



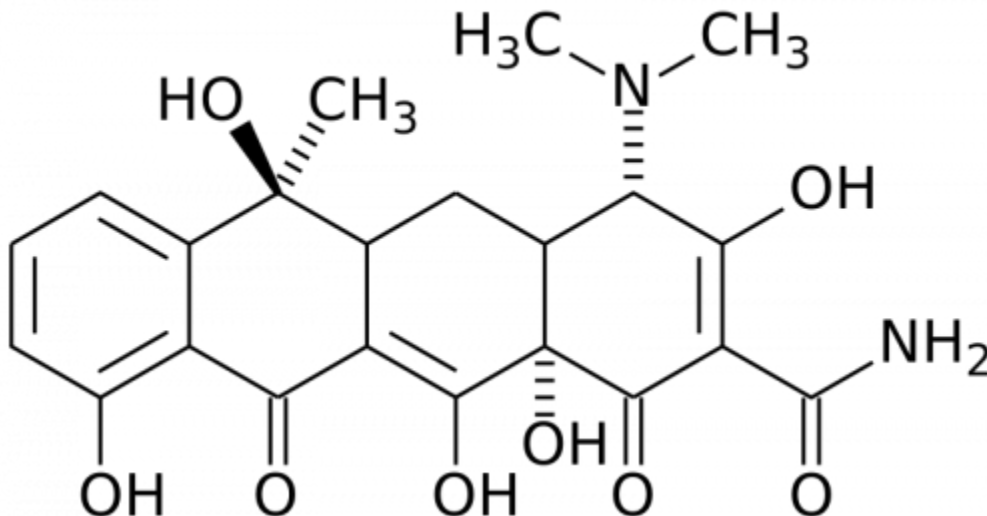
# The United Sludge-Free Alliance Recommended Reading

*From Ecocalizer.com*

## Antibiotic Resistant Genes Increasing in Soil Microbes

Written by Michael Ricciardi

Published on December 31st, 2009



Chemical structure of the antibiotic tetracycline—one of the four classes of antibiotics that sampled soil microbes showed increased resistance to in the 2009 Study.

The prevalence of antibiotic resistant genes (ARG) in soil bacteria has been increasing steadily over the past seven decades, despite tighter controls on the use of antibiotics for agricultural purposes (in Europe). This is according to a recent benchmark study/analysis\* of soil samples from five sites in the Netherlands. The research team, lead by David Graham of Newcastle University in the UK, found that “Seventy-eight percent of detected resistance genes, associated with four classes of antibiotics, showed increasing levels since 1940.”

- » See also: [Endangered Leatherback Sea Turtles: 70,000 Square Miles of U.S. Pacific Coast Habitat Proposed](#)
- » [Get EcoWorldly by RSS](#) or [sign up by email](#).

Since the end of WW II, antibiotic use has grown increasingly common—expanding beyond merely the treating of sick animals to include various antimicrobial applications. It was also discovered

that feeding low levels of antibiotics to livestock increased their growth significantly compared to standard feeding methods.

Despite this increased practice, baseline levels of antibiotic resistance (AR) have yet to be adequately determined. According to the research paper, “This is relevant because exposure of environmental organisms to antimicrobial agents, heavy metals, and resistant commensal (symbiotic) and pathogenic species might create reservoirs of resistance traits in soil organisms that may have broader consequences to public health.”

The validity of this concern is supported by an earlier, 2008 paper (Dantas et al, *Bacteria Subsisting on Antibiotics*, Science, 4 April, 2008) which found that “Bacteria subsisting on antibiotics are surprisingly phylogenetically diverse, and many are closely related to human pathogens.” Further, each resistant bacterium was found to be resistant to *multiple* antibiotics—yielding an “unappreciated reservoir” of AR microbes that might contribute to multiple AR in pathogenic bacteria (presumably meaning human-affiliated pathogens).

Although soil microbe AR is a natural phenomenon (in fact, many bacteria *make* as well as “eat” antibiotics), how this natural resistance capability is related to the emergence of super bugs is not known.

This writer contacted lead researcher David Graham and asked him to explain how these AR soil microbes and/or genes might impact humans: “The genes themselves do not get passed directly to humans per se. The genes get passed from exposed bacteria to bacteria whom might ultimately end up in humans, some of which might be pathogenic. An example is on food or in water that has been exposed to resistance bacteria.”

This “passing” of resistant genes between microbes is known as “lateral” or “horizontal gene transfer”, or sometimes, *conjugation*; a mechanism of “gene sharing” that has shed light on the rapid acquisition of resistance amongst bacterial species. This activity, it is postulated, has played a major role in the evolution of life on earth since the very first *prokaryotes* (cells without nuclei) emerged.

Although detailed estimates of total antibiotic production and use are not available, the paper cites trade data showing an “exponential growth” in their use prior to 1990, with greater than 50% of antibiotic production going towards agricultural purposes.

The research team acknowledges the limited scope of their analysis (using just five, archival soil samples from the TAGA archives at Wageningen University, NL) and call for wider, more global, studies and research on this apparent trend.

Concern over the rise of “super bugs” from the over-prescribing and use of antibiotics in the medical field has prompted widespread concern, and also the search for new antibiotic “scaffolds” upon which to build new classes of the germ-killing molecules. The recent outbreaks of MRSA (Methicillin Resistant *Staphylococcus Aureus*; also referred to as “multi-drug resistant”) is perhaps the most well-known example, but other AR bugs include vancomycin-resistant enterococci (VRE), resistant *Clostridium difficile*, and multi-resistant *pseudomonads*. An estimated 19, 000 patients die each year in the U.S. from super bug infections (primarily Staphylococcus infections). One possible solution to this problem is the complete cessation of antibiotic use in hospitals—and there is recent evidence that this approach, though radical, is working (see: [Solution to Super Bug Found in Norway](#)).

Meanwhile, calls for the cessation or tight limiting of antibiotics in U.S. agriculture are growing (see: [Pressure rises to stop antibiotics in agriculture](#)) although there are many opponents to such a change in practice. Most advocates of the use of antibiotics point to a general lack of evidence

of any resistant bacteria in livestock “jumping” and spreading to a larger, human population (although individual farmers have developed persistent, AR infections).

Alternatives to antibiotics are being considered, including the use of silver *nanoparticles*, which are highly toxic to bacteria. However, the use of such nanoparticles carries its own dangers, such as from accidental inhaling of the particles.

The acquisition of antibiotic resistance in bacteria, as noted, is a natural occurrence. It is the result of both mutation and natural selection (plus, recent research has observed bacteria actively “pumping” antibiotics *out* of the cytoplasm through their membranes). In this case, what is enabling the “selection” is the application of the antibiotic molecule (there will always be sufficient mutations to insure some resistance amongst some microbes in a given population, which then propagate). It has been suggested that the best way to prevent wide-spread selection *for* resistance, is to remove the agent of selection (the antibiotic) from the equation altogether. The above-cited Norwegian example seems to be the proof of this principle.

The “four classes” of antibiotics cited in the paper (that the sampled soil microbes show resistance to) are: tetracyclines (the most common type of AR), penicillins, macrolides, and aminoglycosides.

**\* *Evidence of Increasing Antibiotic Resistance Gene Abundances in Archived Soils Since 1940***, Charles W. Knapp, Jan Dolfing, Phillip A. Ehlert, David W. Graham (published in the December 8, 2009 edition of the journal Environmental Science and Technology)

<http://ecoworldly.com/2009/12/31/antibiotic-resistant-genes-increasing-in-soil-microbes/>