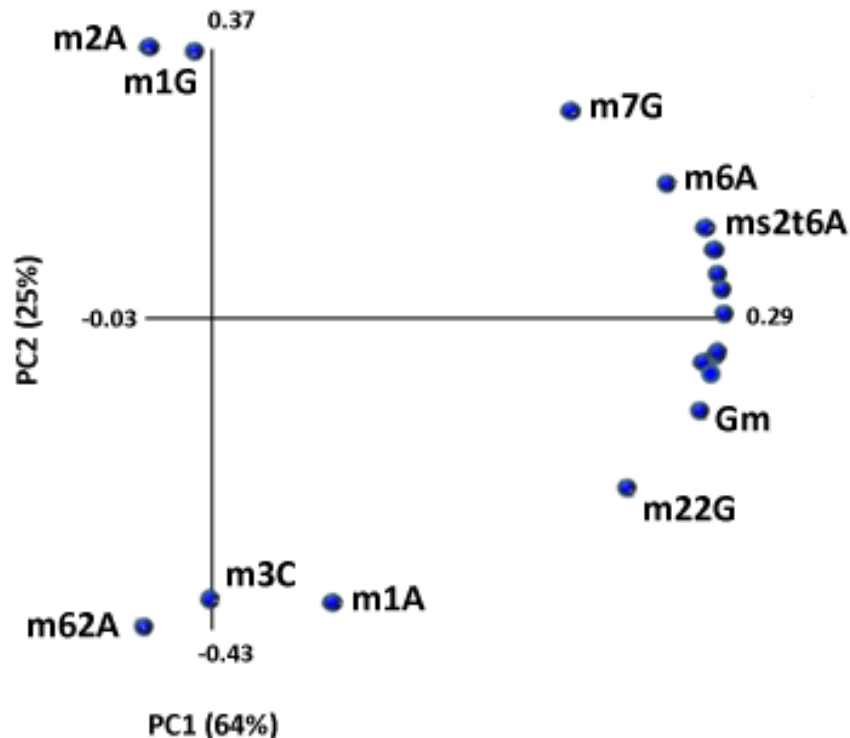
14

Principal component analysis to reveal hidden associations

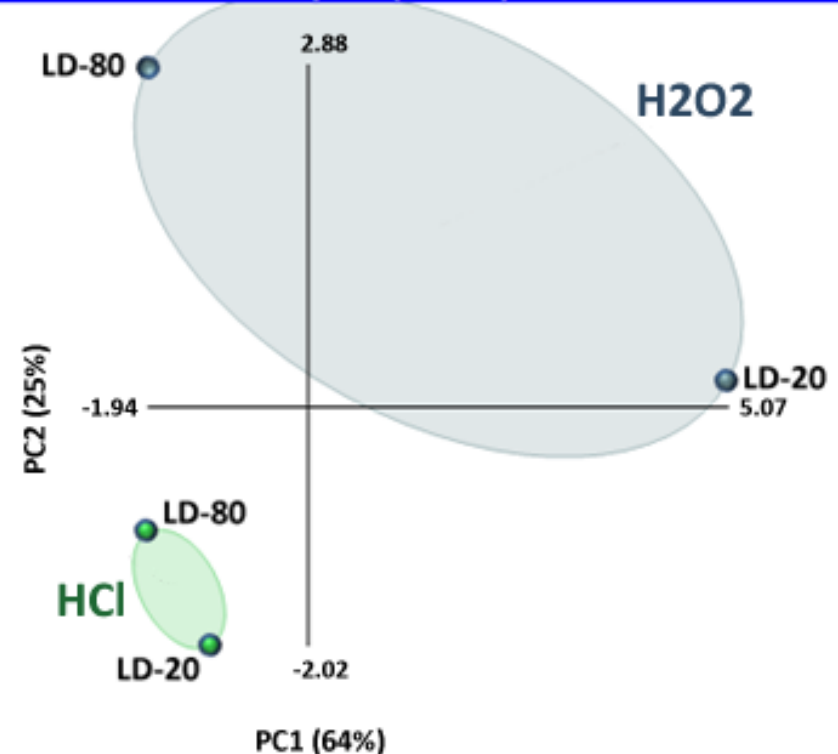
First two PCs capture 89% of the variance – highly predictive

Key modifications separate stresses into distinct classes

Variables (Loadings)



Samples (Score)



Summary and future directions

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First example of tRNA modification profiling in *H. pylori*

First report of tRNA modification reprogramming in a pathogen

- Distinct patterns of modifications by stress
- Clear biomarker signature predicts exposure mechanism of action

First report of specific modifications associated with stress

- m^6_2A also found in *Mycobacterium* tRNA – another harsh niche pathogen
- m^7G conserved across species and critical for stress response in yeast
- ms^2t^6A occurs adjacent to the wobble position, may stabilize translation

Modifying enzymes may represent new antibiotic targets

- Use sequence alignment to identify key enzymes
- Use targeted knockouts to identify critical modifications

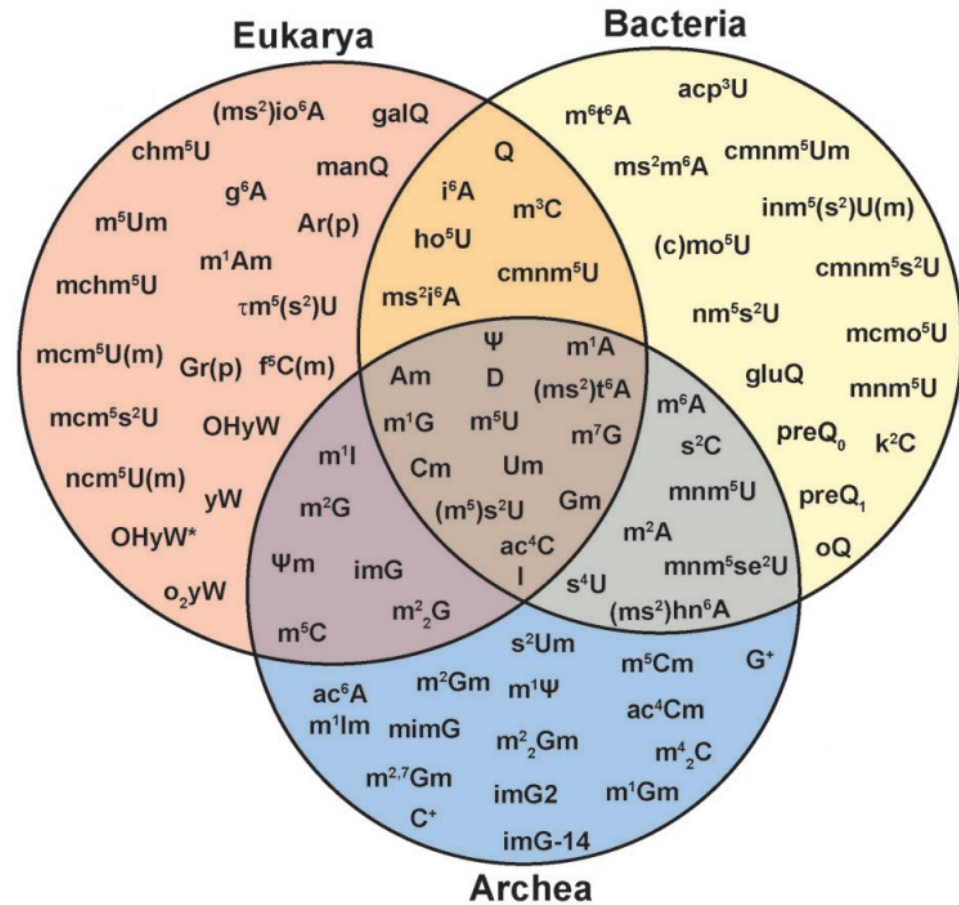
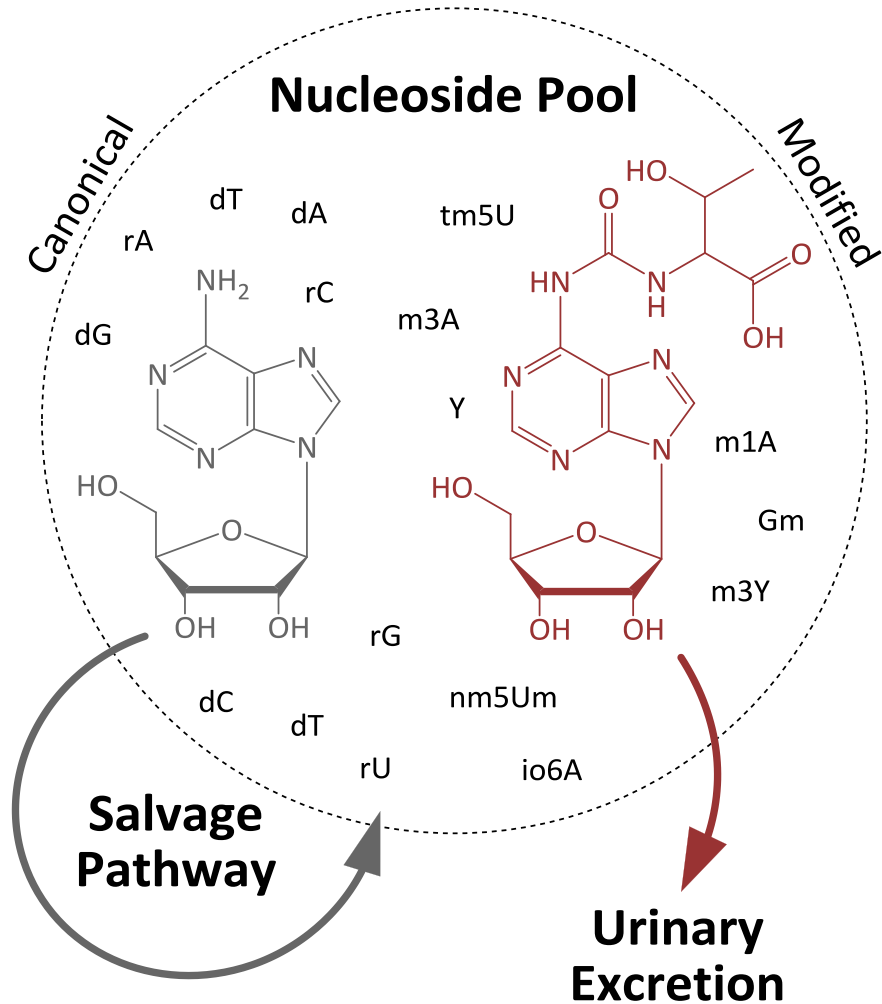
tRNA modifications appear to play a key role in pathogenesis

Development of a novel BSL-2 animal model of mycobacterial lung infection and assessment of RNA modifications as urinary biomarkers

In collaboration with Megan McBee, Sasilada Sirirungruang, Nicola Parry, and Sureshkumar Muthupalani

RNA modifications as urinary biomarkers

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Tuberculosis (TB) is a major global health threat

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Widespread disease

- 33% of the world infected
- 10 million new cases annually
- 2 million deaths annually

Complicated treatment

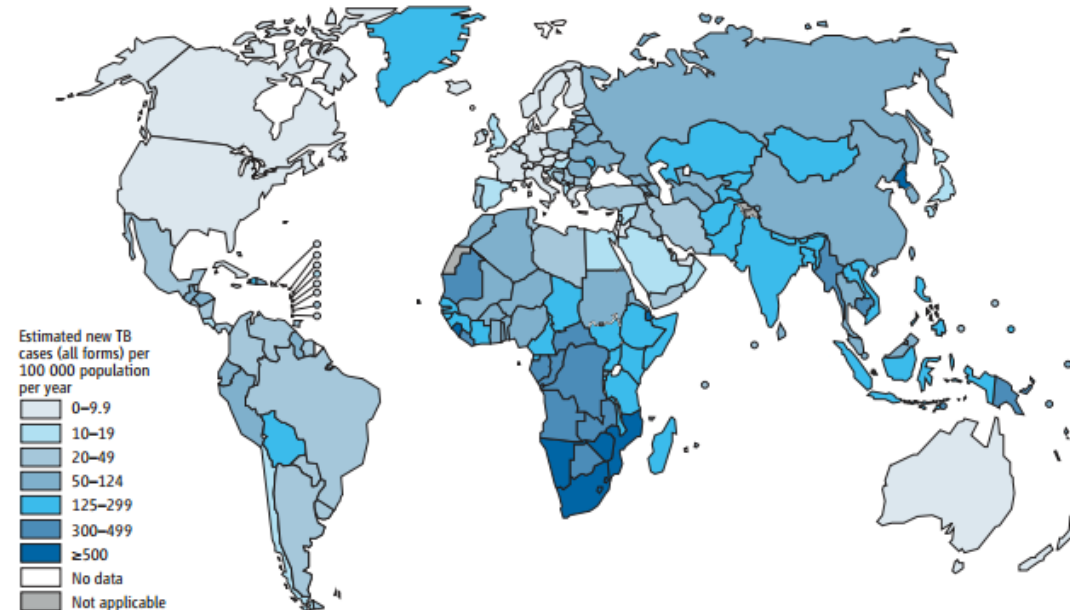
- Antibiotic therapy lasts years
- Same drugs for decades
- Resistance very common

Diagnosis shortcomings

- Sputum smear is insensitive
- Sputum culture is slow

Problem: no BSL-3 facility

Estimated TB incidence rates, 2012



WHO 2013

BSL-2 models of TB are important

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Relatively small number of BSL-3 laboratories in the USA

- Majority are in public research facilities
- Building and operating costs prohibitive for many
- In contrast, virtually any laboratory can operate at BSL-2

BSL-2 models of TB are commonly used in research

- Zebrafish + *M. marinum*
- “Fish tuberculosis”
- Utility limited by biology

No current BSL-2 model is amenable to urine biomarker or drug development studies

Table 2: BSL-3 Labs Registered with the CDC and USDA

Sector	CDC-registered labs	USDA- registered labs	Total
	Number	Number	Number
Federal	291	167	458
Academic	429	58	487
State	248	20	268
Private	74	69	143
Total	1042	314	1356

Spotlight

Insights into tuberculosis from the zebrafish model

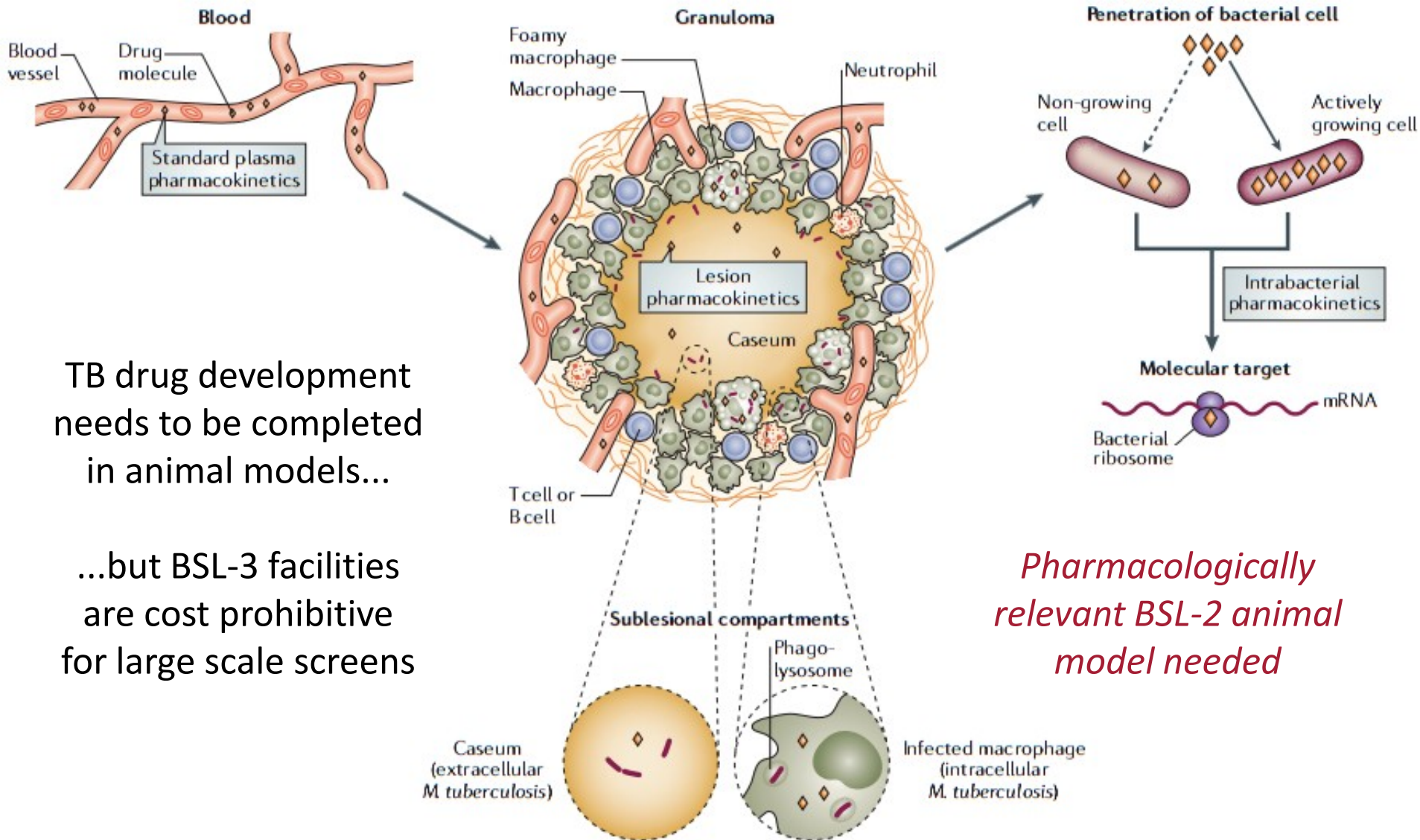
Russell D. Berg and Lalita Ramakrishnan

Cell
PRESS

GAO-08-108T

Animal models are essential to TB drugs

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TB drug development needs to be completed in animal models...

...but BSL-3 facilities are cost prohibitive for large scale screens

Pharmacologically relevant BSL-2 animal model needed

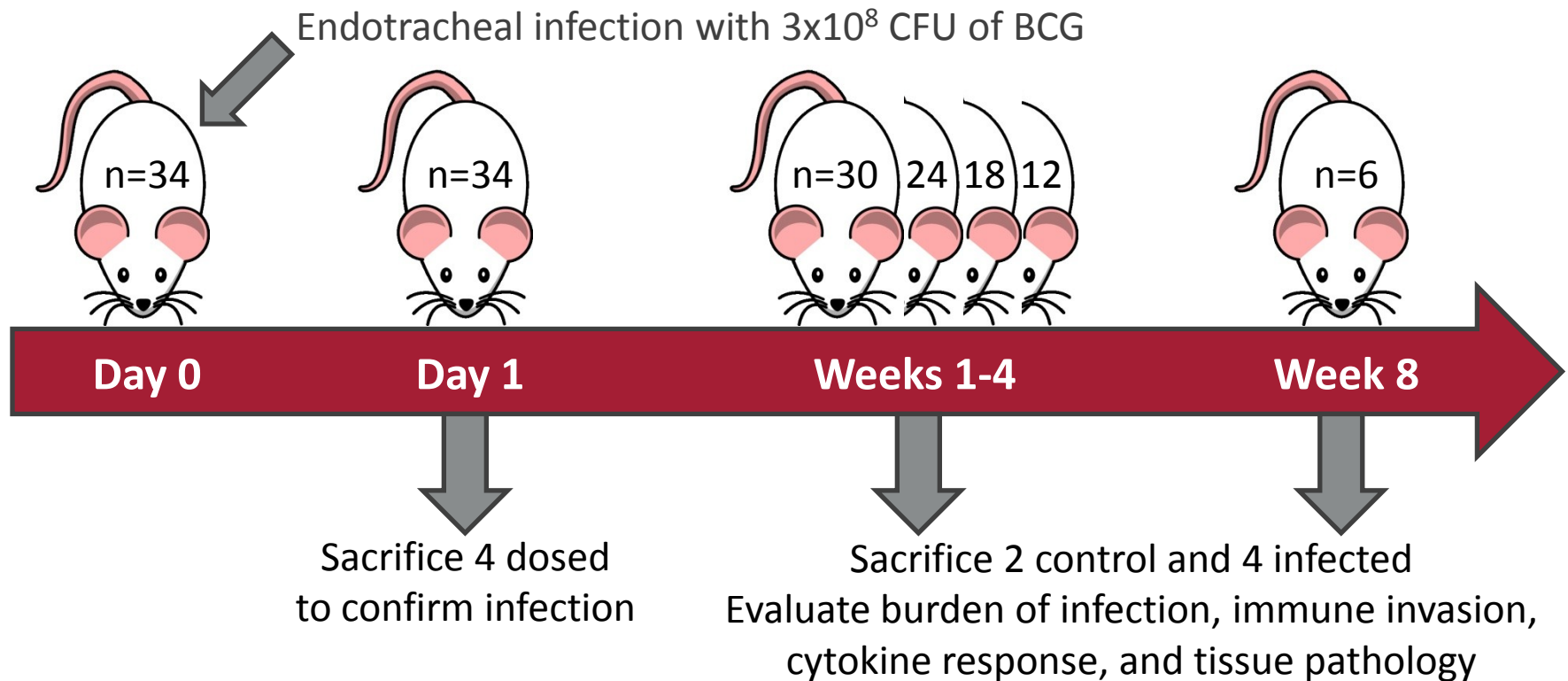
Study design and goals

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M. bovis BCG: BSL-2 vaccine strain, 99.9% sequence identity to Mtb

Endotracheal infection: reproducible, controllable lung infection

Wistar rats: pharma workhorse, outbred for genetic variability



Infection is robust and sustained

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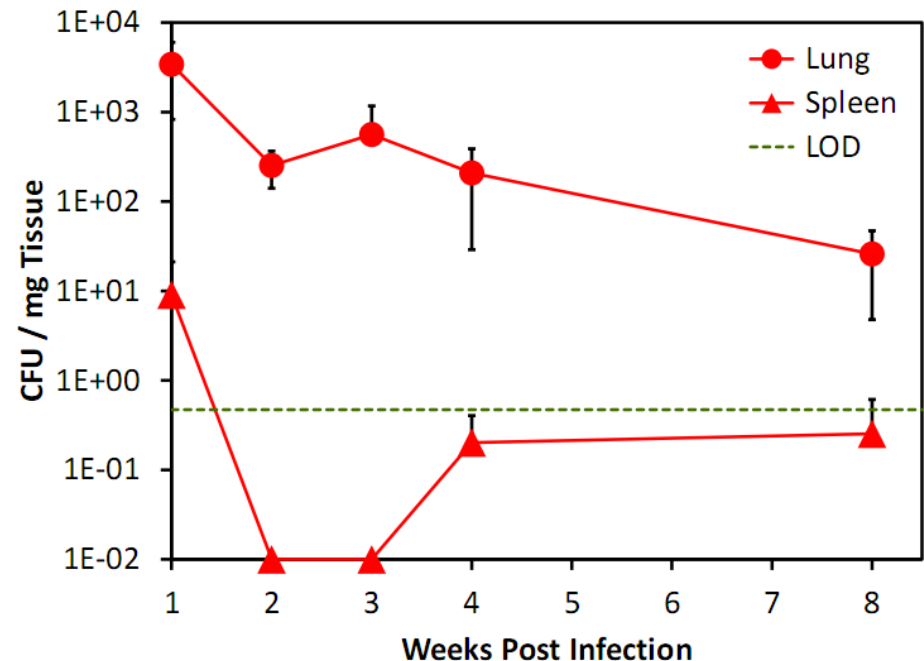
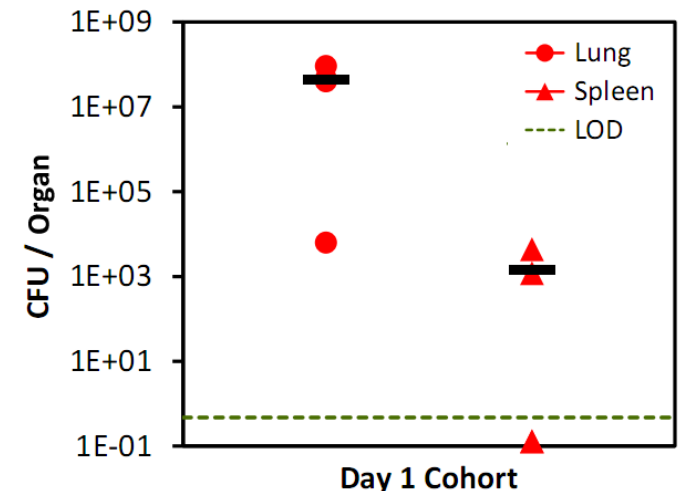
Infection confirmed at day 1: all CFU+

Infection success rate of at least 85%

- 20 of 24 dosed animals were CFU+
- 6 of 26 dosed animals were spleen CFU+
- One CFU- animal confirmed infected by qPCR

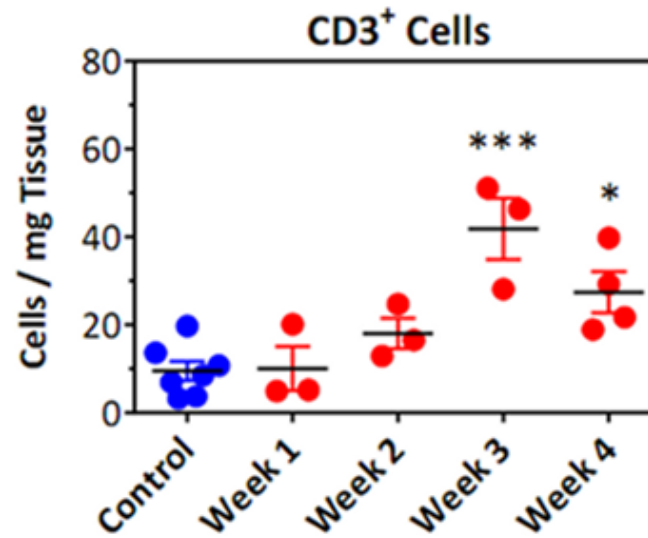
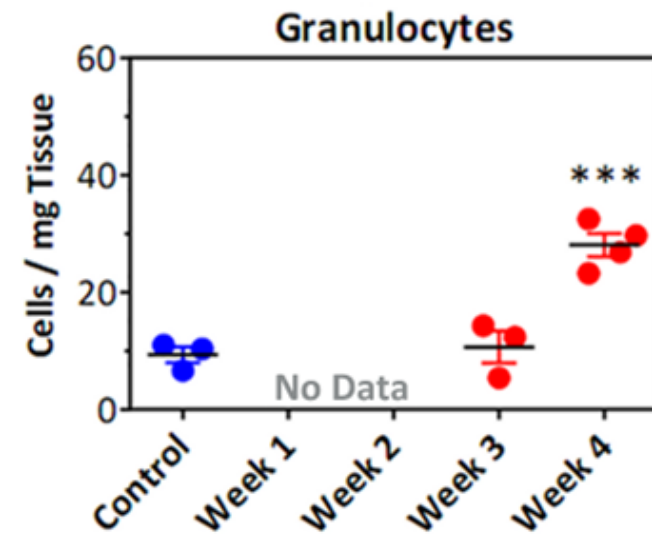
Sustained CFU load through week 8

Cohort	Dosed	CFU +	CFU -	Success
Day 1	4	4	0	100%
Week 1	4	3	1	75%
Week 2	4	3	1	75%
Week 3	4	4*	0	75%
Week 4	4	4	0	100%
Week 8	4	3	1	75%
Total	24	21	3	87.5%



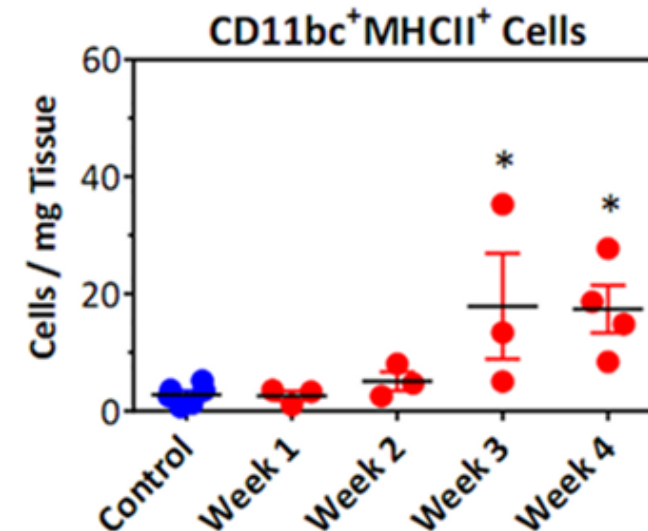
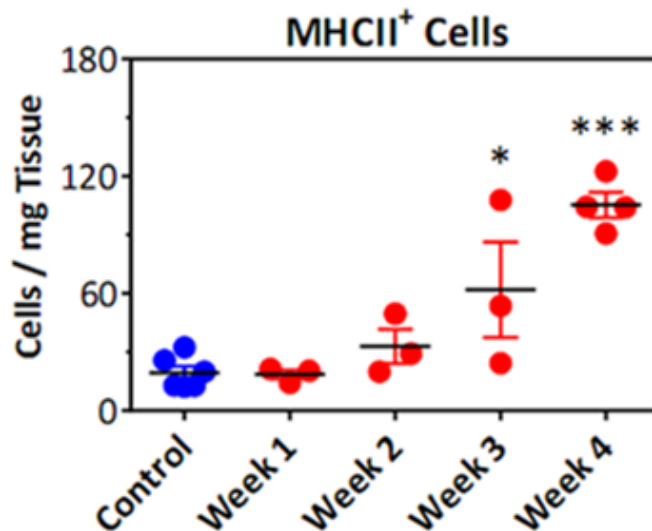
Lung immune infiltration is significant

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Granulocytes:
innate immune
cells (neutrophils)

CD3⁺: adaptive
immune T cells

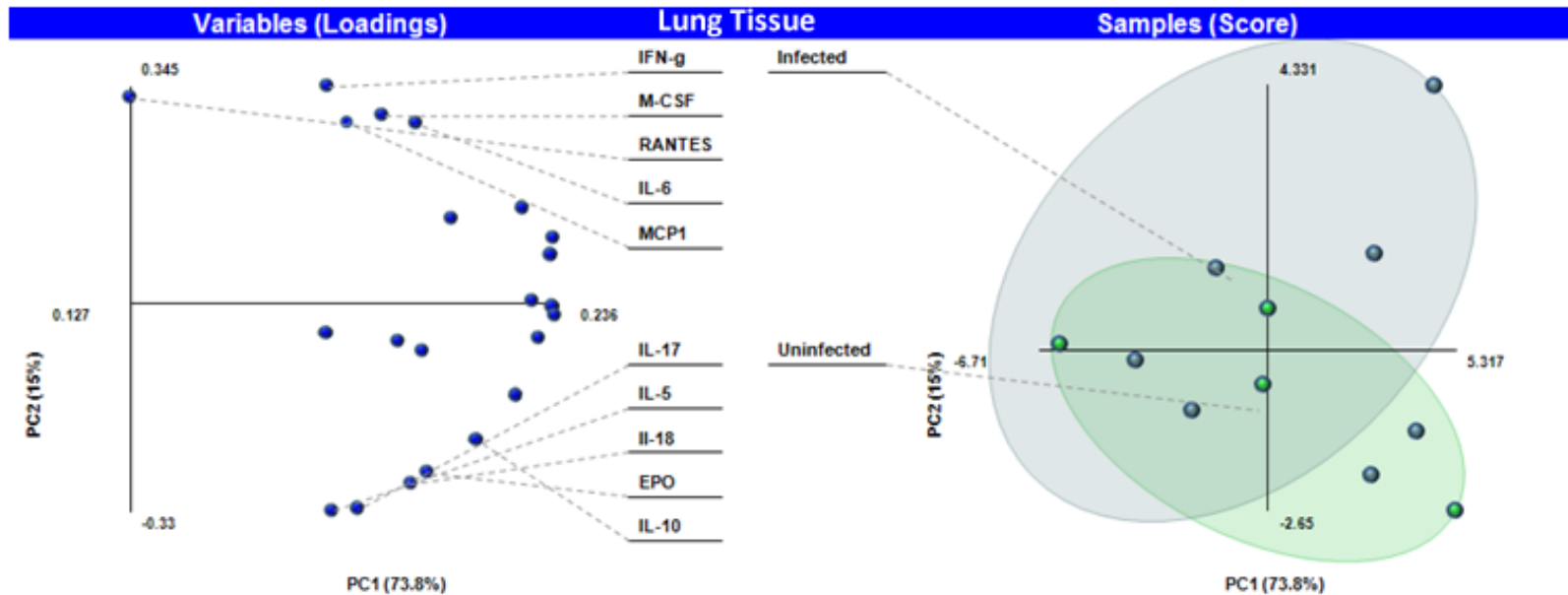
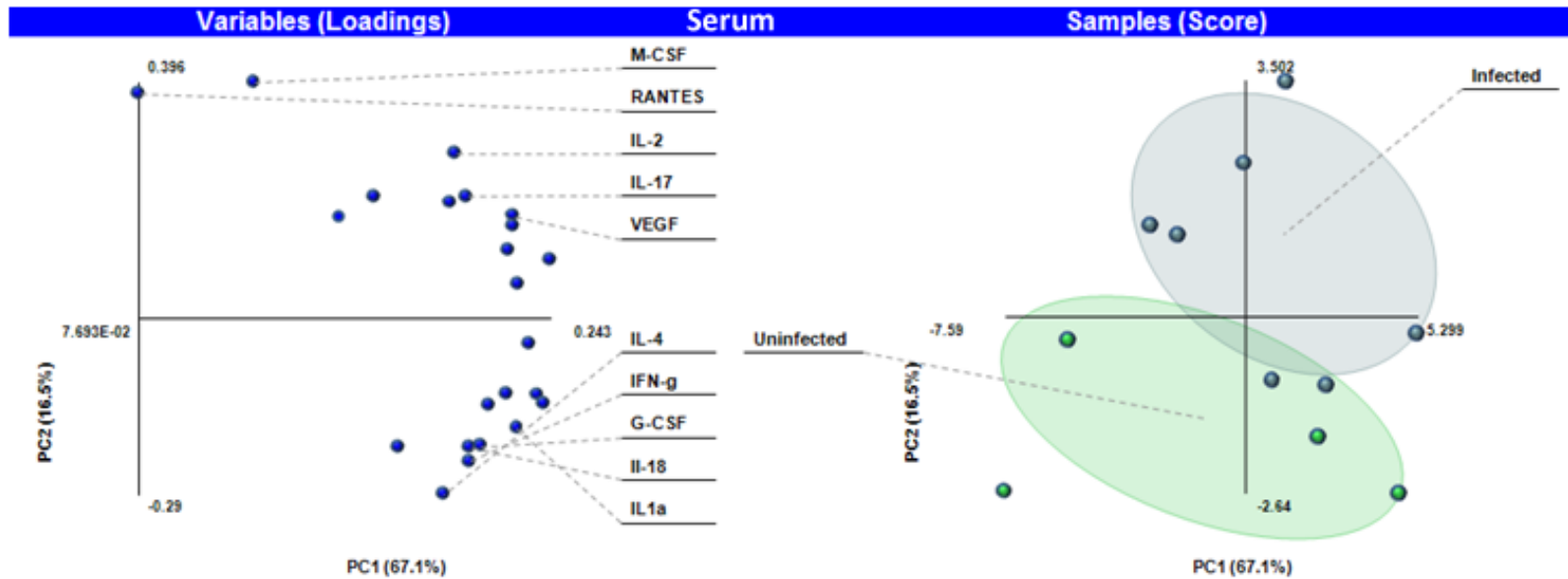


MHCII⁺: antigen
presenting cells

CD11bc⁺MHCII⁺:
lung-derived antigen
presenting cells

Cytokine response peaks late

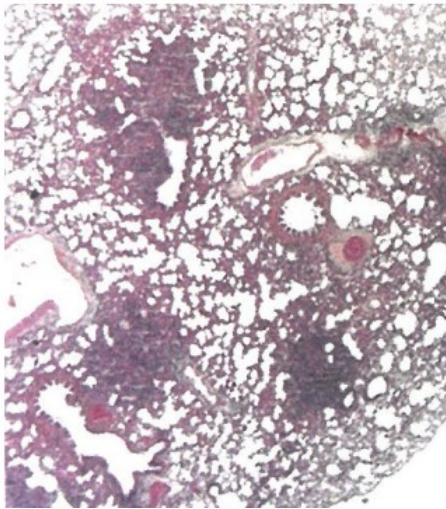
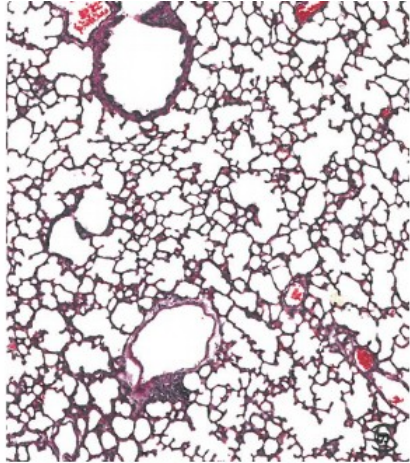
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Significant lung inflammation and pathology

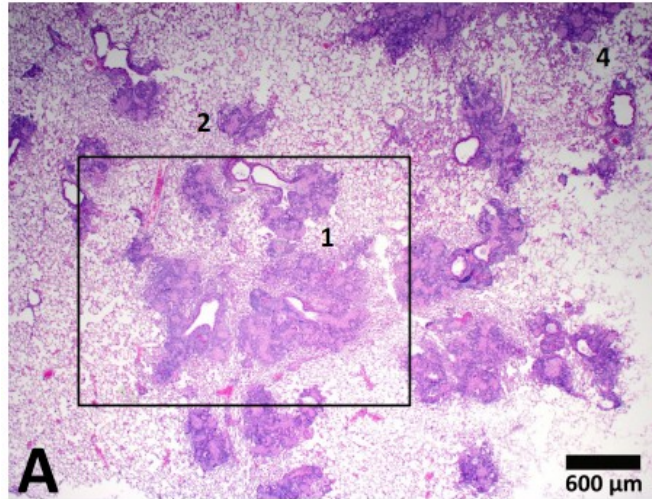
25

Control rat lung

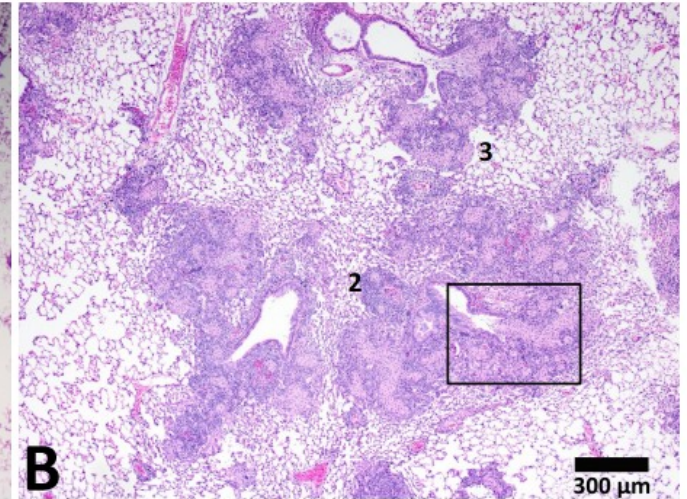


Mtb infection week 2

1 week post infection – representative micrographs

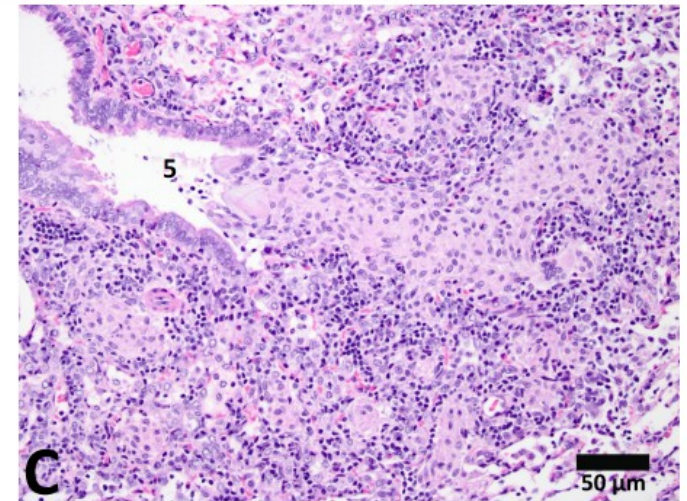


(A) 2x



(B) 4x

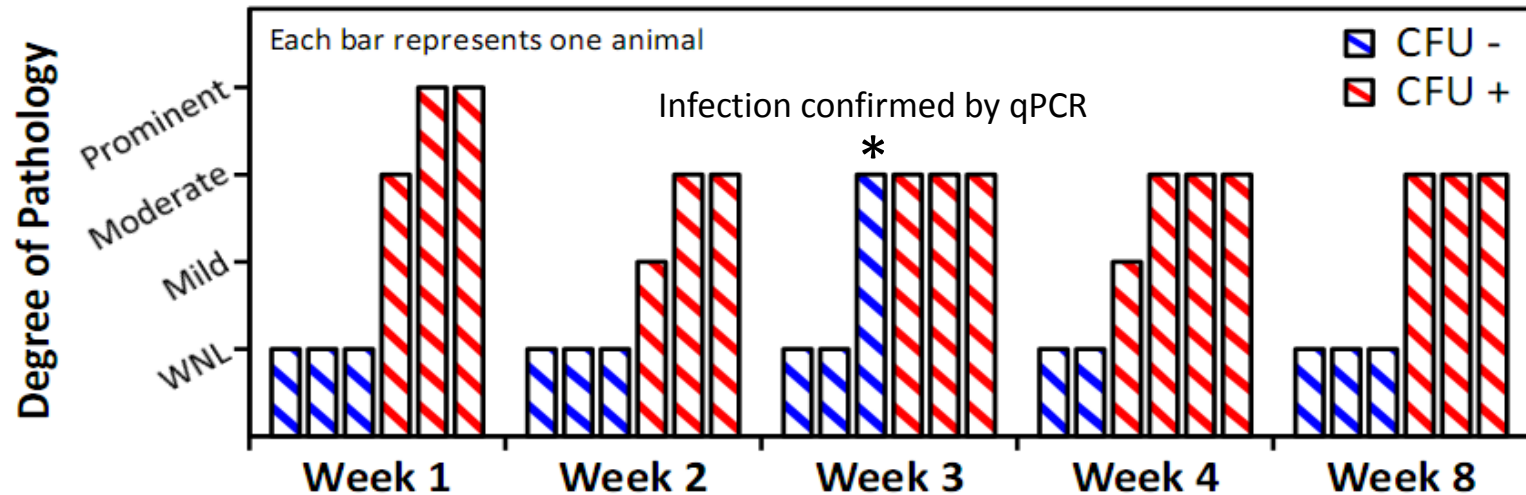
(C) 20x



1. Increased cellularity
2. Coalescing granulomas
3. Peribronchiolar location
4. Scattered small granulomas
5. Bronchiolar attenuation

Pathology is prominent throughout infection

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Pathology remains high even as bacterial burden drops off

Several key features recapitulate the human response to Mtb

- Presence of multinucleated giant cells
- Formation of well organized granuloma and mineralization foci
- Breakdown of bronchiolar wall and invasion into the air space

Model validated – do modified nucleosides serve as biomarkers?

Urine collection and processing

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Modified metabolic cage

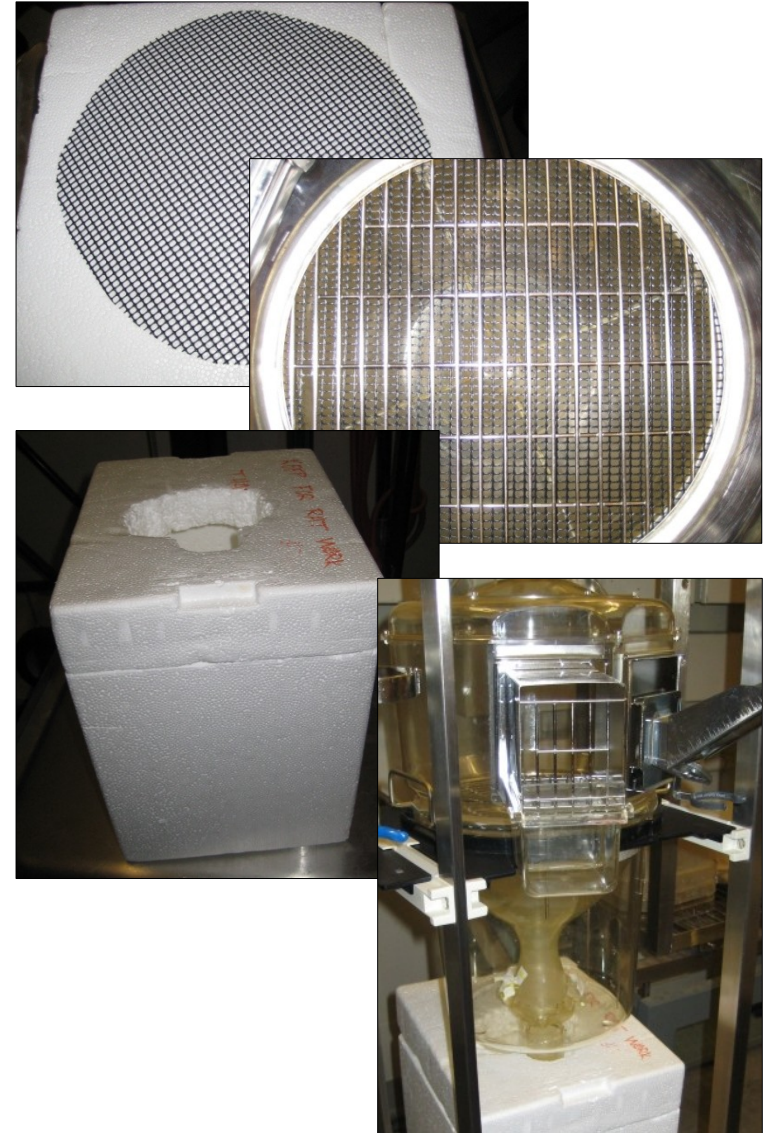
- Mesh screen under floor (0.2 mm)
- Collection tubes suspended in dry ice
- Flash frozen urine

Overnight (8 – 12 hour) collection

- Fasting, unrestricted water
- Volumes from 4 to 12 mL

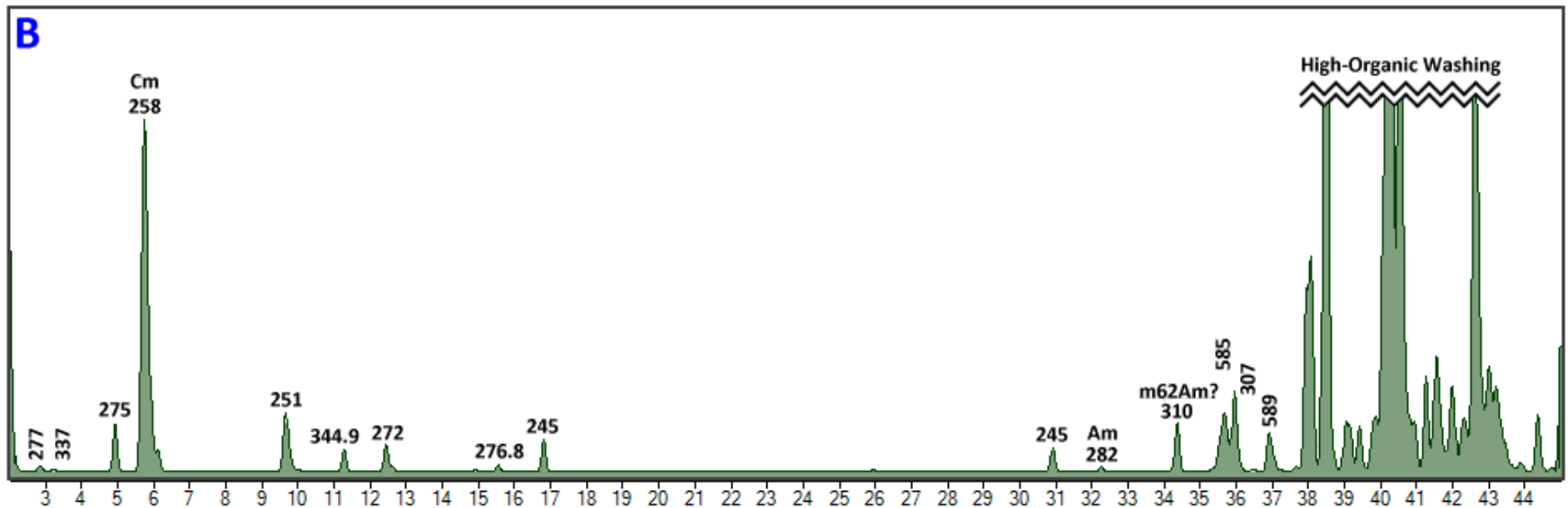
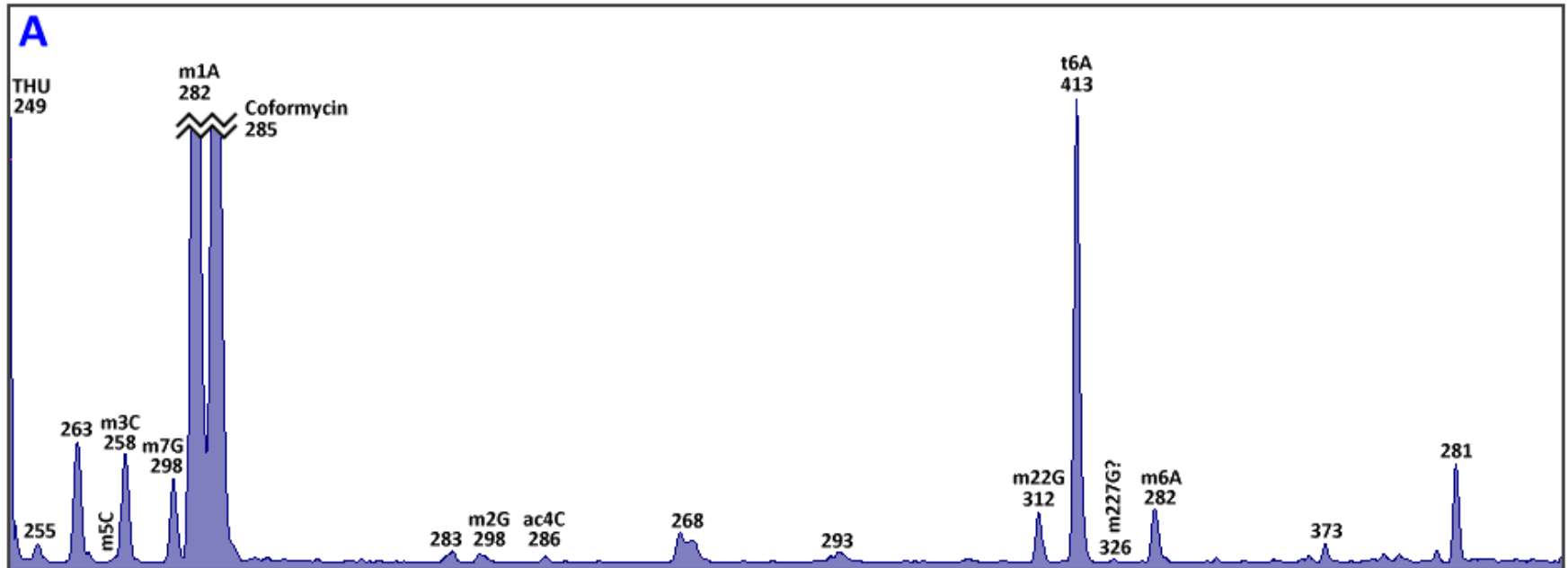
Minimal sample processing

- Thaw on ice
- Antioxidant cocktail
- Centrifuge and aliquot
- Benzonase digest
- 10 kD MW filter



Nucleosides are common in urine

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Introduction

Pathogenesis

Diagnosis

Therapy

Contributions

Nucleoside profile does not predict infection

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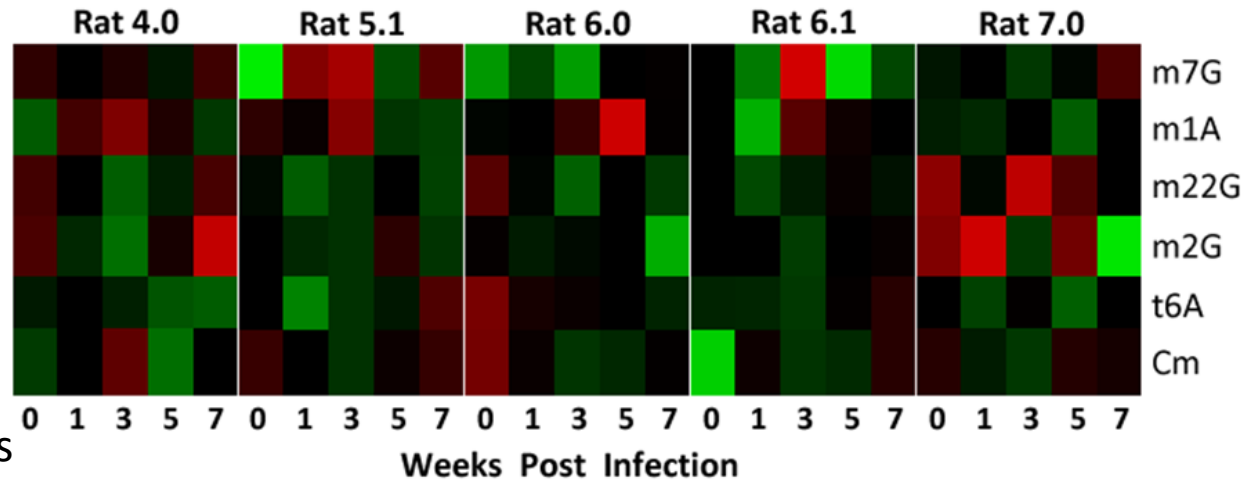
No species unique to infected

No species unique to control

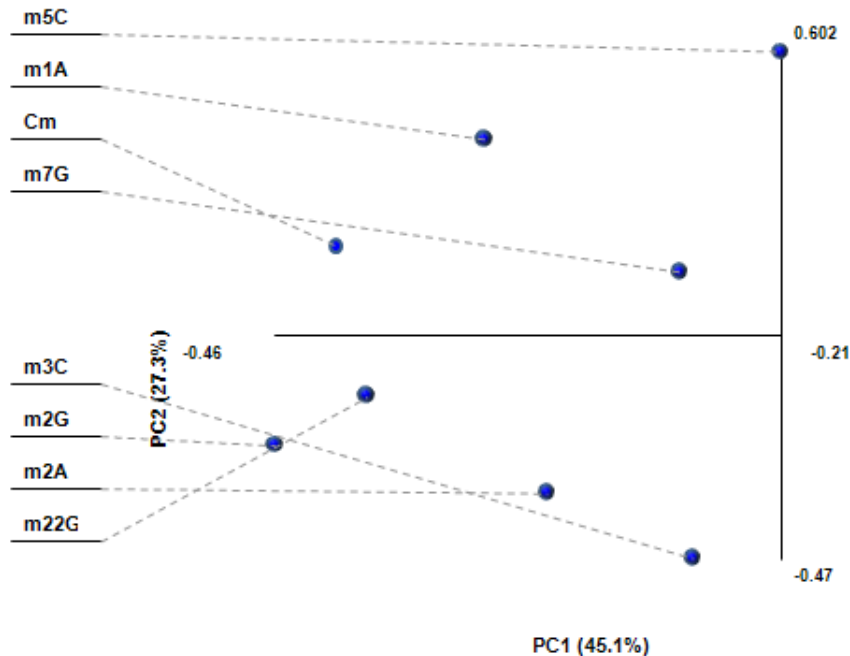
No BCG-specific species

Verified species do not form
a consistent pattern

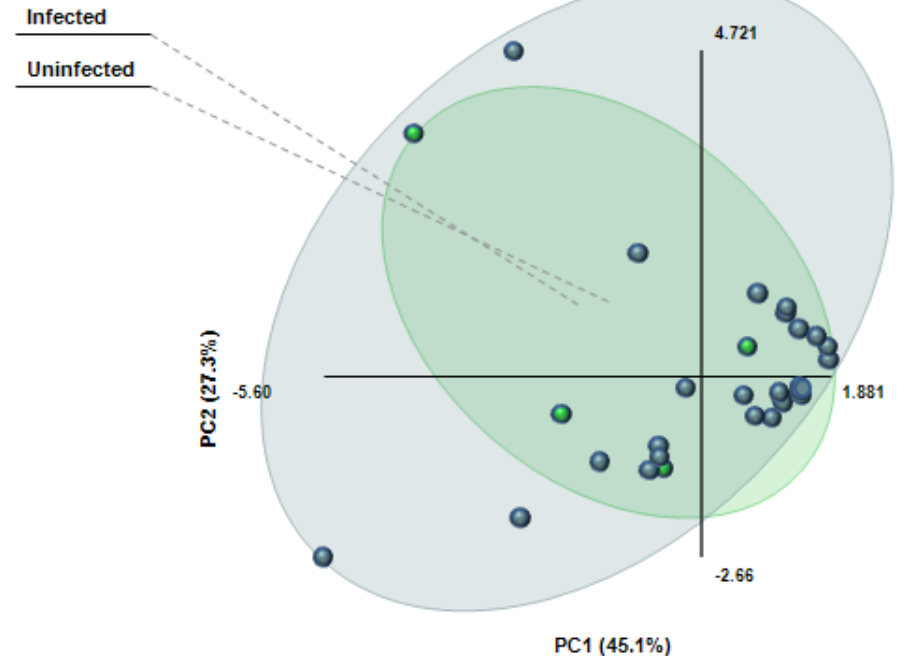
Individual variability dominates



Variables (Loadings)



Samples (Score)



Summary and future directions

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First pharmacologically useful BSL-2 animal model of Mtb

- Rat is ideal for size, ease of use, cost, and availability of reagents
- Disease is consistent even in outbred animals – human relevance

New insights into granuloma formation

- BCG lacks ESAT-6, which some reports have implicated in formation
- Most mice do not form granulomas, even with ESAT-6
- Mice lack MMP-1, but Wistar rats have it – further evidence for importance

First report of modified nucleoside profiling for infection biomarkers

- Large number of species present; patterns may emerge
- Sensitivity advances may reveal species below our limit of detection

New platform for testing RNA modifications as therapeutic targets

Our model will accelerate TB drug and diagnostic development

The role of bacterial DNA phosphorothioation in resistance to oxidative and antibiotic stresses

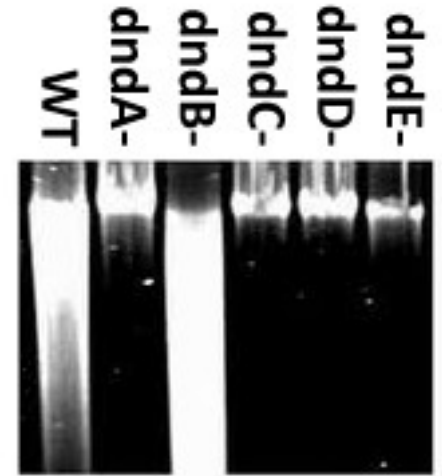
In collaboration with Michael DeMott, Bo Cao, Stefanie Kellner, Megan McBee, Emily Kolenbrander, and Aislyn Schlack

DNA degradation, sulfur, and *dnd* genes

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DNA degradation phenotype in *S. lividans*

- Genomic DNA subjected to Tris electrophoresis
- Knockouts of an uncharacterized gene cluster
- Phenotype could be ablated or enhanced

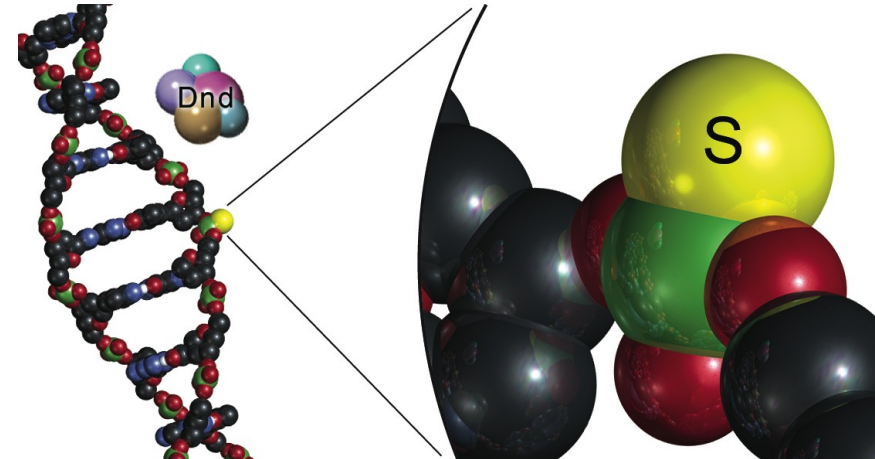


Caused by DNA phosphorothioation (PT)

- Phosphate oxygen replaced by sulfur
- Previously known synthetically
- Two diastereomers, *Sp* and *Rp*

Found in >200 bacterial species

- 5-gene cluster *dnd*
- Distantly related organisms
- Mobile genetic elements
- Many clinical isolates



Xu *et al.* 2009 | Wang *et al.* 2007 | Makarova *et al.* 2013

PT as a restriction-modification system

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PT serves as a restriction system

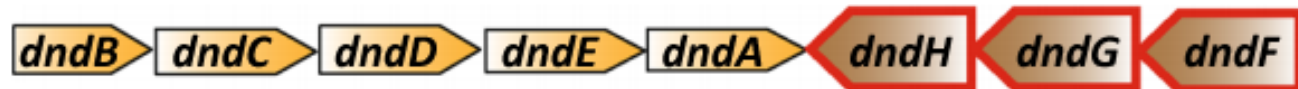
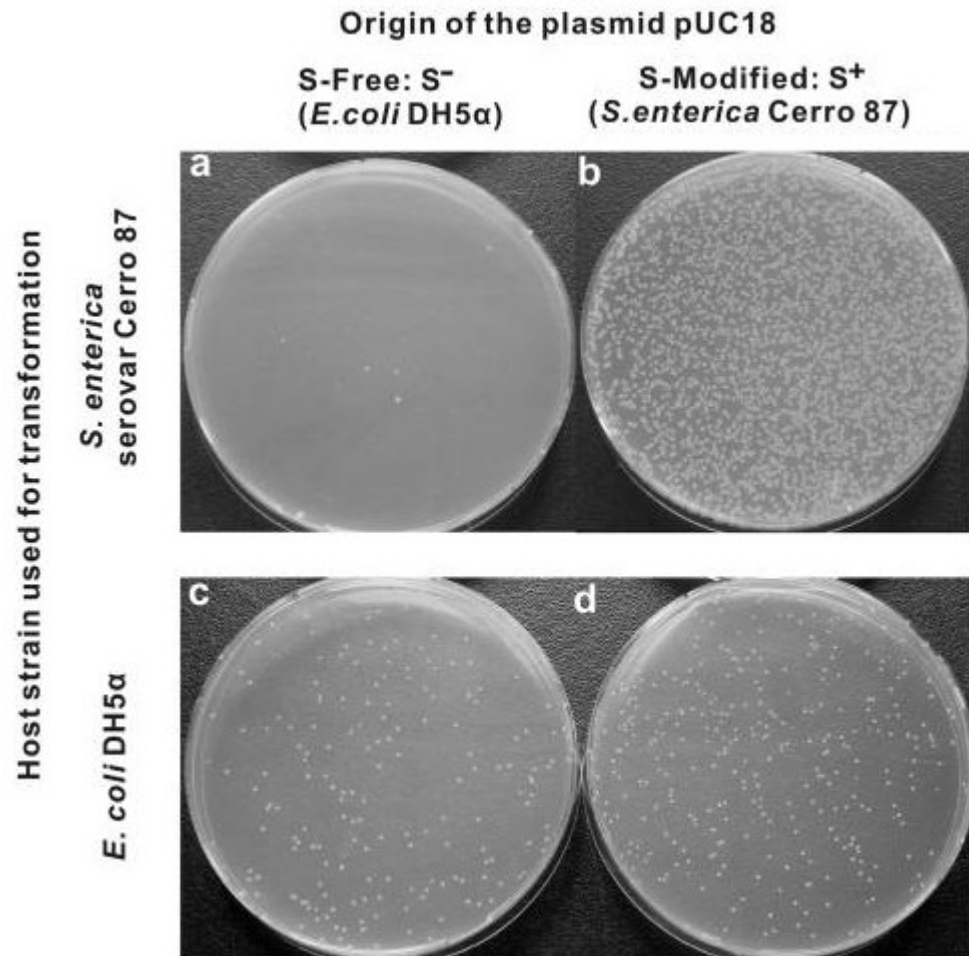
- DNA lacking PT is not taken up
- Cells lacking PT take up DNA

Additional *dnd* genes

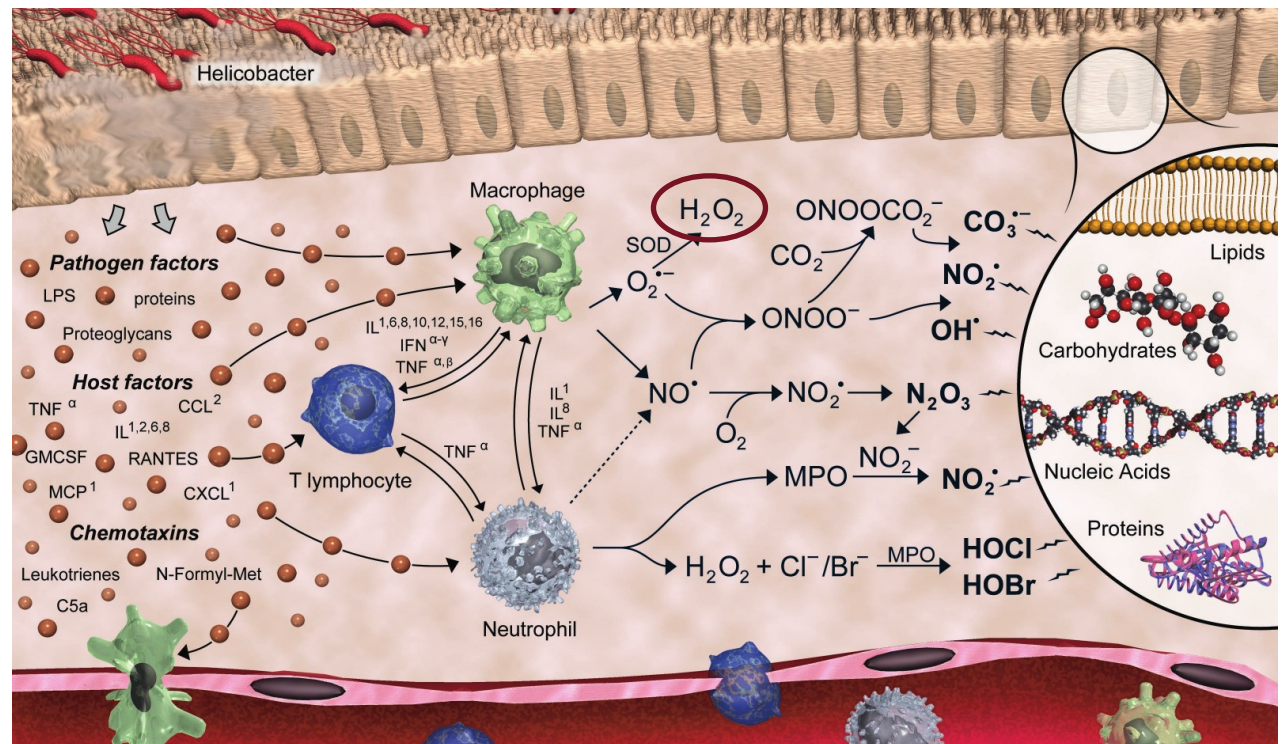
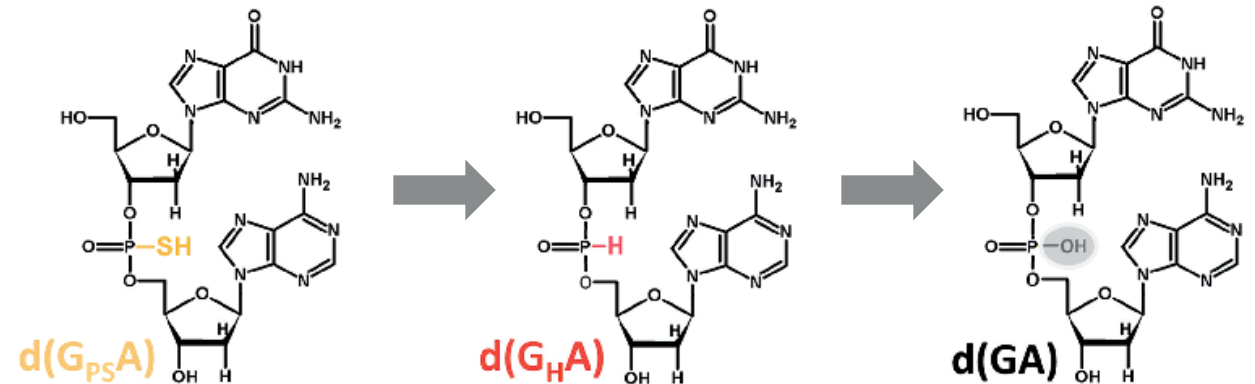
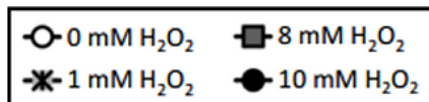
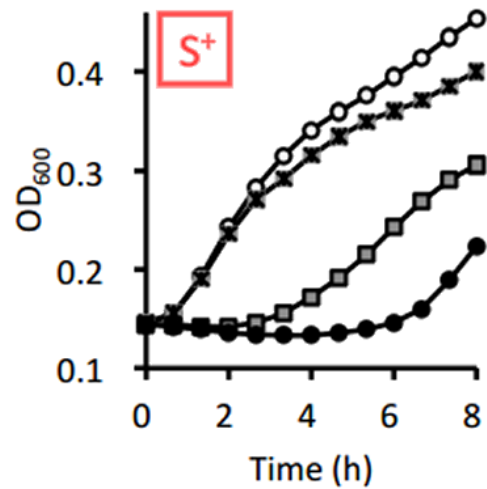
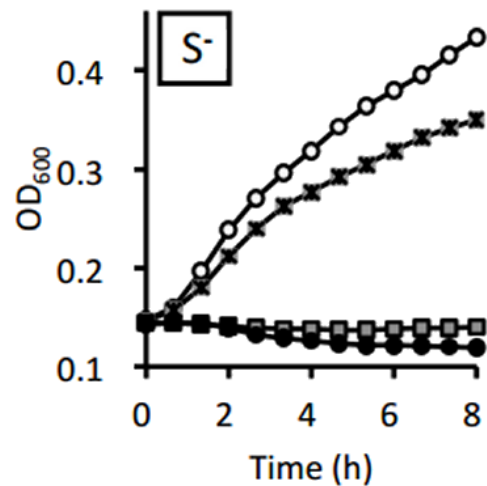
- 3 gene cluster *dndF-H*
- Clustered with *dndA-E*
- Located on the same elements

Most species lack restriction

- More than half lack *dndF-H*
- *dndF-H* toxic without PT
- Other function for PT alone?



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Xie *et al.* 2012 *Nucleic Acids Res* | Jeff Dixon

Organisms and assays

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Organism	PT Source	Restriction
<i>Citrobacter rodentium</i>	Artificial	No
<i>Salmonella enterica</i>	Native	Yes
<i>Streptomyces lividans</i>	Native	No

C. rodentium Agents

- H_2O_2
- Streptomycin
- Kanamycin
- Gentamycin

S. enterica Agents

- H_2O_2
- Kanamycin
- Gentamycin
- Spectinomycin

S. lividans Agents

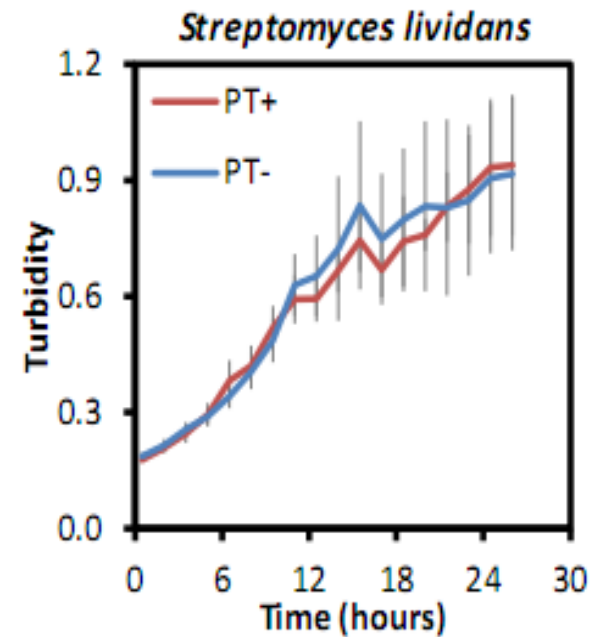
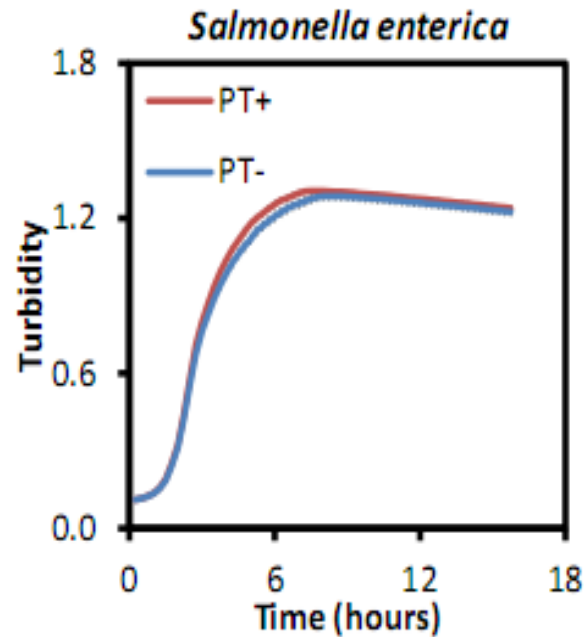
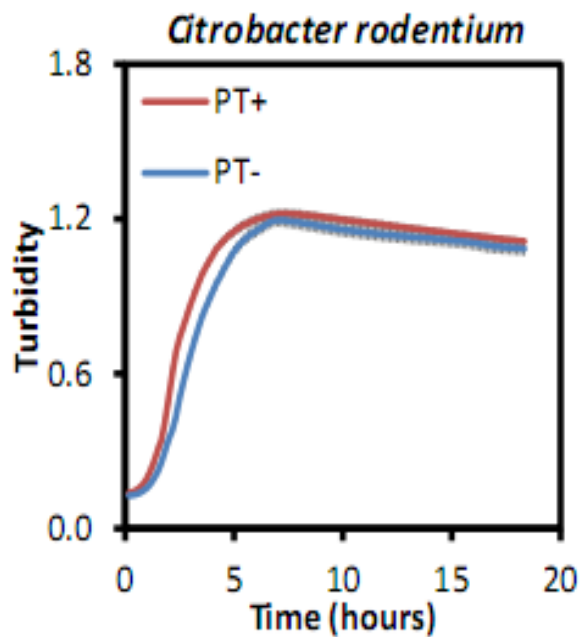
- H_2O_2
- Ampicillin
- Penicillin

Growth curves show inhibition; platings show active killing

Representative data are shown for each organism; highly reproducible

PT genotypes do not alter growth rate

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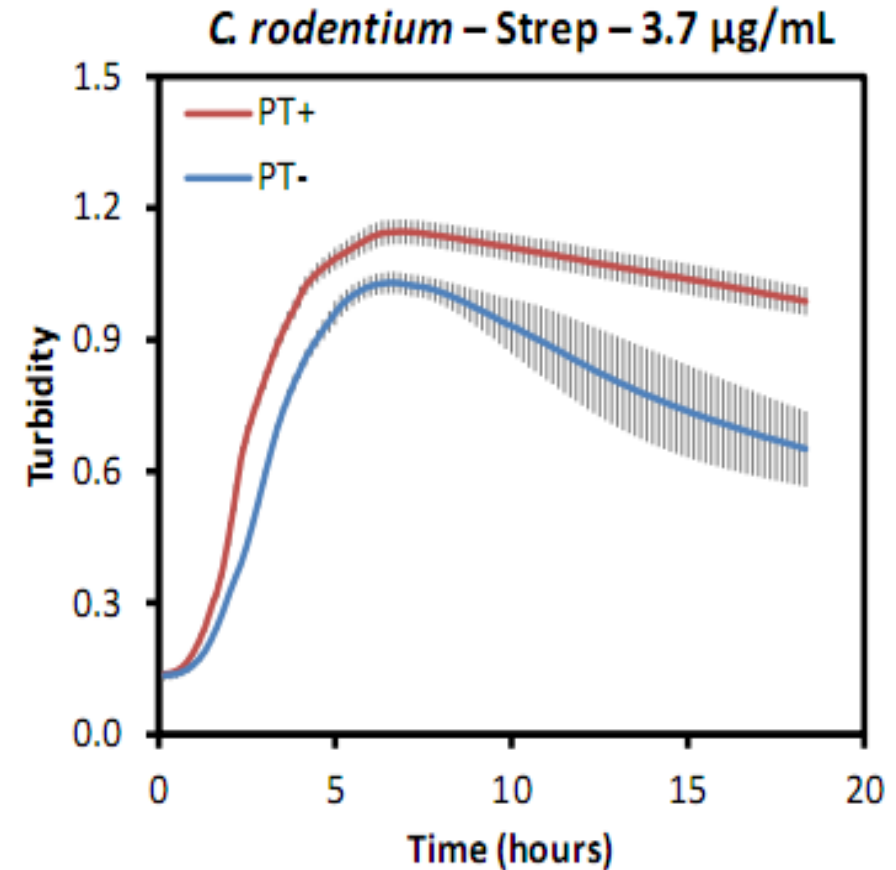
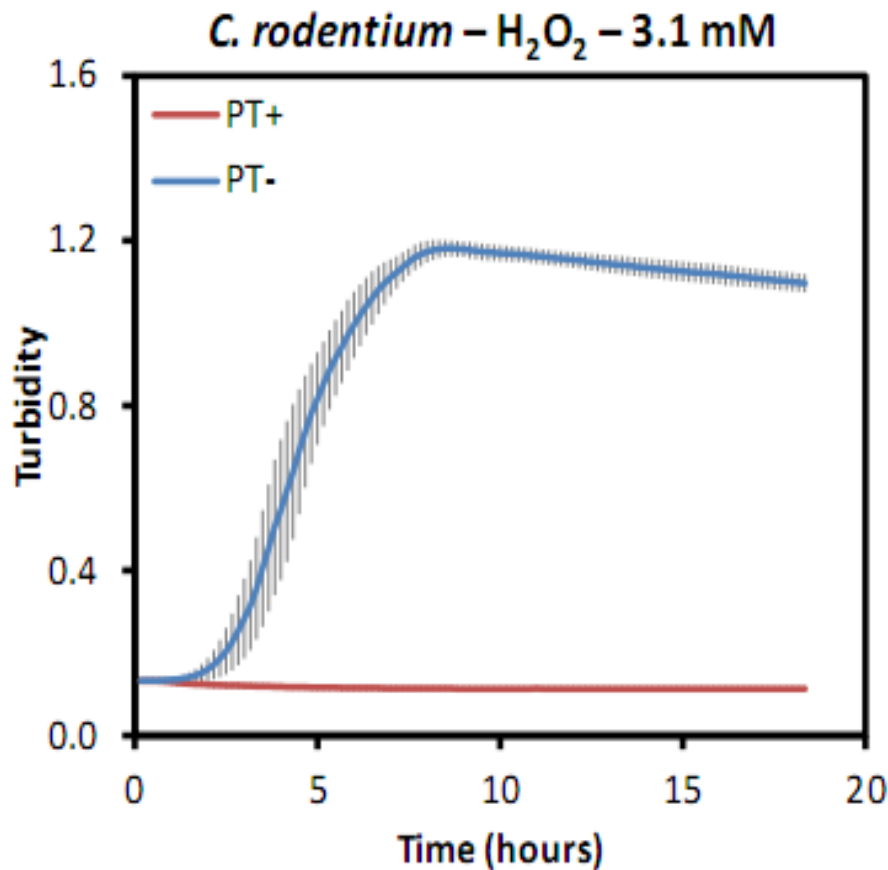


Artificial PT confers only antibiotic resistance

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PT+ strain is much more sensitive to H_2O_2 stress

PT+ strain is more resistant to antibiotic stress

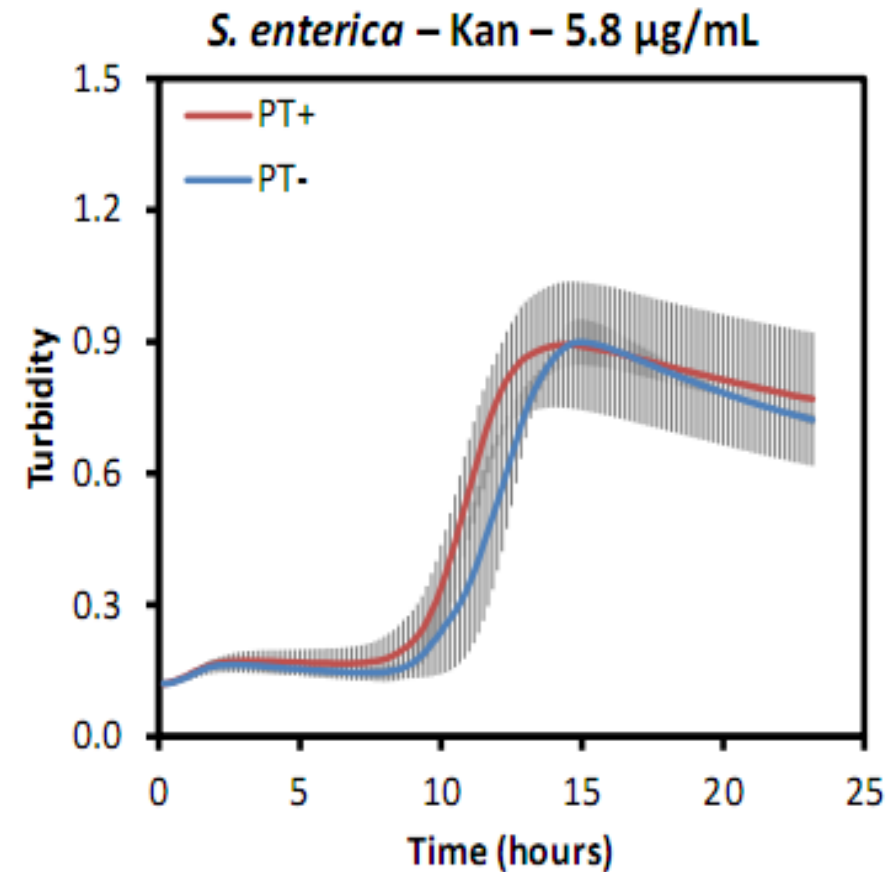
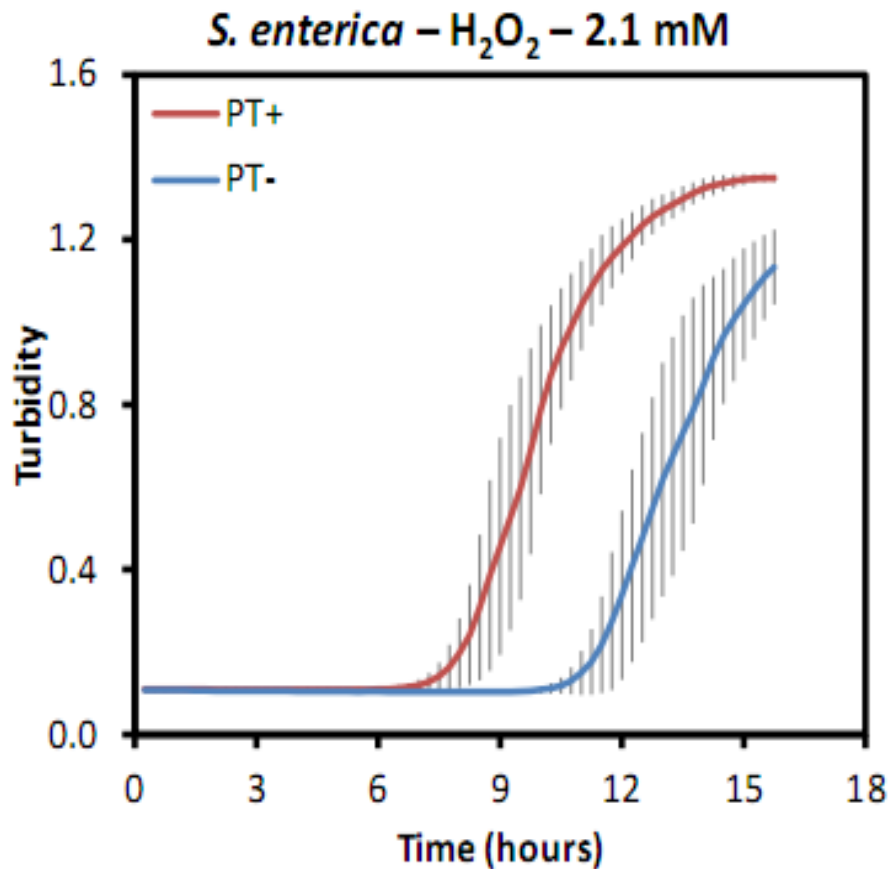


Native PT and restriction: only oxidative resistance

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PT+ strain is more **resistant** to H_2O_2 stress

Strains are **equivalent** in their response to antibiotic stress

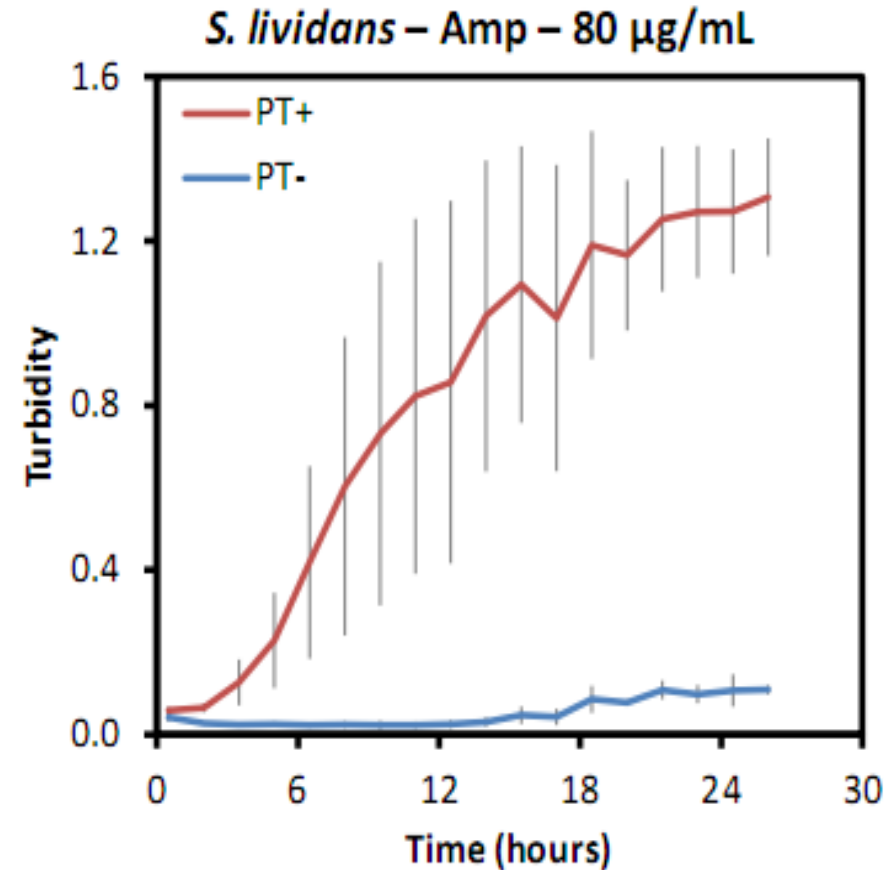
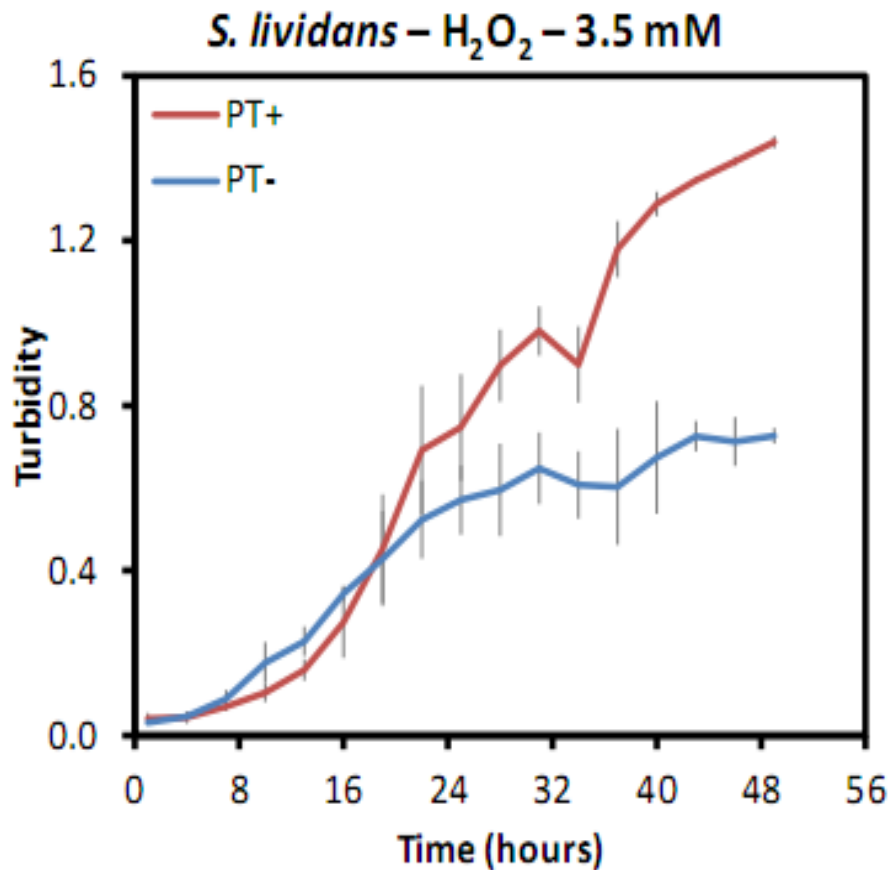


Native PT lacking restriction: complete resistance

39

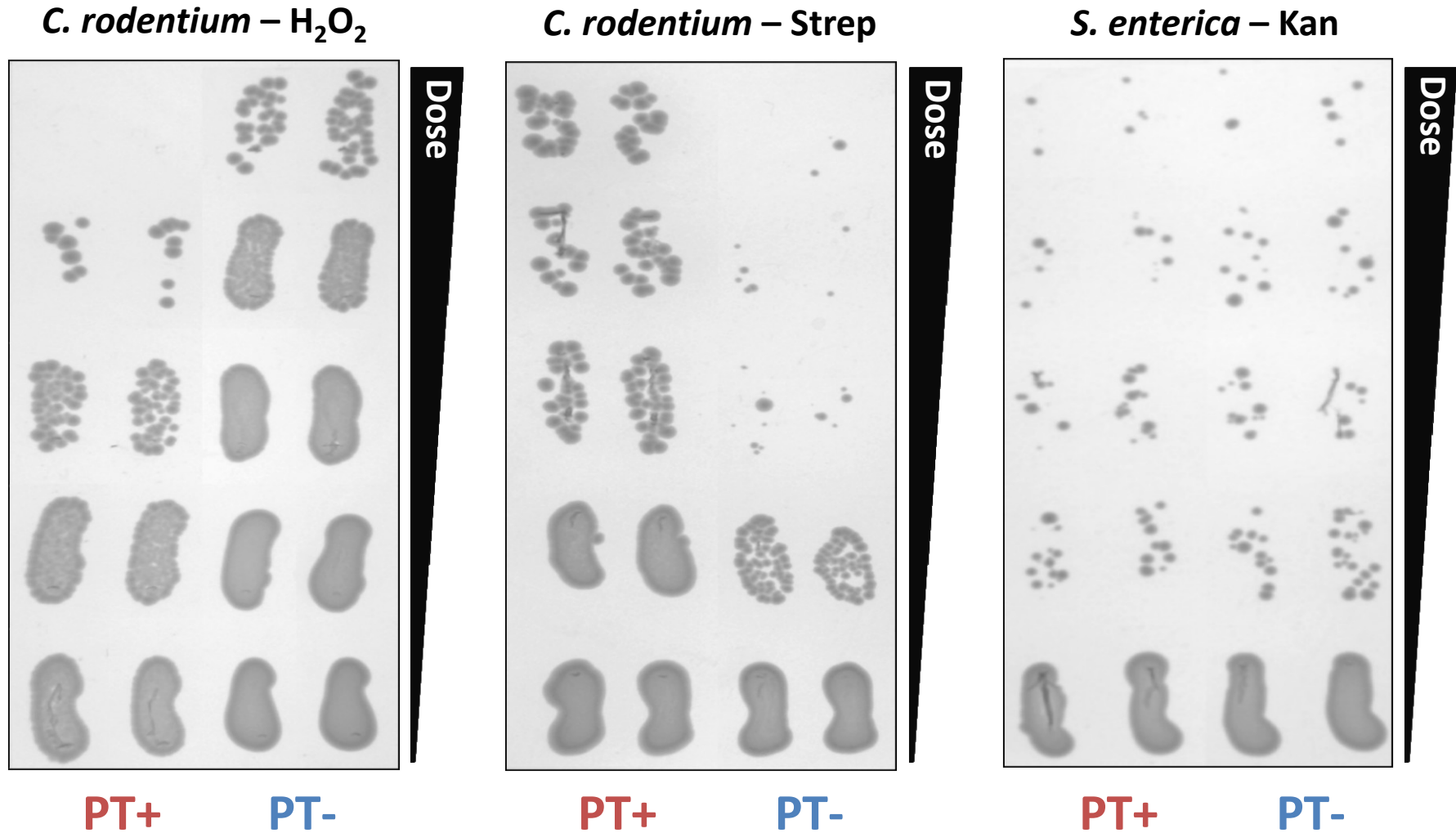
PT+ strain is more **resistant** to H_2O_2 stress

PT+ strain is much more **resistant** to antibiotic stress



PT effects are mediated by cell death

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Summary and future directions

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First systematic profiling of the effect of PT

First report of PT conferring antibiotic resistance

- Significant effect: more than doubles the minimum inhibitory concentration
- Substantial growth advantage might allow PT-positives to take over

First report of organism- and toxicant-dependent PT effect

- Not all antibiotics causing oxidative stress?
- H_2O_2 not causing oxidative stress?

Many potential human health impacts

- PT widespread in clinical isolates – should we be testing for it?
- Can targeting PT synergize with antibiotics or immune system?
- Gut microbes known to harbor PT – role in disease?

Phosphorothioation may serve as a novel therapeutic target

Summary of contributions

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First report of RNA modifications involved in bacterial pathogenesis

- New targets for antibiotic development
- Possible prophylaxis to prevent infection

First BSL-2 model of TB suitable for drug and diagnostic development

- Proof-of-concept biomarker study
- Suitable for determining granuloma targeting

First report of PT DNA conferring transferable antibiotic resistance

- Possibly important clinical parameter
- New target for antibiotic adjuvant

Pathogenesis

- Establish infection
- Target: stop disease



Diagnosis

- Confirm infection
- Target: faster therapy



Therapy

- Clear infection
- Target: cure disease

RNA and DNA modifications are critical in fighting bacterial disease

Important acknowledgments

43

Thesis Committee

- Prof. Peter Dedon (Advisor)
- Prof. James Fox (Chair)
- Prof. Uttam RajBhandary
- Dr. Pete Wishnok

Dedon Laboratory

- Yok Hian Chionh
- Dr. Michael DeMott
- Chen Gu
- Dr. Ramesh Indrakanti
- Watthanachai Jumpathong
- Dr. Stefanie Kellner
- Dr. Megan McBee
- Dr. Joy Pang

Dedon Lab Alumni

- Dr. Clement Chan
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- Dr. Erin Prestwich
- Dr. Dan Su

UROP Students

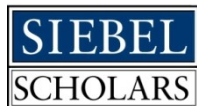
- Emily Kolenbrander
- Aislyn Schlack
- Sasilada Sirirungruang

Division of Comparative Medicine

- Dr. Zhongming Ge
- Melissa Mobley
- Dr. Sureshkumar Muthupalani
- Dr. Nicola Parry
- Joanna Richards
- Dr. Alexander Sheh
- Gladys Valeriano

Funding Sources

- NSF Graduate Research Fellowship
- NIEHS Training Grant
- Siebel Scholars Fellowship



Final thoughts and words

44

Graduate school is hard [citation needed]

Kimberly Russell



1964 – 2009

Shirley Russell



1942 – 2012

Alexander McAdams



Peter Dedon



Thank you all from the bottom of my heart!