



Antibiotic Resistance in the Environment: Factory Farming and Superbug Genes in Rural Streams and Soils

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Executive Summary

The health and wellbeing of animals, people, and the planet are interconnected. The poor conditions and welfare of farmed animals in factory farms directly and indirectly harms food safety, public health, and the environment.

Stopping the growth of factory farming is integral to curbing the spread of antibiotic-resistant bacteria that pose risks to humans.

Despite the United Nations, G20 and many world leaders recognizing superbugs as a global health emergency and calling for comprehensive actions across medicine, the community and agriculture, excessive use of antibiotics in animal farming continues. In the US, an estimated 75% of all antimicrobials sold domestically are marketed to the food animal industry.

To date, US agencies and the industry have failed to adequately assess levels of use on farms, a knowledge gap that continues to impede progress. The data available tell a story of heavy use of important medicines in cows and pigs in the US, in particular.

We can no longer tolerate the many externalities of the factory farming model.

This report summarizes the results of testing conducted by World Animal Protection documenting the presence of antibiotic resistance in the environment surrounding intensive pig farms in the US, including widespread resistance to drugs commonly used by the pork industry. The presence of resistance elements in water and soil surrounding the farms suggests that these farms may be playing a substantial role in the spread of antibiotic resistance to the environment and putting nearby communities that rely on or interact with the environment at risk.

In October 2020, water samples and soil samples were taken across 8 sites in eastern North Carolina, both downstream and upstream of intensive confinement farms. These samples were then tested in a lab to identify whether specific antibiotic resistance genes (ARG) were present.

The key aim of this study was to determine the presence of ARGs in public waterways and soils near industrial farms, which discharge waste into waterways and apply manures to local crop fields. The testing looked for resistance genes because, while they do not confirm that resistant bacteria were necessarily present, they are indicators of the genetic potential for resistance.¹

The results of this testing showed that

- All 90 samples tested returned a positive result for at least 1 resistance gene.
- Ninety-two percent of samples (83/90) had positive PCR results for 3 or more resistance genes, with the largest number of genes in a single sample being 10.
- Fifteen samples (17%) had positive PCR results for 7 or more resistance genes.
- Genes conferring resistance to **tetracyclines** were identified in nearly all samples (89/90), with roughly half of the samples positive for 3 or more tetracycline-resistance genes. Available data indicate widespread use of tetracyclines (categorized as highly important by the World Health Organization (WHO)) by the US pork industry.
- Resistance to **streptomycin**, an aminoglycoside (categorized as critically important by WHO) was identified in 59/90 samples.
- Genes conferring resistance to **beta lactam** antibiotics, which include **penicillin** (critically and highly important), **cephalosporins** (critically and highly important), and **carbapenems** (critically important), were identified in 23/90 samples.
- The *mphA* gene, conferring resistance to **macrolides** (categorized as a class of Highest Priority Critically Important Antimicrobials by WHO), was identified in 9/90 samples and found predominantly in samples taken downstream from target farm sites.

The results also show notable differences in samples taken downstream from the target farms, which are more likely to be directly impacted by the farms' operations, emissions, and discharges. Streptomycin-resistance genes were found predominantly in downstream samples, as was the gene conferring resistance to florfenicol. At a majority of the sites, the macrolide-resistance gene *mphA* was found only in downstream samples.

It is important to note that the region of North Carolina in which samples were collected is heavily concentrated with large intensive confinement operations. There are roughly 2,200 pig producers operating in North Carolina today.² Due to this concentration, collection sites upstream from target farms may be downstream from other facilities nearby.

Further analysis of upstream versus downstream soil samples demonstrated that at most sites the relative abundance of a tetracycline-resistance gene (*tetA*) was higher downstream from target farms than upstream. In other words, there was a higher relative quantity of *tetA* genes in the environment likely directly impacted by farm emissions and discharges than the upstream environment, suggesting that the farm sites are contributing to contamination of ARGs.

There is a better way. Higher welfare animal husbandry can drastically reduce the need for antibiotics and eliminate common, routine uses. Providing animals with sufficient space, enriching their environment to enable them to exhibit their natural behaviors, keeping young animals with their mothers longer, and selecting breeds with better health outcomes, as examples, can protect animals' immune systems and development while giving them lives worth living.

Introduction

In the United States today, more than 9 billion land animals are raised each year to produce the meat, poultry, eggs and dairy consumed here or exported to other countries. The vast majority of these animals are raised in intensive confinement systems that house thousands of animals together.

Intensive systems (also called "factory farms" or "confined animal feeding operations (CAFO)") pack farmed animals tightly together in barren pens or cages to maximize space. The animals are bred for rapid growth rates and fed high-energy diets to further speed up weight gain. Their genetic uniformity, cramped conditions, and propensity for injuries makes them highly susceptible to diseases and infections that emerge and can spread quickly through a barn or feedlot.

It is unsurprising, then, that the intensification of farmed animals in the US has coincided with increased use of veterinary antibiotics. In addition to relying on antibiotics to treat animals should they get sick, antibiotics are routinely administered via feed, water, and injection to entire groups of animals housed together as a strategy to keep them from getting sick in such conditions—called "disease prevention" or "prophylactic" use. As the industry has scaled up it has relied on more and more doses of antibiotics, many of which are also used in human healthcare.

Routine and continuous use of antibiotics increases the selection of resistance among the bacteria the drugs are meant to kill. Bacteria may naturally evolve resistance to antibiotics over time, but the rampant use in factory farm settings is driving this process at a rapid pace and an extreme scale. Antibiotic resistance is now recognized as a global health crisis. Antibiotic-resistant bacteria—also known as "antimicrobial resistant bacteria" or "superbugs"—that develop on farms can then be spread via food, animals, manure, insects, and the environment and pose major risks for people and public health.



Despite the United Nations, G20 and many world leaders recognizing superbugs as a global health emergency and calling for comprehensive actions across medicine, the community and agriculture, excessive use of antibiotics in animal farming continues. In the US, an estimated 75% of all antimicrobials sold domestically are marketed to the food animal industry. To date, US agencies have failed to adequately assess levels of use on farms, a knowledge gap that continues to impede progress.

There is a better way. Higher welfare animal husbandry can drastically reduce the need for antibiotics and eliminate common, routine uses. Providing animals with sufficient space, enriching their environment to enable them to exhibit their natural behaviors, and selecting breeds with better health outcomes, as examples, can protect animals' immune systems and development while giving them lives worth living. Increasing the weaning age—the time they spend nursing their mothers—is a strong example of how higher welfare and reduced antibiotics go hand-in-hand. Progress by industry in several European Union countries has shown that increasing the age of weaning for pigs can lead to significant reductions in overall antibiotics use.³

We can no longer tolerate the many externalities of the factory farming model. The industry's role in driving the spread of antibiotic-resistant bacteria is just one example.

This report summarizes the results of testing conducted by World Animal Protection documenting the presence of antibiotic resistance in the environment surrounding intensive pig farms in the US, including widespread resistance to drugs commonly used by the pork industry. The presence of resistance elements in water and soil surrounding the farms suggests that these farms may be playing a substantial role in the spread of antibiotic resistance to the environment and putting nearby communities that rely on or interact with the environment at risk.



Antibiotic use and regulations in the United States

While the US Food and Drug Administration (FDA) has implemented measures that aim to eliminate the use of medically important antibiotics to promote fast growth of farm animals, their use to prevent disease across entire herds is still allowed and likely widespread. As early as the 1970s FDA signaled an intent to implement measures to restrict the use of important antibiotics in farmed animals for sub-therapeutic uses—those uses other than to treat an infection—and included

restrictions related to both growth promotion and disease prevention. These plans were halted by industry pressure on Congress.⁴ The Agency changed course when it issued definitions in 2012, which included use of antibiotics in feed and water to prevent disease as appropriate use.⁵ Additionally, any antimicrobials not currently defined as medically important by FDA are still permitted to promote fast growth without restriction.

Data from 2016 show that 95% of US swine operations used antimicrobials in their production, and 90% of sites administered medically important antibiotics via feed or water.⁶ Producers were also likely to administer several different

antibiotics to their pigs. For example, roughly 2 out of 3 sites gave nursery-age pigs 3 or more individual antimicrobials via feed.⁷ The pig industry continues to use antimicrobials in feed for growth-promotion purposes as well. Antimicrobials not important to human medicine are still approved at growth promotion doses, and 26% of operations indicated they feed antimicrobials to grower/finisher pigs for this purpose. Further, despite efforts by FDA to phase-out growth promotion uses of medically important drugs, research by Pew Charitable Trusts demonstrates loopholes in the regulations that allow several products to be used for their growth promotion benefits.⁸

In addition to growth promotion, operators indicated respiratory diseases and diarrhea as common reasons for administering antibiotics. Swine disease is exacerbated by low-welfare conditions and practices. Higher welfare strategies can play a role in preventing disease and the need for antibiotic treatments. Among US operators surveyed, 31.3% indicated that weaning pigs at older ages (21 or more days old) as a “very important” practice for reducing the need to use antimicrobials in pigs.⁹ Higher importance was given to adjusting diets to meet pigs’ nutritional needs and making facility management adjustments with 97.8% and 81.9% of operators, respectively, citing these strategies as “very important” for reducing antimicrobials.

Annual antimicrobial sales data published by FDA show that domestic sales of medically important antibiotics intended for farmed animals increased by 3% from 2018 to 2019, with 13.4 million pounds of medically important antibiotics sold. An additional 11.5 million pounds of antibiotics not considered medically important were sold that year for use in domestic farmed animals.¹⁰

Tetracyclines were the largest class of drug sold by volume in 2019, accounting for 67% of all medically important antibiotics sold, and total sales of tetracyclines increased by 4%. The pork industry alone accounted for 50% of these sales. The pork industry was also the largest purchaser of lincosamide antibiotics.

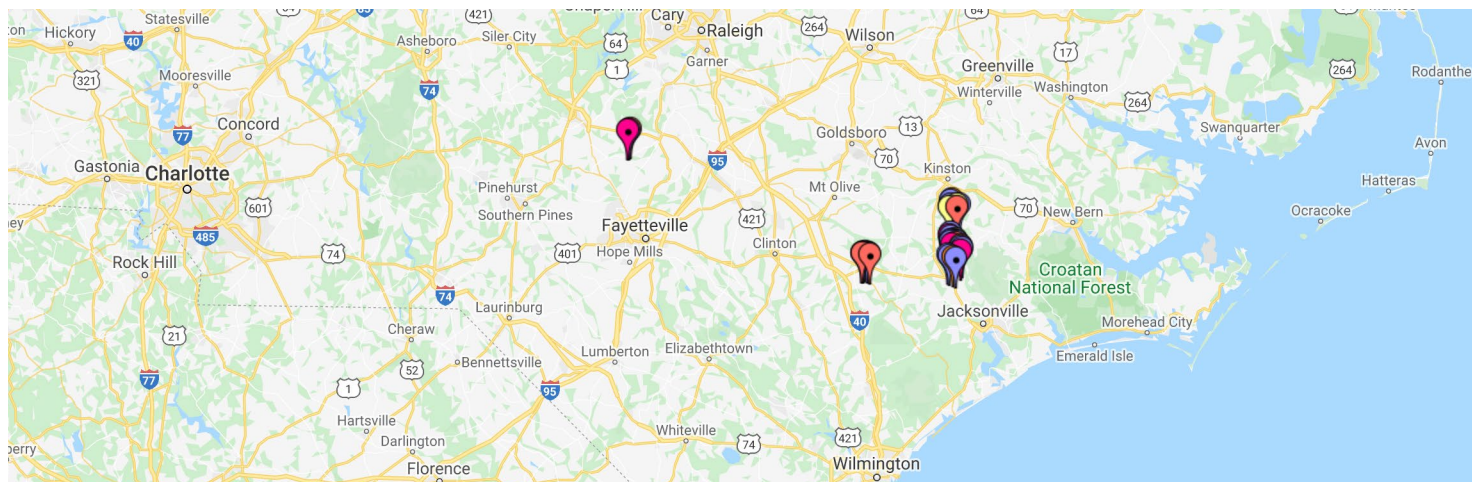
A recent study¹¹ surveyed 9 pig producers in the US on their antibiotic use in 2016 and 2017. Across the 9 farms in both years, the majority of antibiotics (approximately 70%) were administered via feed with roughly 30% administered via water and a small percentage via injection. While use of critically important classes was relatively low (about 5% of total use), use of classes considered highly important made up about 80% of total use. Tetracyclines and lincosamides—both categorized as highly important—made up roughly 60% and 9% of overall use, primarily through feed. Beta Lactams—a broad group of antibiotics that includes some critically important classes—constituted about 7% of total use, largely via water. Beta Lactam antibiotics, macrolides, and aminoglycosides were also used across all 9 farm sites as well as a small percentage of quinolones and cephalosporins.

FDA, US Department of Agriculture (USDA), and Centers for Disease Control and Prevention (CDC) collaborate on surveillance of antibiotic-resistant bacteria and infections in the US, called the National Antimicrobial Resistance Monitoring System (NARMS). NARMS¹² monitors resistant bacteria of concern in humans, farmed animals, and retail meat. In 2017, 32% of Salmonella isolates, 72% of E. coli isolates, and 78% of Enterococcus isolates taken from market pigs were resistant to tetracycline. For isolates taken from sows, 66% of E. coli and 70% of Enterococcus isolates were resistant. Forty-five percent of Enterococcus isolated from market pigs and 27% from sows were resistant to erythromycin, a macrolide. Nearly 100% of Enterococcus isolates from market pigs (97%) and from sows (91%) were resistant to lincomycin, a lincosamide. Twenty-five and 20% of E. coli isolated from market pigs were resistant to ampicillin and sulfonamides, respectively.

National surveillance and reporting of antibiotic use and surveillance for superbugs are still nascent. There are plans for NARMS to begin investigating levels of resistance in surface waters in the US, but there are no internationally agreed maximum environmental safe levels or resistance indicators. Antibiotics most critical for use in humans have been the focus of discussion to date, but antimicrobial resistance is transferable between classes and types of antibiotics. Swapping for another antibiotic considered less important for humans, or replacing antibiotic use with a probiotic, herb or tightened hygiene and biosecurity isn't the answer.

World Animal Protection's water and soil testing project

In October 2020, 45 water samples and 45 soil samples were taken across 8 sites in eastern North Carolina, both downstream and upstream of intensive confinement farms. These samples were then tested in a lab using Polymerase Chain Reaction (PCR) to identify whether 23 target antibiotic resistance genes (ARG) were present. The key aim of this study was to determine the presence of ARGs in public waterways and soils near industrial farms, which discharge waste into waterways, apply manures to local crop fields, and emit particles into the air.



The testing looked for resistance genes because, while they do not confirm that resistant bacteria were necessarily present, they are indicators of the genetic potential for resistance¹³. The genes can be transferred from one bacteria to another, even within a distantly related genus, through horizontal gene transfer (HGT)¹⁴. As such their detection in the environment is indicative of the presence of resistance elements that can be shared among bacteria in that same environment. Resistant bacteria originating on farms can spread their resistance genes to harmful bacteria already present in the surrounding environment, with the genes persisting beyond the viability of the bacteria themselves. Further, bacteria originating on farms that are still susceptible to antibiotics can then pick up resistance to important drugs if genes are widely present in the environment.



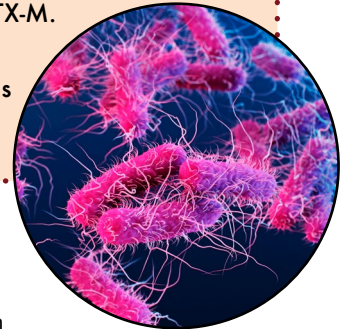
The 23 target genes included in the testing were selected based on relevant literature and included genes that confer resistance to the critically important macrolides (*mphA*, *ermF*), quinolones (*gyrA*), aminoglycosides (*strA*, *strB*), as well as the highly important tetracyclines (*tetA*, *tetB*, *tetC*, *tetQ*, *tetB(P)*), *otrA*, amphenicols (*floR*), and sulfonamides (*sul1*, *sul2*). The target genes also included several genes (*blaCTX-M*, *blaOXA*, *blaCMY*, *blaTEM*) indicating resistance to a broad spectrum of antibiotics called Beta Lactams.

[see break out box on the next page]

ESBL-producing bacteria - An emerging global threat

Extended-spectrum- β -lactamases (ESBLs)-producing bacteria (a family of bacteria which includes *Salmonella*, *E. coli*, and *Klebsiella*) have been identified by the World Health Organization (WHO) as an emerging global threat, and the geographical distribution of ESBL-producing bacteria has increased dramatically in recent years.¹⁵ At least one study has shown that ESBL genes have been shared between farmed animals and humans. Another study documented that ESBL-producing *Escherichia coli* (*E. coli*) in the air surrounding chicken farms were genetic variants of *E. coli* found on the farm.¹⁶

The prevalence of ESBL-producing bacteria on swine farms has been reported to range from 10-45%¹⁷, and ESBL genes have been identified at swine farms including, most commonly, *bla*CTX-M. ESBL-producing bacteria can confer resistance to the critically important carbapenem antibiotics, as well as penicillin and cephalosporins, which cover drugs categorized as critically or highly important, and some fluoroquinolones (critically important).



Overall, the testing results indicate that all samples were positive for the presence of at least one of the target resistance genes. Ninety-two percent of samples (83/90) had positive PCR results for 3 or more resistance genes, with the largest number of genes in a single sample being 10. Fifteen samples (17%) had positive PCR results for 7 or more resistance genes. Seven resistance genes—*flbR*, *gyrA*, *strB*, *sul1*, *tetA*, *tetB*, and *tetC*—were each found in at least 1 out of 3 of all samples, with *tetA* found in nearly all (83/90) samples taken.

- Nearly all of the samples (89/90) had positive PCR results for at least 1 of the **tetracycline-resistance** genes included in the analysis, with roughly half of the samples positive for 3 or more tetracycline-resistance genes, typically *tetA*, *tetB*, and *tetC*. Given the widespread use of tetracyclines (categorized as highly important by WHO) by the US pork industry—based on annual sales data and voluntary surveys—it is unsurprising that tetracycline-resistance would be prolific in the surrounding environment.
- Positive PCR results for resistance to **streptomycin**, an aminoglycoside (categorized as critically important by WHO) was identified in 59/90 samples. *StrA* was found less frequently, but where found was predominantly in downstream samples. Similarly, *strB* was found in 78% of downstream samples compared to 45% of upstream samples.
- The *gyrA* gene was found in 31/90 samples. It was more likely to be detected in downstream samples from the target farm sites and a greater number of soil samples had positive PCR for the gene as compared to water. Fluoroquinolones are listed in the WHO's Highest Priority Critically Important Antimicrobials (HPCIA) list. The PCR primer was developed to identify the region in which a mutation of the *gyrA* gene that confers resistance to **fluoroquinolones** is known to occur, however a positive result in this test is not a guarantor that this mutation was present.
- Genes conferring resistance to **beta lactam** antibiotics, which include **penicillin** (critically and highly important), **cephalosporins** (critically and highly important), and **carbapenems** (critically important), were identified in 23/90 samples. *Bla*CTX-M and *bla*CMY were most commonly found. Samples from site 5 had 3 beta lactam genes detected—*bla*CMY, *bla*CTX-M, and *bla*TEM.
- The *mphA* gene, conferring resistance to macrolides, was identified in 9/90 samples and found predominantly in samples taken downstream from target farm sites. The gene was found upstream at only 2 sites and only in soil samples, indicating that the genes could have been carried by air rather than water. Macrolides are listed as HPCIA by WHO.

Indications of greater contamination downstream from target sites

While samples taken upstream and downstream across all sites had positive PCR for resistance genes, the results show notable differences in samples taken downstream from the target farms, which are more likely to be directly impacted by the farms' operations, emissions, and discharges.

It is important to note that the region of North Carolina in which samples were collected is heavily concentrated with large intensive confinement operations. There are roughly 2,200 pig producers operating in North Carolina today.¹⁸ Due to this concentration, collection sites upstream from target farms may be downstream from other facilities nearby.

Seven of the 8 sites had both upstream and downstream samples taken. At site 4 access to the nearby waterway upstream from the target farms was cut off due to construction. As such, no upstream to downstream comparisons can be made for this site. Additionally, while this study aimed to collect samples at 10 total sites, sites 3 and 8 were inaccessible during the collection period.

- At 5/7 sites (sites 1, 2, 7, 9, and 10), the *bla*CTX-M ESBL gene was found only in downstream samples.
- At site 2, the *bla*CMY ESBL gene was found in water samples both downstream and upstream from the target farms. However, downstream water samples had a higher relative abundance of the gene compared to upstream.
- At 5/7 sites, analysis of upstream and downstream soil samples showed higher abundance of the tetracycline-resistance gene, *tetA*, downstream.
- The *mphA* gene, conferring resistance to macrolides—an HPCIA class—was found at 6 total sites and more likely to be found in downstream samples. The gene was only in downstream samples at 4/7 sites (sites 5, 6, 7 and 10).
- *FloR* and *strB*—conferring resistance to florfenicol and streptomycin, respectively—were found both downstream and upstream at nearly all sites. However, both genes were found in a higher number of downstream samples, suggesting they are more abundant downstream from the target farms.
- At 3/7 sites (sites 6, 7 and 9), the *gyrA* gene was identified only in downstream samples.

Interpretation: Antimicrobial resistance in the farm environment in the United States

The results of this testing project are supported by previous studies identifying antibiotic-resistant bacteria and/or antibiotic resistance genes are widespread on farms, in manures, and in the environment near farms in the US—particularly the environment directly downstream from manure applications or discharges. The frequency of which genes were identified that confer resistance to specific classes of antibiotics heavily used by or sold to the pork industry add to the mounting evidence that routine use on farms negatively impacts public health via the spread of antibiotic-resistance off farm.

Testing at monitoring wells and groundwater sites near 2 swine farms in North Carolina found *E. coli* resistant to antibiotics approved for use in pig production. At the first site, 37% of *E. coli* isolates were resistant to at least 1 antibiotic, with resistance to chlortetracycline, tetracycline, and sulfamethoxazole identified. At the second site, 79% of *E. coli* were resistant, with resistance predominantly to tetracycline and chlortetracycline, as well as ampicillin, streptomycin, chloramphenicol, sulfamethoxazole, trimethoprim, florfenicol, and neomycin.¹⁹

A study of *Salmonella* isolated from manure and environmental samples in North Carolina after manure application on commercial swine farms found ARGs in the bacteria on plasmids—meaning they could be transferred to other bacteria. Five of the 14 plasmids were considered multidrug resistant. The *Salmonella* carried genes conferring resistance to sulfisoxazole, tetracyclines, and beta lactams.²⁰

Another study identified ARGs conferring resistance to tetracycline in samples taken from groundwater and lagoons on 2 swine production sites. All 8 target genes were found in the samples overall, whereas samples taken from upstream wells for background control found none of the target genes at 1 control site and only 1 target gene in a single sample at the other.²¹

Yet another study sampled lagoons on 3 types of swine operations in the southeastern US. All of the samples taken from a sow (breeding) farm and all samples from a nursery farm were positive for tetracycline resistance genes (tetA) and macrolide resistance genes (ermF). Nearly all (90%) of samples from a finisher farm were positive for those same genes.²²

Environmental risks from factory farming

Superbugs do not remain on the farm. Intensive animal production generates large quantities of animal waste, which is often spread on land for use as a fertilizer or discharged into public waterways. It can also seep into groundwater.

Waterways can be flash points for toxic pollutants and create reservoirs where superbugs accumulate and mix. However, there are no national standards for identifying the concentration at which superbugs or resistance genes in the environment become a hazard. As such, there is no mechanism for holding companies accountable for discharging them into the environment and the issue is not currently monitored by any government agency. This is despite the United Nations identifying superbug contamination as one of the most important global environmental issues.

As animals do not metabolize around 70% of the antibiotics that are administered to them, antibiotics can transfer into animal waste. Bacteria can survive in untreated farmed animal waste for 2 to 12 months.²³ As these antibiotics pass through the animals and into the environment via manure, they speed the evolution of antibiotic-resistant bacteria in soil and water.²⁴

Soil treated with animal manure as fertilizer has greater levels of antibiotic-resistant organisms and antibiotic resistance genes (ARG) compared to soils not treated with manure.²⁵ Once present in the soil, resistant bacteria persist even when residues of the antibiotic drugs are no longer present. What's more, the genetic elements conferring resistance can be detected for at least 6 months at levels greater than before the application of manure, suggesting ARGs accumulate over time.²⁶ Researchers have suggested that certain ARGs, given their maintenance in natural ecosystems, should be considered pollutants.²⁷

Antibiotic-resistant bacteria can also be found in the air surrounding livestock farms.²⁸ Flies and insects also come into contact with livestock and manure, contract antibiotic-resistant bacteria and transmit it to humans. Research from Johns Hopkins University found that many houseflies near chicken operations carried antibiotic-resistant bacteria strains.²⁹

It is recognized that livestock production and areas with livestock manure applied can result in the contamination of nearby surface and groundwater resources with resistant bacteria.³⁰ Aquatic environments, therefore, can act as reservoirs for antimicrobial resistance (AMR), especially as they are often endpoints for agricultural runoff and discharge from human wastewater treatment plants.³¹

Communities at Risk

An analysis of county and satellite data by the NGO Environmental Working Group found that roughly 160,000 people in North Carolina live within a half-mile of a pig or poultry farm, and nearly 1 million live within 3 miles of a farm.³² These residents endure noxious odors as well as particulate matter that drifts onto their property and into their homes from the ventilation systems, manure lagoons, sprayed manures, and carcasses of animals that did not survive to slaughter. The

stench attracts buzzards, gnats, and flies. Residents complain that their eyes burn and their noses runs when spending time outside.³³

Research has shown a correlation between air pollution from pig farms and higher rates of nausea, increases in blood pressure, respiratory issues, increased asthma symptoms for children, and diminished quality of life for local residents.³⁴

A 2018 study published in the North Carolina Medical Journal demonstrated a clear link between zip codes, demographics, and proximity to CAFOs that correlated with an uptick of health issues such as anemia, kidney disease, tuberculosis, septicemia, and higher rates of emergency care visits for infants.³⁵

The impacts of pig operations in the state disproportionately affect African Americans, Hispanics, and Native Americans, a pattern of placing the burden of pollution on marginalized communities known as “environmental racism”.³⁶

Research investigating rates of antibiotic-resistant infections among residents living near CAFOs has not been identified at the time of this report.

Conclusion—Increase Welfare to Reduce Risk

The problem of antimicrobial resistance in the farm environment must be addressed at the source—overreliance by the factory farming industry on antibiotics to mitigate harms from cruel, outdated practices. Higher welfare animal husbandry practices are the solution. Waste treatment technologies do not eradicate superbugs and once in the environment superbugs cannot be cleaned from waterways.

Dependence on antibiotics must be addressed through building the wellbeing and immunity of farmed animals. This means eliminating the worst welfare abuses in factory farming: cage confinement, painful physical alterations, weaning animals from their mothers too young, and using high-growth breeds.

A recent study demonstrated that pigs given regular in-feed antibiotics showed an increase in aggressive behaviors, such as biting and fighting, and were more likely to have tail lesions and other injuries as a result of attacks from their pen mates, compared to pigs not fed antibiotics. The authors surmised this could be due to one of two factors: pigs fed antibiotics had greater motivation to eat, potentially leading to an increase in feed competition; antibiotics are known to alter the microbiome in the gut, which has been linked to increases in anxiety and aggression. Further, while the pigs not given in-feed antibiotics did require a larger number of injection doses throughout the trial, this nevertheless translated to roughly 95% less antibiotics used compared to the group receiving regular in-feed doses.³⁷ The same study also found a correlation between temperature, carbon dioxide, and stocking density with increased aggressive behaviors and lesions, suggesting that management practices addressing these common welfare issues can also contribute to reduced use of antibiotics.³⁸

In general, animals in higher welfare systems have reduced stress and greater immunity and resilience to disease, which in turn reduces the need for antibiotics.³⁹ Achieving measurable reductions in total antibiotics used in farmed animals is vital to curbing the resistance crisis, preserving critical medicines, protecting public health, and improving the lives of billions of animals every year.



Recommendations

Recommendations for the global retail sector, animal protein production sector, governments and intergovernmental organizations, and the global finance sector follow.

Global food retail and animal protein production sectors:

- Develop an overarching animal welfare policy aligned with the five Domains⁴⁰ framework and phase in procurement requirements in line with the Farm Animal Responsible Minimum Standards (FARMS) animal welfare requirements as a minimum.
- Commit to using antibiotics responsibly in farming: ending the routine use of antibiotics including to promote fast growth and to prevent disease across groups. They should not, however, pursue “antibiotic free” or “no antibiotics ever” or “raised without antibiotics” policies or product lines; this can create a disincentive for producers to treat sick animals and does not address underlying welfare issues.
- Increase the proportion of plant-based protein options to support an average global reduction in meat production and consumption of 50% by 2040.
- Publish annual reports on their progress towards implementing high welfare commitments in conjunction with antibiotic use data on supplier farms; and progress on humane and sustainable protein diversification.

Governments and intergovernmental organizations:

- Introduce and enforce regulations in line with FARMS animal welfare requirements as a minimum.
- Introduce and enforce regulations ending the routine use of antibiotics including to promote fast growth and to prevent disease across groups.
- Commit to national surveillance and public reporting of antibiotic use at farm level in conjunction with reporting on welfare practices on farms.
- Redirect subsidies and financial incentives to high welfare systems that align with the 5 Domains welfare framework and in support of an average global reduction in meat production and consumption of 50% by 2040.

For financial investors in food systems:

- Require companies to develop overarching animal welfare policies aligned with the Five Domains framework and to meet FARMS animal welfare requirements as a minimum.
- Require companies to commit to using antibiotics responsibly in farming: ending the routine use of antibiotics including to promote fast growth and to prevent disease across groups. They should not, however, pursue “antibiotic free” or “no antibiotics ever” or “raised without antibiotics” policies or product lines; this can create a disincentive for producers to treat sick animals and does not address underlying welfare issues.
- Increase the proportion of plant-based protein in the investment portfolio to support an average global reduction in meat production and consumption of 50% by 2040.
- Influence policy such as supporting regulations on stricter animal welfare requirements, antibiotic use, mandatory disclosures, and due diligence processes.

Methodology

Over a period of 2 days in October 2020 water and soil samples were collected at 8 sites near to factory farm operations in eastern North Carolina.

Downstream from the manure storage and likely discharge points of the target operations, water was collected from a nearby stream in 3 sterile 1-Liter bottles. Dry soil near to the same waterway was collected in 3 sterile 60-gram sample containers.

Upstream from the manure storage and likely discharge points of the target operations, water from the same stream was collected in 3 sterile 1-Liter bottles. Dry soil near to the same waterway was collected in 3 sterile 60-gram sample containers. At 1 site, site 4, no upstream samples were collected due to accessibility issues.

With the exception of site 4, each collection site resulted in 3 1-Liter downstream water samples, 3 60-gram downstream soil samples, 3 1-Liter upstream water samples, and 3 60-gram upstream soil samples. Samples were sealed and labeled with a corresponding code denoting the site number, sample medium, whether collected upstream or downstream, and the sample number.

Samples were delivered within 8 hours of collection to Environmental Chemists Inc. (EnviroChem) in Jacksonville, NC, and transported to a second EnviroChem lab in Wilmington, NC. EnviroChem filtered all 45 1-Liter water samples using membrane filtration to capture the organisms and froze the membrane filters. The frozen filters and 45 60-gram soil samples were packaged in insulated containers with dry ice and shipped to TACGen in California.

The labs at TACGen developed polymerase chain reaction (PCR) primers and oligos for 23 target resistance genes identified by World Animal Protection for inclusion in the project. The full list of targeted genes follows this section. TACGen provided World Animal Protection with agarose gel images, data result tables, and summary tables grouped by collection site and indicating whether the PCR analysis returned a positive or negative result for each target gene in each sample. For the purposes of this report, a positive PCR result served as evidence that the gene was present in the sample. However, a small percentage of false positives are possible.



Target genes prioritized in this study:

Gene	Relevant Antimicrobial Classes	# Samples with Positive PCR
<i>mphA</i>	macrolides	9/90 (10%)
<i>blaCMY</i>	penicillins, cephalosporins, carbapenems	12/90 (13%)
<i>blaCTX-M</i>	penicillins, cephalosporins, carbapenems	15/90 (17%)
<i>blaTEM</i>	penicillins, cephalosporins, carbapenems	3/90 (3%)
<i>blaOXA</i>	penicillins, cephalosporins, carbapenems	1/90 (1%)
<i>floR</i>	amphenicols	31/90 (34%)
<i>strA</i>	streptomycin	14/90 (16%)
<i>strB</i>	streptomycin	54/90 (60%)
<i>sul1</i>	sulfonamides	30/90 (33%)
<i>sul2</i>	sulfonamides	4/90 (4%)
<i>tetA</i>	tetracyclines	82/90 (91%)
<i>tetB</i>	tetracyclines	55/90 (61%)
<i>tetC</i>	tetracyclines	62/90 (69%)
<i>tetO</i>	tetracyclines	0/90 (0%)
<i>tetQ</i>	tetracyclines	7/90 (8%)
<i>tetM</i>	tetracyclines	0/90 (0%)
<i>tetS</i>	tetracyclines	0/90 (0%)
<i>tetB(P)</i>	tetracyclines	2/90 (2%)
<i>otr(A)</i>	tetracyclines	1/90 (1%)
<i>ermA</i>	macrolides	0/90 (0%)
<i>ermF</i>	macrolides	1/90 (1%)
<i>mecA</i>	penicillins	0/90 (0%)
<i>gyrA</i>	quinolones	14/90 (16%)

Endnotes

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