What is the Biggest *inadvertent* Biology *Experiment ever Performed: That with the Grandest Scale?*

- *Rise and persistance of antibiotic resistant strains of human pathogens is a public health nightmare*
- In this respect hospitals are on of the scariest places to be



Oct, 22, 2007

Hospital screens for super bug

St. Joseph taking steps to isolate MRSA infections

MARY LANE GALLAGHER

BELLINGHAM — St. Joseph Hospital has just begun screening all intensive-care patients for the drug-resistant staph infection M n an effort to stop the spread of the dangerous bacteria.

The Centers for Disease Control released a report last week that estimates MRSA is responsible for about 94,000 serious infection each year and 19,000 deaths. Methicillin-resistant Staphylococcus aureus is a type of souped-up staph bacteria that resists the antibiotics traditionally used to fight staph infections.

MRSA (pronounced "mer-sa") infections commonly show up as small pimples or boils on the skin. But invasive MRSA that gets ir the body through a surgical wound, for example, can be deadly.

It's difficult to know how widespread the bug is in Washington state because MRSA infections don't have to be reported to state h authorities. But there have been reports of MRSA in Whatcom County since at least 2003, said Greg Stern, Whatcom County hea officer.

Nearly half, 47 percent, of the staph infections confirmed in the laboratory at St. Joseph Hospital were MRSA in 2006, hospital off say.

But that may not tell the whole story, either, because not all patients are tested for the presence of MRSA, which can live in some nose or folds of skin without causing an infection.

'It's very difficult to determine how big of a problem it is." said Joni Och, director of the hospital's center for health-care improveme 'There may be colonized patients that show no signs or symptoms. It's kind of difficult to put your hands on."

The hospital routinely tests heart surgery patients whose lives could be jeopardized by a MRSA infection around the heart. Other surgeons can order a MRSA test on a patient, but not all surgery patients are screened.

The hospital just started screening all patients coming into the intensive-care unit on the recommendation of a national quality eff the Institute for Healthcare Improvement.

A patient who is found to have the bacteria in the body is put in a single-patient room with a sign outside telling all those who enter wear a gown and gloves to help stop the spread of the infection.

Some health-care advocates say hospitals should fight the infection by testing all patients, as have European countries who have nearly eradicated MRSA.



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Table 1. Dates of deployment of representative antibiotics and herbicides, and the evolution of resistance. [Source (75)].

EVOLUTION OF RESISTANCE TO ANTIBIOTICS AND HERBICIDES

Antibiotic or herbicide	Year deployed	Resistance observed					
Antibiotics							
Sulfonamides	1930s	1940s					
Penicillin	1943	1946					
Streptomycin	1943	1959					
Chloramphenicol	1947	1959					
Tetracycline	1948	1953					
Erythromycin	1952	1988					
Vancomycin	1956	1988					
Methicillin	1960	1961					
Ampicillin	1961	1973					
Cephalosporins	1960s	late 1960s					
Science 293: 1786 Sept. 7, 2001							

How do antibiotic resistance genes/alleles confer resistance?

How do antibiotic resistance genes/alleles confer resistance? BMJ VOLUME 317 5 SEPTEMBER 1998 www.bmj.com



Fig 1 Four major biochemical mechanisms of antibiotic resistance



BMJ VOLUME 317 5 SEPTEMBER 1998 www.bmj.com

Where do these antibioticresistance alleles/genes come from? Antibiotic resistance acquired by two fundamental mechanisms:

- Sustain a mutation that confers resistance in a gene already present in the bacteria's genome: this mechanism explored in the mutagenesis lab
- Acquire a new gene from somebody else via horizontal gene transfer: this strategy mechanism explored the next bacterial genetics lab

Target site alterations $rif^{s} \rightarrow rif^{r}$ (rif = the antibiotic rifamycin = rifampin)



As tuberculosis took off in Russia in the 1990s, one antibiotic after another failed; the state of Tomsk responded with an epidemic-fighting strategy pioneered by the Boston nonprofit Partners in Health. Deaths have declined, but resistance to drugs remains high

Rifampin (rifamycin) is a major drug used in the treatment of tuberculosis infections, and increasing rifampin resistance represents a worldwide clinical problem. *Resistance to rifampin is caused by mutations in the rpoB gene, encoding the betasubunit of RNA polymerase.*

Tough bug. Mycobacterium tuberculosis (red) likes nothing better than to be ingested by a macro- phage, its usual home.



• The rifamycin antibacterial agentsrifampin (also known as rifampicin) function by binding to and inhibiting bacterial RNA polymerase

• The wildtype *Mycobacterium tuberculosis* RNA polymerase is 1000X more sensitive to this antibiotic than the wildtype *E. coli* RNA polymerase.

• Rifamycins are first-line antituberculosis agents, and are among

the few antituberculosis agents that can kill nonreplicating tuberculosis bacteria.

- For all major bacterial pathogens, including the tuberculosis pathogen, strains resistant to rifamycins have arisen
- Resistance to rifamycins involves substitution of residues within the rifamycin-binding site on bacterial RNAP, i.e., substitutions that directly decrease rifamycin binding

"What we really need," Rich (a Russian health professional) adds, "is a good, cheap, point-of-service test." Wealthier countries have access to polymerase chain reaction tests that monitor variable TB organism genes, signaling within 24 hours whether the strain is resistant to the first-line drugs isoniazid and rifampin (rifamycin). "

Xpert[®] MTB/RIF Two-hour detection of MTB and resistance to rifampicin.

Specific

• The Xpert MTB/RIF assay uses 3 specific primers and 5 unique molecular probes to ensure a high degree of specificity

• Assay targets the rpoB gene, which is critical for identifying mutations associated with rifampicin resistance

No cross reactions were observed with many other bacterial species tested, including a comprehensive panel of Mycobacteria

 PROBE D

 PROBE D

 PROBE C

 5" - GCACCAGCCAGCTGAGCCAATTCATGGACCAGAACAACCCGCTGTCGGGGTTGACCCACAAGCGCCCGACTGTCGGGCGCTG - 3"

 3" - CGTGGTCGGTCGGCGCGACAGCCCGGGTTAAGTACCTGGTCGGCGCACAGCCCCAACTGGGGTGTTCGCGGCGTGACAGCCCGCGAC

 PROBE B



Follow-up on rifR mutants We will follow up on our rifR mutations by determining the location and nature of mutatgenic changes that can confer resistance to the antibiotic without severely compromising the ability of RNA polymerase to perform its cellular function



Part 3: orient our PCR primers and sequence output with respect to this cartoon of the rpoB protein

Figure 1. The Rif-Resistant Regions of the RNAP b Subunit

The bar on top schematically represents the *E. coli* b subunit primary sequence with amino acid numbering shown directly above. Gray boxes indicate evolutionarily conserved regions among all prokaryotic, chloroplast,

archaebacterial, and eukaryotic sequences. indicate the four clusters where RifR mutations have been identified in E. coli. Mutations that confer RifR in E. coli and M. tuberculosis are indicated directly above (for E. coli) or below (for M. tuberculosis) as follows: D for deletions, V for insertions, and colored dots for amino acid substitutions (substitutions at each position are indicated in single amino acid code in columns above or below the positions).

Color coding for the amino acid substitutions is as follows:

yellow, residues that interact directly with the bound Rif

green, residues that are too far away from the Rif for direct interaction

purple, three positions that are substituted with high frequency (noted as a % immediately below the substitutions) in clinical isolates of RifR M. tuberculosis



BMJ VOLUME 317 5 SEPTEMBER 1998 www.bmj.com

Where do these antibioticresistance alleles/genes come from?

Weapons of Microbial Drug Resistance Abound in Soil Flora

http://fire.biol.wwu.edu/trent/trent/microbialresistance.pdf

Multidrug Resistance in S. aureus				
Antibiotic	MSSA (1930)	MRSA (1994)	Resistance mechanism	
Penicillin	S	R	+ (1945)	
Streptomycin	S	R	+ (1948)	
Tetracycline	S	R	+ (1950)	
Methicillin	S	R	+ (1961) <i>mecA</i>	
Oxacillin	S	R	+	
Cephalothin	S	R	+	
Cefotaxime	S	R	+	
Imipenem	S	R	+	
Chloramphenicol	S	R	+	
Ciprofloxacin	S	R	А	
Clindamycin	S	R	+	
Erythromycin	S	R	+	
Gentamycin	S	R	+	
Rifampin	S	R	А	
Vancomycin	S	S	A (1997) VISA	
Vancomycin	S	S	+ (2002) vanA	
Teichoplanin	S	S	+	
Trimeth/Sulfa	S	R	A	

A = adaptive

implying a
darwinian process
+ = acquired from
an extra species
source

Emergence of multidrug resistance in *Staphylococcus aureus.* The Brazilian clone of methicillin-resistant *S. aureus* (MRSA), isolated in 1994 (*2*), was resistant (R) to nearly all the antibiotics listed. Most of the resistance mechanisms were not adaptive (A), but acquired (+) from an extraspecies source. In contrast, an invasive strain of *S. aureus* (MSSA), recovered in 1930, was susceptible (S) to all the agents.

A recent article on antibiotic resistance is titled *The bacteria fight back*

This is misleading: as we have already seen in the mutagenesis lab, "adaptive" resistance happens because mutation happens and the antibiotic is simply selecting for preexisting mutations in the vast bacterial populations

Antibiotic resistance acquired by two fundamental mechanisms:

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Cephalothin	S	R	+	
Cefotaxime	S	R	+	
Imipenem	S	R	+	
Chloramphenicol	S	R	+	
Ciprofloxacin	S	R	A	
Clindamycin	S	R	+	
Erythromycin	S	R	+	
Gentamycin	S	R	+	
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(+) = acquired from
an extraspecies source
what do we know about
the transfer
mechanisms?
what types of genetic
elements are involved?

Similar Themes in Eukaryotic and Prokaryotic Genetics:

- Use model organisms to explore basic questions about heredity
- Use phenotypic variation to explore hereditary processes and to define the existence of specific genes
- Cross males and females with different phenotypes!

In other ways, doing genetics with bacteria is fundamentally different

- number of organisms handled is off the scale used by eukaryotic geneticists
- ability to detect very rare events is one of the most powerful aspects of bacterial genetics

Prokaryotes the unseen majority

From PNAS 95: 6578 June 1998

Most of the earth's prokaryotes occur in

- open ocean: 1.2×10^{29} cells
- soil: 2.6 X 10²⁹ cells
- oceanic subsurfaces (marine sediments below 10cm): 3.5 X 10³⁰ cells
- terrestrial subsurfaces (below 8 meters): $0.25 - 2.5 \times 10^{-30}$ cells

Other habitats

- animals -- many vertebrate and invertebrate animals contain dense populations of prokaryotes that play important roles in nutrition and disease
- leaves
- air

Microbes maketh man

People are not just people. They are an awful lot of microbes, too

Aug 18th 2012 | The Economist

POLITICAL revolutionaries turn the world upside down. Scientific ones more often turn it inside out. And that, almost literally, is happening to the idea of what, biologically speaking, a human being is.

We and other complex organisms are composed of an interconnected ecosystem of eukaryotic and prokaryotic cells:

Density of prokaryotes on human skin: 10^3-10^4 per cm² [except in groin and axilla where it is 10^6 per cm²]

Total estimated number of prokaryotes on the skin of an individual is 3×10^8 cells

In the human colon: 3.2×10^{11} *cells/g* (colon is about 220 g)

Compare to # of people on earth-- which is?

http://www.census.gov/main/www/popclock.html



Current Population Clock



20:00 UTC (EST+5) Nov 06, 2012

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How do bacterial acquire genes from each other?

What are the mechanisms of horizontal gene transmission?







We will examine plasmid transfer between E. coli cells in the lab

It is well documented that many cases of AR acquisition involve transfer of plasmid encoded genes between cells that are not necessarily closely related



Decoding bacterial genotypes: We know that sex in humans is determined by the presence or absence of the Y chromosome and by the number of X chromosomes on fruitflies and worms,

But how is sex determined in bacteria?





IS 3 & IS 2 = insertion sequences $\gamma\delta$ = transposon Tn1000 oriV = origin of replication oriT = origin of conjugal transfer tra = tra functions The tra (transfer) gene specify structural proteins that are required for pili formation and various enzymes required for "mobilization" of the DNA

Transfer of the plasmid DNA starts at ori-T and proceeds counterclockwise on the drawing shown above

Horizontal gene transfer during conjugation F' X F- or F^+XF-

Animation of gene transfer http://www.blackwellpublishing.com/trun/artwork/Animations/conjugation/conjugation.html Some thoughts for the curious: Why aren't all bacterial cells male? http://fire.biol.wwu.edu/trent/trent/Ffactorpopulationgenetics.pdf

We will examine plasmid transfer between E. coli cells in the lab





bacterium bacterium Whole plasmid transfer does not require sequence homology between incoming DNA and resident genome to generate a stable recombinant

Why is the homology issue so important in the movement of antibiotic resistance genes?

Important implications of whole plasmid transfer

- *This is a great way for a bacterial cell to acquire novel genes:* since no requirement for cross over, resident genome does not have to have homology to incoming genes
- Also plasmid packaged AR genes come with their own transfer genes

Pathogenecity genes are often coded on plasmid or phage genes

see Nature News 6/14/11: Phage on the Rampage

http://fire.biol.wwu.edu/trent/trent/PhagerampageNatureNews.pdf

Page encoded genes code for Shiga toxin in pathogenic E. coli