Antibiotic resistance
is in the air
But what does that mean?

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Antibiotic resistance

Data from EARS-Net

The role of the environment
The role of the environment
The role of the environment

Enrichment

Transmission

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The role of the environment

- Enrichment
- Recruitment of novel genes
- Transmission
The role of the environment

Enrichment

Transmission

Recruitment of novel genes
Study background

- Environments with high abundance and diversity of ARGs are candidates for selection and transmission of resistance
- Large-scale data on ARGs distribution is lacking
- This prevents identification of risk environments
- Characterization of resistance genes in 864 samples
- Humans (350) Animals (145) External environments (369)
  - Skin, airways, oral, feces, sediment, water, soil, sewage sludge, air, pharmaceutical pollution
Scientists find bacteria in Beijing smog that lead to antibiotic resistance

Findings are reason for global concern, warn study’s authors
DRUGS

Why Drug-Resistance Genes Are Showing Up In Smog

Alexandra Sifferlin
Dec 08, 2016

Antibiotic resistant bacteria is becoming a greater medical threat, with estimates suggesting that by 2050, 10 million people will die from infections that are resistant to drugs each year.

In a recent study, scientists discovered the genes that make bacteria resistant to antibiotics in polluted air in China. That does not mean people can get drug-resistant infections from the air, but the aerial spread of such genes should be the subject of further study, the researchers say. The report was published in the journal Microbiome.

In the study, researchers at the University of Gothenburg analyzed DNA sequencing from 864 different samples from humans, animals and the environment. A few of those samples came from the air in Beijing, and from
Fear, Then Skepticism, Over Antibiotic-Resistant Genes in Beijing Smog

People in Beijing wearing masks this month, after the government declared an orange alert for air pollution, the second-highest level in a four-tier warning system. ©Giles Clarke/Getty
Methodology

ATTGCTCTGCGTAGCTTAGGCTTACGT
ATCGACTTGTCGATGCTACGTACGACG
ACTACGACTAGCTACGACGACTACGAC
TACGACTACTCTACGACTATCTACTCG
AGCTACGTCACCATTACTATGACTCGT
GATCTTCTATCGGACTATCTACTTATC
TATCGGCATGCTAGCTAGCTAGCTACT
CGTACGACTACGTAGCTAGCTAGCTACG
AGCGACTACGAGCTACGATCAGCT...

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ARGs are abundant in polluted samples...

Pal et al. Microbiome (2016)
...but highly diverse in Beijing smog

Pal et al. Microbiome (2016)
ARG composition in Beijing smog is unique.

Pal et al. Microbiome (2016)
Taxonomic diversity is also high in air

Pal et al. Microbiome (2016)
Not unique to Beijing smog

Pal et al. Microbiome (2016)
How could this affect our health?

- Air samples from WWTPs, animal slaughter houses, swine feeding operations carry live resistant bacteria

- Airborne infections?

- Resistance genes in harmless bacteria

- Reflection of that air comes into direct contact with many other types of environments -> accumulation of highly diverse collection of bacteria
How severe is the threat?

- Lots of air collected on filter
- Infectious doses very likely higher
- Only DNA sampled, bacteria may be dead
- No selection pressure for resistance
- Other health problems with smog more acute
More research is needed

- Sources of resistant bacteria in urban air unknown
- Air transmission of resistance is under-investigated
- Is this a general feature of air? Air samples from other environments are needed
Prioritising risk environments

- Selection enrich for resistant bacteria
- Nutrient availability enhances growth
- Close contact to humans eases spread
- Presence of human-associated bacteria
Prioritising risk environments

- Humans under treatment
- Farmed animals and fish farms
- Environment subjected to pollution with antibiotics
  - Drug production facilities
  - Sewage treatment plants?
  - Landfills?
- Food?
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