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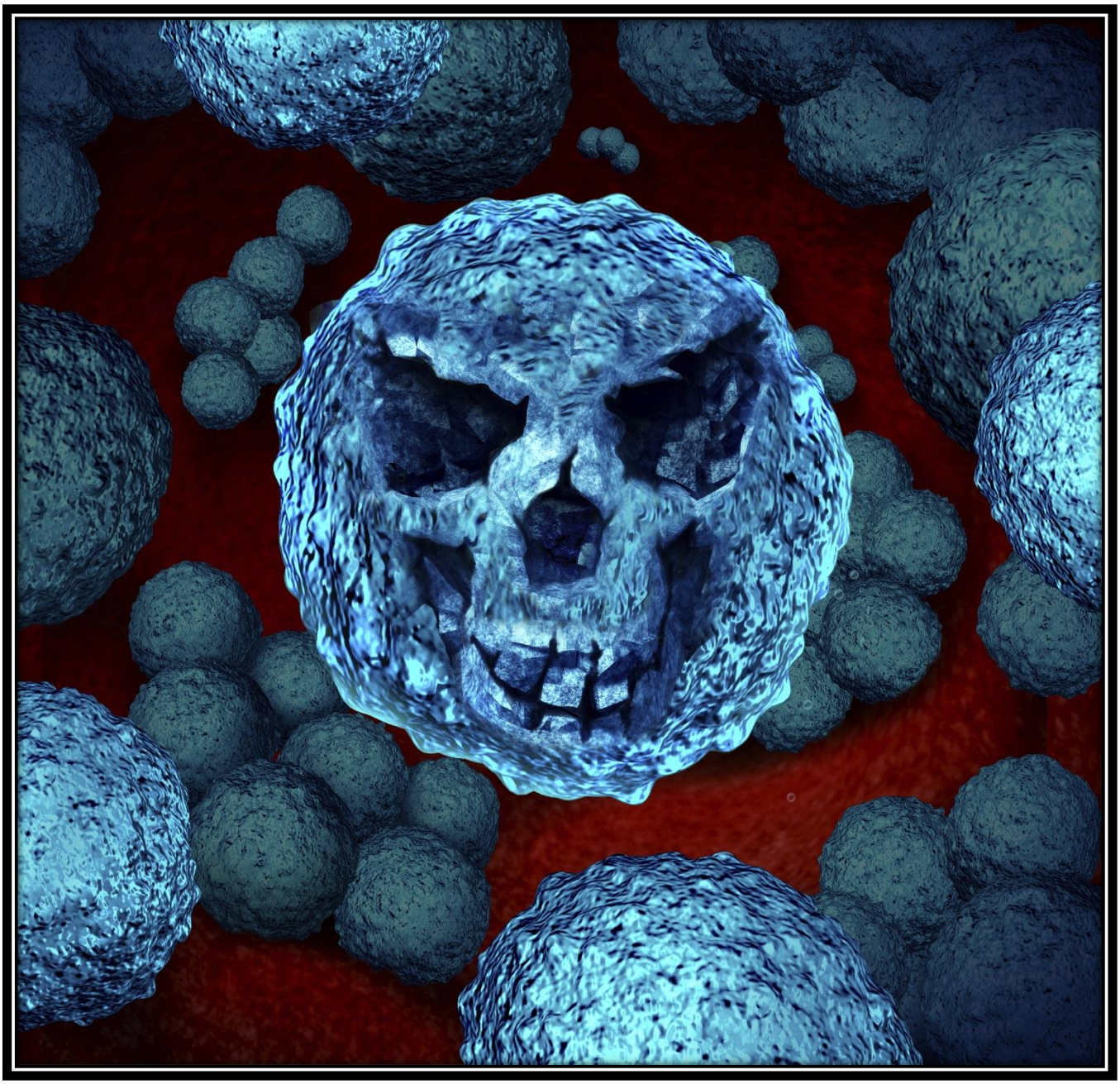

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INSTRUCTIONS TO CONTRIBUTORS

ENVIS Newsletter on 'Microorganisms and Environment Management', a quarterly publication, brings out original research articles, reviews, reports, research highlights, news-scan etc., related to the thematic area of the ENVIS Centre. In order to disseminate the cutting-edge research findings to user community, ENVIS Centre on Microorganisms and Environment Management invites original research and review articles, notes, research and meeting reports. Details of forthcoming conferences / seminars / symposia / trainings / workshops also will be considered for publication in the newsletter.

The articles and other information should be typed in double space with a maximum of 8 - 10 typed pages. Photographs/line drawings and graphs need to be of good quality with clarity for reproduction in the newsletter. For references and other details, the standard format used in refereed journals may be followed.

Articles should be sent to:

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Cover page : Superbug danger concept as a killer bacteria shaped as a death skull face as a Symbol for MRSA medical health care risk hazard icon as a bacterium infection inside the human body.

Courtesy: Shutter Stock © Lightspring.

ENVIS Newsletter
on
Microorganisms and Environment Management

Contents

Dear Readers,

Greetings!

The discovery of antibiotics has revolutionized healthcare practices and made it possible now to treat and cure many infections. Pathogens such as bacteria, virus, fungi and parasites have evolved to resist these drugs by the process termed Antimicrobial Resistance (AMR). Naturally microbes develop AMR due to selection pressure of the antimicrobials present in the environment typically through genetic changes in-order to survive. But in the last few decade high levels of AMR is observed in microbes, due to overuse and misuse of antibiotics/antimicrobials such as in humans, animals (including farmed fish), crops, as well as the spread of residues of these medicines in soil, crops, and water. This resistance has become a problem at present as the already discovered antibiotics are becoming ineffective against pathogens and the discovery of new antibiotics has also slowed down. Hence, AMR is considered as the greatest and most urgent risk requiring immediate attention globally.

This issue contains a scientific article on the environmental and public health impact of sub-therapeutic use of antibiotics in poultry industry along with some other interesting topics such as development of AMR in bacteria, programming DNA to reverse AMR in bacteria, how teamwork enables bacterial survival in the presence of antibiotics and many more. Hope this issue would trigger awareness among the readers in this regard.

Kindly send your feedback @ www.envismadrasuniv.org/send_feedback.php

Prof. N. Munuswamy

For further details, visit our website.

In House News

Dr. C. Arulvasu, Department of Zoology, University of Madras assumed charge as the new Co-ordinator of ENVIS – Microorganisms and Environment Management (MEM) with effect from 01 July, 2016.

SCIENTIFIC ARTICLE

Environmental and public health impact of sub-therapeutic antibiotic use in the poultry industry

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Abstract

The use of antibiotics at sub-therapeutic concentrations in poultry farm is believed to be an important factor for development of antibiotic resistance genes (ARGs) thereby resulting in proliferation of antibiotic-resistant bacteria in farm environment. ARGs are emerging environmental contaminants and pose threat to human health. In our study, the persistence of antimicrobial resistance genes in bacteria from poultry and farm soils from some districts of Tamil Nadu were assessed. Mean resistance levels were highly variable for tetracyclin and erythromycin antibiotics. These high resistance determinants were observed inside poultry farms. The prevalence of resistance in staphylococcal and enterobacterial isolates against antibiotics commonly used as growth promoters in poultry farms was evident. These results indicated the need for monitoring the use of antibiotics in poultry industry.

Introduction

Antibiotics are routinely used in the livestock industry to treat and prevent diseases. In the modern poultry industry, antibiotics are used in high quantities not only for therapy and prophylaxis, but also as antimicrobial growth promoters in animal feeds (Singer and Hofacre, 2006). Sub-therapeutic use of antibiotics in poultry industry resulted in the development of antimicrobial resistance (AMR) in intestinal microbiota of broilers and through the animal excreta it is disseminated to soil and aquatic environments (Ji *et al.*, 2012). Antibiotic resistance genes (ARGs) responsible for AMR traits are recognized as environmental pollutants posing potential worldwide human health risk (Apata, 2009). The environmental burden of imprudent antimicrobial use in poultry farms and its impact on human health is discussed in this article.

Poultry Industry in India

Poultry industry is a fast growing and dynamic subsector of agriculture, recognized for sustainable employment, income generation that ensures food security through egg and meat production. Production of chicken meat is growing into the largest component of the poultry industry in India. India ranks third in poultry egg and meat production in the world. In India Andhra Pradesh ranks first in top five states of meat production followed by Maharashtra, Tamil Nadu, Haryana and West Bengal. The main hubs of broiler production in Tamil Nadu are Thiruvallur, Namakkal and Salem districts.

Commercial Poultry Production

Chicken is the most common type of poultry in the world. The term broiler is applied to chickens that have especially been bred for meat that grow rapidly (35-42 days) to attain the average slaughter weight (2 kg approx.). Broiler strains are based on hybrid crosses between Cornish White, New Hampshire and White Plymouth Rock. Their life-cycle is categorised into pre-starter (1-10 days), starter (11-25 days) and finisher (26^{th} day onwards). They are fed with antibiotics mixed feed throughout the life-cycle, as an integral part of commercial farming (Prabakaran, 2003).

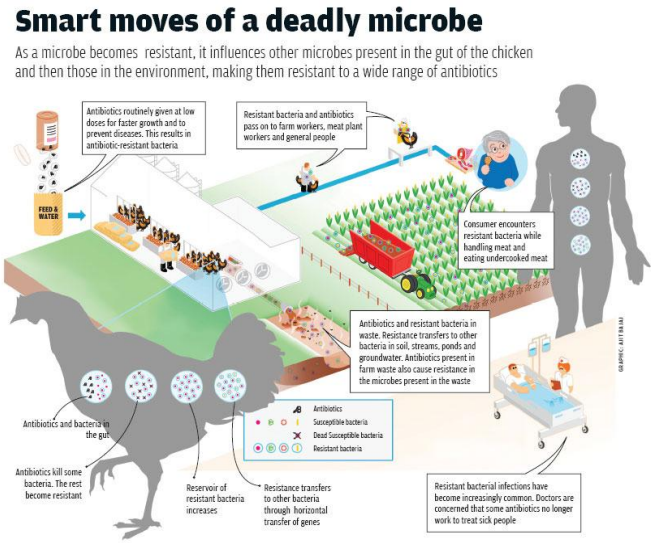
Use of Antibiotics in Poultry Farming

Antibiotics are used in poultry farming as: (i) therapeutic agents for treatment of diseases, (ii) prophylactic agents for prevention of diseases and (iii) growth promoters to increase growth-rate and productivity. Its use as growth promoters, especially in poultry production is quiet prevalent in India primarily due to economic considerations as they are inexpensive, safe, easy to use and they tend to improve growth performances, laying capacity, general confirmation in consistent manner regardless of the system of husbandry. Antibiotic growth promoters are known to suppress the gut bacteria leaving more nutrients for chicken to be absorbed for greater weight gain. In particular broilers are mostly fed with antibiotic mixed diet and the antibiotics used were also shown to control endemic disease in poultry population. Classes of antibiotics that are used in poultry production include ß-Lactams (Penicillins and Ceftiofur), Macrolides (Azithromycin, Spiramycin and Tylosin), Quinolones (Fluoroquiniolones- Sarafloxacin and Enrofloxacin), Polypeptides (Bacitracin), Streptogramins (Virginiamycin), Sulphonamides (Sulphadimethoxine, Sulphamethazine and

Sulphisoxazole), Tetracyclines (Chlortetracycline, Oxytetracycline and Tetracycline) and Ionophores (Monensin, Salinomycin, Semduramicin and Lasalocid). Antibiotics of same classes are used in animals and humans. This overlap significantly contributes to the emergence of resistant bacteria in human (Apata, 2009).

Development of Antimicrobial resistance

Antimicrobial resistance (AMR) is strongly linked with antibiotic use, misuse and overuse in humans and animals. Overuse in animals occurs in the treatment of mild and self limiting infections and long-term low dose administration for prophylaxis. Under-use of antibiotics is common in poultry practice as in group dosing which often results in uneven consumption and also in use of antibiotics in sub-therapeutic concentration as in growth promoters. They inhibit sensitive flora and select resistant flora which multiply and pass to environment may thereby transport resistant gene to other bacterial species present in the host and environment. Sub-therapeutic concentration may induce antimicrobial resistance including transfer of R-factor. The resistant bacteria from animals may be transferred directly to humans via food chain (Barton, 2000; Barton and Hart, 2001). Although most of the AMR is carried by commensal bacteria, ARGs can be transferred to pathogens of both animals and humans through horizontal gene transfer (HGT).



(**Source:** CSE Study: Antibiotics in Chicken Meat, 2014)

Impact of AMR in Environment

Antibiotic resistance genes (ARG) can be transferred to other bacteria via AMR bacteria present in water, soil and air. Animals excrete a significant amount of the antibiotics to the environment, making their manure a potential source of both antibiotics and antibiotic-resistant bacteria (Grohmann and Arends, 2012; Yannarell and Mackie, 2012).

In a study conducted in Delmarva Peninsula of the United States, resistance genes *erm(B), erm(A), msr(C), msr(A/B)* and mobile genetic elements associated with the conjugative transposon Tn916, were found in isolates recovered from poultry farm environment. *erm(B)* was the most common resistance gene in enterococci, while *erm(A)* was the most common resistance gene in staphylococci (Graham *et al.*, 2009). Similarly our study had quantified antibiotic-resistant bacteria in eight different broiler farms located in Nammakal, Salem and Thiruvallur districts of Tamil Nadu and investigated the prevalence and persistence of antimicrobial resistance genes such as tetracycline resistant and macrolide resistant determinants. Bacteria resistant to tetracycline and erythromycin were detected in soil samples of eight different farms. Antibiotic resistance levels were calculated as the ratio of bacteria able to grow on plates supplemented with antibiotics against no antibiotics. Mean resistance levels were highly variable for tetracycline and erythromycin antibiotics, ranging between 59–93% and 23–78% respectively. Statistical significance was observed among the eight sites based on resistance levels. The most frequent gene was *erm(A)* (56.2%) followed by *tet(K)* (43.7%) and *erm(C)* (32.2%). Higher tetracycline and macrolide resistance determinants were observed inside the farms compared to outside.

Incidence of Antibiotic Resistance in Broilers and its Impact on Public Health

The use of antibiotics as growth promotors that are critically important in human medicine is concerned with the emergence of new forms of multi-drug resistant bacteria that infect people. These include new strains of multi-resistant food borne bacteria such as *Salmonella sp.*, *Campylobacter sp.*, Methicillin-Resistant *Staphylococcus aureus* (MRSA), Vancomycin Resistant *Enterococci* (VRE) and *E. coli* that produce the Extended-spectrum beta-lactamases (ESBL) and/or AmpC enzymes that inactivate nearly all beta-lactam antibiotics (which include penicillins and the critically important 3rd and 4th generation Cephalosporins) (Phillips *et al.*, 2004; Furtula *et al.*, 2013; Mehndiratta and Bhalla, 2014).

In a study conducted in our laboratory, we assessed the prevalence of antibiotic resistant *Enterobacteriaceae* and

Staphylococcus sp. from broilers. Among the enterobacterial isolates, highest resistance was observed to amikacin (27%) followed by cotrimoxazole (12.2%), ciprofloxacin (5.6%), cefotaxime (3.1%) and gentamicin (3.1%). Among the staphylococcal isolates, highest resistance was observed to penicillin (86.6%) followed by tetracycline (73.7%), erythromycin (60%), clindamycin (60%), cotrimoxazole (26.6%) and ciprofloxacin (20%).

Antibiotic Residues in Meat

Antibiotics administered in poultry feed may result in minute residues of antibiotics in meat and eggs. The possible adverse effects of antibiotic residue were first reported in UK in 1969. In India, Pollution Monitoring Laboratory (PML), at the Centre for Science and Environment, New Delhi tested for antibiotics in chicken samples. Twenty eight samples of chickens out of 70 (40%) showed the presence of antibiotic residues. Tetracyclines were detected in 10 samples (14.3%) in the range of 16.01 – 46.02 µg kg^{-1}. Fluoroquinolones were detected in 20 samples (28.6%) in the range 3.37 – 131.75 µg kg^{-1}. (CSE Study: Antibiotics in Chicken Meat, 2014).

Conclusion

Antimicrobial resistance is becoming an increasing health concern because antimicrobial resistant commensal bacteria function as a huge resistance reservoir and can spread ARGs to the environment and humans. The results of our study and others clearly indicated the impact of AMR in environment and the persistence of resistant bacteria in broilers, and highlighted the role of antibiotics with its use as feed additive in poultry production to be the inducer of resistance in microbes. There is an urgent need for monitoring the use of antibiotics in poultry industry and a regulatory body may be constituted for the same in India with a viewpoint of containing antibiotic resistance.

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RESEARCH REPORTS

Programming DNA to reverse antibiotic resistance in bacteria

New research introduces a promising new tool to combat the rapid, extensive spread of antibiotic resistance around the world. It nukes antibiotic resistance in selected bacteria, and renders other bacteria more sensitive to antibiotics.

The research, if ultimately applied to pathogens on hospital surfaces or medical personnel's hands, could turn the tide on untreatable, often lethal bacterial infections.

The World Health Organization at its annual assembly in Geneva approved a radical and far-reaching plan to slow the rapid, extensive spread of antibiotic resistance around the world. The plan hopes to curb the rise caused by an unchecked use of antibiotics and lack of new antibiotics on the market.

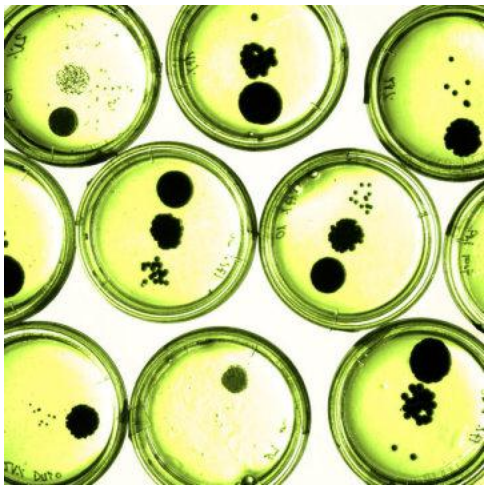
New Tel Aviv University research published in *PNAS* introduces a promising new tool: a two-pronged system to combat this dangerous situation. It nukes antibiotic resistance in selected bacteria, and renders other bacteria more sensitive to antibiotics. The research, led by Prof. Udi Qimron of the Department of Clinical Microbiology and Immunology at TAU's Sackler Faculty of Medicine, is based on bacterial viruses called phages, which transfer "edited" DNA into resistant bacteria to kill off resistant strains and make others more sensitive to antibiotics.

According to the researchers by choosing suitable combinations of DNA-delivering phages specifically designed for appropriate sensitization treatments for each pathogen and selecting suitable combination of 'killing' phages antimicrobial resistance could be countered. In short the injected DNA eliminates the genes that cause resistance to antibiotics and confers protection against lethal phages.

The researchers have managed to devise a way to restore antibiotic sensitivity to drug-resistant bacteria, and also prevent the transfer of genes that create that resistance among bacteria.

Earlier research by Prof. Qimron revealed that bacteria could be sensitized to certain antibiotics and that specific chemical agent could "choose" those bacteria more susceptible to antibiotics. His strategy harnesses the CRISPR-Cas system a bacterial DNA-reprogramming system Prof. Qimron pioneered as a tool to expand on established principles.

According to the researchers, "selective pressure" exerted by antibiotics renders most bacteria resistant to them hence the epidemic of lethal resistant infections in hospitals prevail. No counter-selection pressure for sensitization of antibiotics is currently available. Prof. Qimron's strategy actually combats this pressure selecting for the population of pathogens exhibiting antibiotic sensitivity where in addition to disinfection, could significantly render infections once again treatable by antibiotics.



Growing bacteria in Petri dishes.

(**Image credit:** *kasto / Fotolia*)

Source: www.sciencedaily.com

Scientists reveal secret of antibiotic-resistant bacteria

Researchers of MIPT's Laboratory of Systems Biology, have built a computer model to study the interaction between different bacteria, and between bacteria and the gut wall. This has led them to explain how antibiotic-resistant microbes develop and spread.

The human intestine contains trillions of different bacteria, which together are called the microbiome. Bacteria protect us from harmful microorganisms, produce digestive enzymes, and help the immune system to function normally. Many diseases, such as obesity, Crohn's disease, colon cancer, and other inflammatory processes are associated with a change in the gut microbiome. The researchers built a model for the interaction between two types of bacteria in the intestine and they determined the interaction when antibiotics that kill a large number of microorganisms are taken.

Using a simple modelling method, Agent Based Modelling (ABM) they recreated the processes involving bacteria that take place in the gut and explained some interesting effects when resistivity occurs.

The researchers were interested in a number of important issues such as, the speed at which the number of bacteria was restored after antibiotic therapy, finding what proportion of bacteria was not affected by antibiotics and the process of feedback between bacteria and the intestinal wall.

The intestinal wall actively absorbs certain substances and produces others, which affects the number of bacteria and their "state of health": if the numbers of bacteria in these processes are altered, it is difficult to obtain proper results.

The substances produced by bacteria and the intestinal walls were one of the main focal points in the new model. These compounds, which are formed by the bacterial fermentation of carbohydrates, may perform different functions at once: e.g. they can be “toxins” for one type of bacteria, and "food" for another type. If certain bacteria begin to produce too much of a substance that is poisonous to them, their numbers automatically decrease -- scientists call this as negative feedback. The intestinal wall can also produce either compounds that are harmful to bacteria (but not to the intestines themselves!), or carbohydrates that microorganisms can digest as nutrients.

The model also enabled the scientists to observe the location of strains in the gut and how their position changes after various substances are produced by the intestinal wall or bacteria. The visualization of the model showed that the spatial structure is a key factor that helps bacteria to survive and adapt to the changing conditions of their environment.

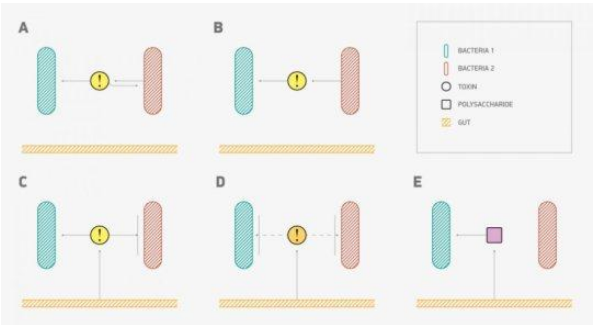
Using the model, the researchers were able to prove that even after antibiotic therapy there may be more bacteria that are sensitive to the effects of the antibiotic drug than those that are resistant to it. This conclusion may seem contradictory, but it is in fact true: the resistance to antibiotics comes at a price to the microorganisms. Antibiotics work by disrupting the biochemical mechanisms that are of vital importance to the function of the microbes (e.g. blocking protein synthesis or respiratory enzymes), which means they can only survive with major changes to the structure of key proteins, or by producing molecules that neutralize the drug. By altering their biochemical properties or using up resources on additional chemical reactions, bacteria inevitably lose out on efficiency: they consume "food" slower, divide slower and therefore it is certainly not the case that these microbes will be able to drive out ordinary microorganisms. The fact that we now have increasing numbers of antibiotic-resistant strains is important both from a scientific, as well as a medical point of view.

The researchers say that regions dominated by one particular type of bacteria play a key role here in these regions the "slow but resistant" strains simply suppress the competition. Feedback mechanisms and the production and absorption of substances in the gut wall also have an effect on the ratio of resistant and sensitive bacteria. The more feedback mechanisms involved, the slower the reduction in the number of sensitive bacteria, while resistant strains die faster. The researchers believe that further studies in this area will be useful to understand the fundamental causes of the emergence of antibiotic-resistant bacteria, and to develop drugs targeted at pathogens.

KNOW A SCIENTIST

Dr. Carlo Urbani

Italian epidemiologist Dr. Carlo Urbani was the first person who identified **SARS** (**Severe Acute Respiratory Syndrome**) as a highly contagious disease. He worked as an infectious disease expert in World Health Organization’s office in the Vietnamese capital, Hanoi, and warned WHO against this deadly disease. As a result of his early warning, millions of lives around the world were saved. But sadly, while treating SARS infected patients, Dr. Urbani himself was infected with the virus and later on died due to complications from the condition.



(A) Toxin-antitoxin system: bacterium produces toxins, which are harmful to itself and digestible to the other bacterial type. (B) Bacteria of one type control abundance of the other bacterial type. (A) and (B) situations have been also examined in inversed edge directions. (C) Gut produces toxins, which are harmful to one bacterial type and digestible to the other one (toxin's type is the same as in A case). (D) Gut controls abundance of bacterial species by producing toxins against one bacterial type (1 or 2). (E) Gut produces digestible substrates for bacteria of type 2.

(**Image credit:** MIPT press office)

Source: www.sciencedaily.com

Teamwork enables bacterial survival

A new study from MIT finds that two strains of bacteria that are each resistant to one antibiotic can protect each other in an environment containing both drugs.

The findings demonstrate that mutualism, a phenomenon in which different species benefit from their interactions with each other, can help bacteria form drug-resistant communities. This is the first experimental demonstration in microbes of a type of mutualism known as cross-protection, which is more commonly seen in larger animals.

The researchers focused on two strains of *E. coli*, one resistant to ampicillin and the other resistant to chloramphenicol. These bacteria and many others defend themselves from antibiotics by producing enzymes that break down the antibiotics. As a side effect, this also protects cells that don't produce those enzymes, by removing the antibiotic from the environment.

"Any time that you're breaking down an antibiotic, there's this potential for cross-protection," says Jeff Gore, the Latham Family Career Development Associate Professor of Physics and the senior author of the study, which appeared in the *Proceedings of the National Academy of Sciences* in May 2016.

The MIT team found that, indeed, both strains could survive in an environment where both antibiotics were present, even though each one was resistant to only one of the drugs. This type of situation is likely also found in the natural world, especially in soil where many strains of bacteria live together.

"Each of them is making different toxins and each of them is resistant to different toxins," Gore says. "A lot of antibiotics are produced by microbes as part of the combat that is taking place between microorganisms in the soil."

Gore and co-authors Eugene Yurtsev and Arolyn Conwill, both MIT graduate students, also found that the populations of the two strains oscillate over time. Population oscillations are common in predator-prey interactions but rare in mutualistic interactions such as the cross-protection seen in this study.

Throughout their experiments, the researchers diluted the bacterial population each day by transferring about 1 percent of the population to a new test tube, to which new antibiotics were added. They found that while the total size of the bacterial population remained more or less the same, there were large oscillations in the relative percentages of each strain, which varied by nearly 1,000 percent over a period of about three days.

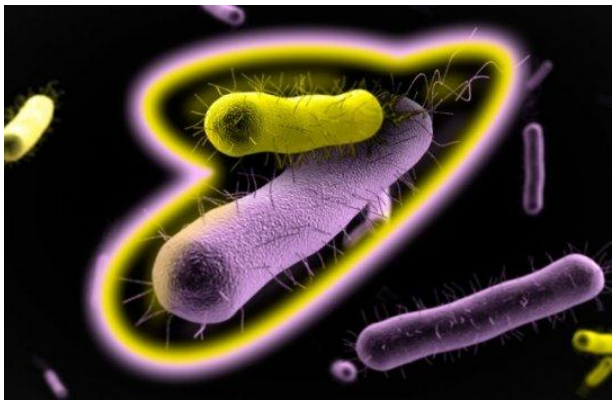
For example, if the ampicillin-resistant strain was more abundant in the beginning of a cycle, it rapidly deactivated ampicillin in the environment, allowing the chloramphenicol-resistant strain to begin growing. The ampicillin-resistant strain only began growing once the other strain had expanded enough to deactivate most of the chloramphenicol, at which point the chloramphenicol-resistant strain had already overtaken the ampicillin-resistant strain.

"The mutualism exhibits oscillations because the strain that is more abundant at the beginning of a growth cycle might end up less abundant at the end of that cycle," Gore says.

At lower antibiotic concentrations, the bacterial population can survive in this oscillating pattern indefinitely, but at higher drug concentrations, the oscillations destabilize the population, and it eventually collapses.

Gore suspects that similar population oscillations may also be seen in natural environments such as the human gut, as bacteria exit the body along with bowel movements, or in soil as bacteria are washed away by rainfall.

Gore's lab is now looking at this type of mutualism in bacteria living in the gut of the worm *C. elegans*. The researchers are also studying how these types of population oscillations can become synchronized over large geographic areas, and how migration between populations influences this synchronization.



Mutualism, a phenomenon in which different species benefit from their interactions with each other, can help bacteria form drug-resistant communities. Pictured is an artist's interpretation of mutualism among bacteria.

(**Image Credit:** Prof. Itamar Willner)

Source: www.sciencedaily.com

Antibiotics don't promote swapping of resistance genes

Researchers have shown that, outside of a few specific examples, antibiotics do not promote the spread of bacterial antibiotic resistance through genetic swapping, as previously assumed.

While the overuse of antibiotics is undeniably at the heart of the growing global crisis, new research published online April 11, 2016 in *Nature Microbiology* suggests differential birth and death rates and not DNA donation are to blame. The results have implications for designing antibiotic protocols to avoid the spread of antibacterial resistance.

According to Lingchong You, the Paul Ruffin Scarborough Associate Professor of Engineering at Duke University and lead author on the paper; bacteria, does not often share resistant genes with each other.

Bacteria can swap DNA through a process called conjugation, which allows helpful genes to spread quickly between individuals and even between species.

Because the number of resistant bacteria rises when antibiotics fail to kill them, researchers assumed that the drugs increased the amount of genetic swapping taking place. But Lingchong You thought maybe the drugs were killing off the two "parent" lineages and allowing a newly resistant strain to thrive instead.

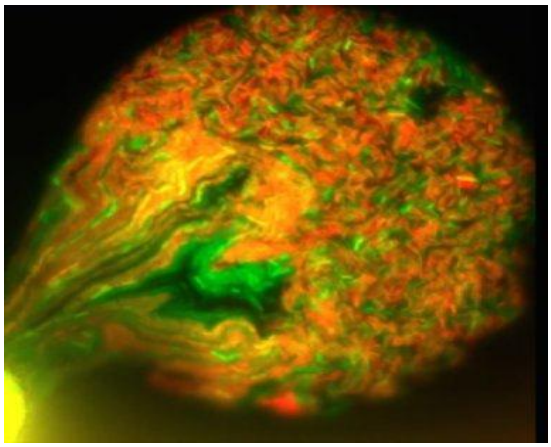
Allison Lopatkin, a doctoral student in You's laboratory and the lead author of the study said they have showed at the single-cell level that the exchange of resistant genes is not influenced by antibiotics at all, which is in contrast to the literature. Previous studies haven't been able to tease these two ideas apart and their work decoupled them.

In their experiments, Bacterial cells were put under a sort of suspended animation where they could neither die nor reproduce but they could still swap genes. With the birth and death rates no longer a variable, the researchers could see how the rate of gene exchanges responded to antibiotics.

They tested nine clinical pathogens commonly associated with the rapid spread of resistance and exposed them to ten common drugs representing each major class of antibiotics. The rates of gene exchange in each test remained flat and, in a few cases, actually decreased slightly as the concentration of antibiotics grew.

Lingchong You points out that there are a few proven examples of antibiotics directly inducing the expression of the genes responsible for donating resistance, but they are very specific. For example, the antibiotic tetracycline induces the expression of genes that only transfer tetracycline resistance.

The new study shows that despite these outliers, antibiotics don't promote resistance spread by inducing global changes at the cellular level. The researchers hope further research will soon help clinicians to design better antibacterial protocols.



Antibiotics can lead to increased populations of resistant bacteria through changes in death-rates rather than an increase in the swapping of resistant genes.
(**Image credit:** Duke University)

Source: www.sciencedaily.com

NEWS

Antimicrobial resistance in soil: Potential impact on the food chain

New research at the University of Southampton is to investigate if large amounts of antibiotic resistant bacteria are present in agricultural soil which may spread into the food chain.

Antimicrobial resistance (AMR) is one of the major issues facing society: by 2050, if not tackled, it will kill more people than cancer deaths and cost, globally, more than the size of the current global economy (Review on Antimicrobial Resistance, 2014).

The aim of the research is to understand how AMR is introduced into natural soil bacteria, for example from manures applied by farmers or exposure to domesticated or wild animal and bird faecal droppings, and how this transfer takes place in different soil types.

The research will help to inform the Government about AMR policy and management strategies.

Professor Bill Keevil and Dr Marc Dumont from the University's Network on Antimicrobial Resistance and Infection Prevention (NAMRIP) are leading the study. Professor Keevil said: "The project addresses if antibiotic resistant bacteria introduced by agricultural practice (animal husbandry, human wastewater disposal, improperly composted manures) or domesticated and wild animal faecal droppings contribute antibiotic resistance genes to the soil microbiome communities or gain resistance genes from the soil antibiotic resistance gene pool (the 'resistome'), becoming more difficult to treat if they are spread in the food chain causing disease."

The work, which has received £198,000 funding from the Natural Environment Research Council (NERC), will take clay, loam and sandy soils obtained from different parts of the country for analysis of their natural antibiotic resistant species before adding important antibiotic resistant or sensitive bacteria to monitor antibiotic resistance transfer.

Source: www.sciencedaily.com

Rare fungus product reduces resistance to antibiotics

Microorganisms, among them fungi, are a natural and rich source of antibiotic compounds. Scientists have succeeded for the first time in extracting the rare compound cPM from a filamentous fungus, applying a special method. Using this substance leads to increased susceptibility of a resistant pathogen against standard antibiotics.

Besides mushrooms such as truffles or morels, also many yeast and mould fungi, as well as other filamentous fungi belong to the Ascomycota phylum. They produce metabolic products which can act as natural antibiotics to combat bacteria and other pathogens. Penicillin, one of the oldest antibiotic agents, is probably the best known example. Since then, fungi have been regarded as a promising biological source of antibiotic compounds. Researchers expect that there is also remedy for resistant pathogens among these metabolites.

It depends on the stimulus

However, agents like penicillin are only produced when necessary, not permanently. "Fungi can even deactivate the respective parts of their genome if a metabolite is not needed anymore. These compounds can't be detected any longer and are classified as cryptic compounds," explained Christoph Zutz from the Institute for Milk Hygiene, Milk Technology and Food Science of the Vetmeduni Vienna.

World Environment Day – June 5, 2016


Creating Awareness among public by issuing pamphlets related to "Fight against the Illegal Trade in Wildlife"




Mr. Magudeswarar, Deputy Tahsildar, Revenue Taluk Office, Karur. Planting sapling and distributing pamphlets to Village people.


Mr. P. Thirumurugan, Information Officer, interacted with School Students to create awareness related to World Environment Day 2016 at **Bharathi Vidyalaya High Schoo**l, Kulithalai, Karur.



Conducted **Drawing Competition** on various topics, related to environment and distributed Prices at **Panjayath Middle School**, Manathattai Village, Karur.
http://dzumenvis.nic.in/wed16.html

The right stimulus can reinduce the production of antibiotic compounds. The researchers used valproic acid which can induce the activation of such deactivated genes in fungi. In the fungus *Doratomyces microsporus*, valproic acid even induced the production of several antimicrobial compounds.

Rare compound detected in fungi for the first time

The gained metabolites were effective against a "normal," as well as resistant *Staphylococcus aureus* pathogens. The team succeeded in filtering out the six most active compounds from all metabolites. These six compounds have been regarded as "cryptic" so far. One compound, cyclo-(L-proline-L-methionine) or cPM, could be detected even for the first time in a fungus. The only source of this compound so far has been a bacterium living in an Antarctic sponge.

Boosting effect as an asset in the fight against resistance

The as yet "cryptic" compound cPM has a special function. It boosts the activity of other antimicrobial compounds. The team assumes that particularly this boosting effect constitutes the effect these compounds have on the tested pathogens.

Therefore, the researchers went a step further and tested the newly detected compound cPM together with ampicillin in two ampicillin-resistant bacteria. The combination has proved successful. "The resistance was demonstrably reduced, even at a lower dose of ampicillin than usually," said co-author and corresponding group leader Kathrin Rychli.

New research platform is looking at the big picture

The team is now going to search for novel antibiotic compounds from other microorganisms by applying similar methods. The new research platform "Bioactive Microbial Metabolites" (BiMM) in Tulln (Lower Austria) provides the facility. BiMM represents the detection of bioactive compounds metabolites in microorganisms. "Valproic acid is not the only way to gain active compounds from fungi or other microorganisms. You can also make bacteria and fungi grow together. This also leads to a natural stimulus," explained Joseph Strauss from the University of Natural Resources and Life Sciences, Vienna, who heads the platform. For this purpose, researchers from the University of Veterinary Medicine, Vienna and the University of Natural Resources and Life Sciences, Vienna founded this new research core facility.

Delivery mode, exposure to antibiotics and feeding method linked to change in baby's microbial communities

Birth by C-section, exposure to antibiotics and formula feeding slow the development and decrease the diversity of a baby's microbes through the first year of life. That is the finding of a study led by researchers from NYU Langone Medical Center and published June 15 in the journal *Science Translational Medicine*.

The study results center on the microbiome, the mix of bacterial species that live on human skin and in our guts, and that co-evolved with humans to play roles in digestion, metabolism and immunity. As rates of children's exposure to C-sections, antibiotic use, and formula feeding have increased in recent decades, the incidence of asthma, autoimmune diseases and obesity has more than doubled. Many studies have now linked these trends, but only a few experiments in mice have shown microbial differences to directly increase disease risk.

"Our results provide evidence that modern practices change a baby's microbial communities in ways that last through the first year," says Martin Blaser, MD, the Muriel G. and George W. Singer Professor of Translational Medicine at NYU School of Medicine, and the study's senior author. "The big, remaining question is whether or not changes in this timeframe, even if resolved later on, affect the founding of microbiomes with lifetime consequences for a child's immune function and metabolism."

Source: www.news-medical.net/

Christoph Zutz identified a significant advantage of this inter-university research platform. "Unlike industrial enterprises, we investigate all promising metabolites in microorganisms, not only single chemical compounds. Thus, we consider known and cryptic compounds in our analyses."

Microorgansims like fungi can be cultivated in the laboratory and stimulated with distinct substances for production of antibiotic metabolic products.

(**Image credit:** BiMM Research/Bioactive Microbial Metabolites)

Source: www.sciencedaily.com

First discovery in United States of colistin resistance in a human *E. coli* infection

The Multidrug Resistant Organism Repository and Surveillance Network (MRSN) at the Walter Reed Army

Institute of Research (WRAIR) characterized a transferrable gene for colistin resistance in the United States that may herald the emergence of truly pan-drug resistant bacteria.

Colistin is the last agent used to combat bacteria that are resistant to the strongest antibiotics. Colistin has remained the best tool available to treat multidrug resistant bacteria because bacteria were not exchanging genes for its resistance. This latest discovery shows that colistin may be losing its effectiveness in antimicrobial therapy. Now, bacteria may be exchanging resistance genes for colistin.

Alarms sounded in the microbiology community in late 2015 when the first transferrable gene for colistin-resistance was identified in China. Since the report, the global health community has monitored and searched for the occurrence of this gene in the food supply and in humans. This colistin-resistance gene has been reported in Europe and Canada and, as of now, is reported in the U.S.

A clinical sample from a urinary tract infection was collected from a patient in a military treatment facility in Pennsylvania. The sample was sent to the Walter Reed National Military Medical Center (WRNMMC) where colistin susceptibility was tested. The results showed that no safe dosage of colistin would be effective to treat such a bacterial infection. WRNMMC recognized colistin-resistance and sent a sample to WRAIR's MRSN for sequencing, which identified the colistin-resistant gene, mcr-1

Through intergovernmental communication, it was learned the CDC and USDA are also reporting a swine intestinal infection with a single mcr-1 positive E. coli strain. While there is no evidence that links these recent findings, the evidence of the strain in the U.S. is a public health concern.

An urgent public health response is underway to contain and prevent potential spread of mcr-1. Active surveillance of multidrug resistant organisms (MDROs), such as mcr-1, allows for earlier and more accurate identification of originating sources. The collection and storage of isolates and samples in the MRSN's growing repository helps researchers identify trends in resistance and prevalence of MDROs and provide best practices for medical providers. The repository also enables them to compare isolates from previous occurrences to better respond to future findings. Recognized as a model program by the White House, the MRSN is a key component of the National Action Plan for Combating Antibiotic Resistant Bacteria (CARB).

This finding has been published by *Antimicrobial Agents and Chemotherapy* (AAC) of the American Society for Microbiology (ASM).

Source: www.sciencedaily.com

Abstracts of Recent Publications

01. Environmental Microbiology, 2016, Vol. **18** (2), Page: 311–313.

Even therapeutic antimicrobial use in animal husbandry may generate environmental hazards to human health. Felipe C. Cabello, Henry P. Godfrey.

Department of Microbiology and Immunology, New York Medical College, Valhalla, New York, USA.

The potential negative impact for human health of veterinary use of antimicrobials in prophylaxis, metaphylaxis and growth promotion in animal husbandry was first established in the 1960s and 1970s. Determination of the molecular structure of antimicrobial resistance plasmids at that time explained the ability of antimicrobial resistance genes to disseminate among bacterial populations and elucidated the reasons for the negative effects of antimicrobials used in food animals for human health. In this issue of *Environmental Microbiology*, Liu *et al*. (2016) show that even therapeutic use of antimicrobials in dairy calves has an appreciable environmental microbiological footprint. We discuss the negative implications of this footprint for human health and the possibility they may lead to calls for increased regulation of veterinary antimicrobial use in terrestrial and aquatic environments.

02. The Lancet Infection Diseases, 2016, Vol. **16** (7), Page: e127–e133.

Aquaculture as yet another environmental gateway to the development and globalisation of antimicrobial resistance. Felipe C Cabello, Henry P Godfrey, Alejandro H Buschmann, Humberto J Dölz.

Department of Microbiology and Immunology, New York Medical College, Valhalla, New York, NY 10595-1524, USA.

Aquaculture uses hundreds of tonnes of antimicrobials annually to prevent and treat bacterial infection. The passage

of these antimicrobials into the aquatic environment selects for resistant bacteria and resistance genes and stimulates bacterial mutation, recombination, and horizontal gene transfer. The potential bridging of aquatic and human pathogen resistomes leads to emergence of new antimicrobial-resistant bacteria and global dissemination of them and their antimicrobial resistance genes into animal and human populations. Efforts to prevent antimicrobial overuse in aquaculture must include education of all stakeholders about its detrimental effects on the health of fish, human beings, and the aquatic ecosystem (the notion of One Health), and encouragement of eco-friendly measures of disease prevention, including vaccines, probiotics, and bacteriophages. Adoption of these measures is a crucial supplement to efforts dealing with antimicrobial resistance by developing new therapeutic agents, if headway is to be made against the increasing problem of antimicrobial resistance in human and veterinary medicine.

03. Antimicrobial Agents Chemotherapy. 2016, Vol. **60** (5), Page: 2972 - 2980.

Distribution and Relationships of Antimicrobial Resistance Determinants among Extended-Spectrum-Cephalosporin-Resistant or Carbapenem-Resistant *Escherichia coli* Isolates from Rivers and Sewage Treatment Plants in India. Masato Akiba *et al*.

Bacterial and Parasitic Disease Research Division, National Institute of Animal Health, National Agriculture and Food Research Organization, Ibaraki, Japan.

To determine the distribution and relationship of antimicrobial resistance determinants among extended-spectrum-cephalosporin (ESC)-resistant or carbapenem-resistant *Escherichia coli* isolates from the aquatic environment in India, water samples were collected from rivers or sewage treatment plants in five Indian states. A total of 446 *E. coli* isolates were randomly obtained. Resistance to ESC and/or carbapenem was observed in 169 (37.9%) *E. coli* isolates, which were further analyzed. These isolates showed resistance to numerous antimicrobials; more than half of the isolates exhibited resistance to eight or more antimicrobials. The bla_{NDM} gene was detected in 14/21 carbapenem-resistant *E. coli* isolates:bla_{NDM-1} in 2 isolates, bla_{NDM-5} in 7 isolates, and bla_{NDM-7} in 5 isolates. The bla_{CTX-M} gene was detected in 112 isolates (66.3%): $bla_{CTX-M-15}$ in 108 isolates and $bla_{CTX-M-55}$ in 4 isolates. We extracted 49 plasmids from selected isolates, and their whole-genome sequences were determined. Fifty resistance genes were detected, and 11 different combinations of replicon types were observed among the 49 plasmids. The network analysis results suggested that the plasmids sharing replicon types tended to form a community, which is based on the predicted gene similarity among the plasmids. Four communities each containing from 4 to 17 plasmids were observed. Three of the four communities contained plasmids detected in different Indian states, suggesting that the interstate dissemination of ancestor plasmids has already occurred. Comparison of the DNA sequences of thebla_{NDM}-positive plasmids detected in this study with known sequences of related plasmids suggested that various mutation events facilitated the evolution of the plasmids and that plasmids with similar genetic backgrounds have widely disseminated in India.

04. mBio , 2016, Vol. **7** (3), Page: 1–8.

How Can Vaccines Contribute to Solving the Antimicrobial Resistance Problem? Marc Lipsitch, George R. Siber.

Center for Communicable Disease Dynamics, Harvard T.H. Chan School of Public Health, Boston, Massachusetts, USA.

There is a growing appreciation for the role of vaccines in confronting the problem of antimicrobial resistance (AMR). Vaccines can reduce the prevalence of resistance by reducing the need for antimicrobial use and can reduce its impact by reducing the total number of cases. By reducing the number of pathogens that may be responsible for a particular clinical syndrome, vaccines can permit the use of narrower-spectrum antibiotics for empirical therapy. These effects may be amplified by herd immunity, extending protection to unvaccinated persons in the population. Because much selection for resistance is due to selection on bystander members of the normal flora, vaccination can reduce pressure for resistance even in pathogens not included in the vaccine. Some vaccines have had disproportionate effects on drug-resistant lineages within the target species, a benefit that could be more deliberately exploited in vaccine design. We describe the effects of current vaccines in controlling AMR, survey some vaccines in development with the potential to do so further, and discuss strategies to amplify these benefits. We conclude with a discussion of research and policy priorities to more fully enlist vaccines in the battle against AMR.

E - Resources on Microorganisms

NATIONAL

National Institute of Technology, Calicut
http://www.nitc.ac.in/

Tezpur University
http://www.tezu.ernet.in/

Indian Institute of Chemical Biology
http://www.iicb.res.in/

Institute of Life Sciences
https://www.ils.res.in/

INTERNATIONAL

Asian Bacterial Bank
http://grbio.org/institution/asian-bacterial-bank

Agricultural Culture Collection of China
http://www.accc.org.cn/htdocs/epages.asp?id=13

Bulgarian Type Culture Collection
http://www.nbimcc.org/en/about.htm

National Culture Collection of Pakistan (NCCP)
http://www.parc.gov.pk/index.php/en/imccp-nccp

EVENTS
Conferences / Seminars / Meetings 2016

Mathematical Modeling and High-Performance Computing in Bioinformatics, Biomedicine and Biotechnology. August 29 - September 02, 2016. **Venue:** Novosibirsk, **Russia**. **Website:** http://conf.bionet.nsc.ru/mm-hpc-bbb-2016/en/2016/04/04/111/#more-111.

XI Meeting of the Molecular Microbiology Group of the Spanish Society for Microbiology. September 06 - 08, 2016 **Venue:** Sevilla, **Spain. Website:** http://micromolecular2016.org/.

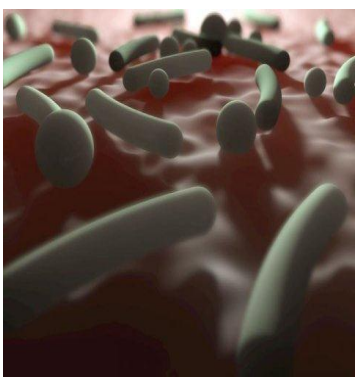
Antimicrobial resistance in biofilms and options for treatment. October 05 - 07, 2016. **Venue:** Ghent, **Belgium. Website:** http://www.biofilmresistance.be/.

From Functional Genomics to Systems Biology. November 12 - 15, 2016. **Venue:** Heidelberg, **Germany**. **Website:** http://www.embl.de/training/events/2016/OMX16-01/index.html.

ASM Conference on Antibacterial Development. December 11 - 14, 2016. **Venue:** Washington, DC, **USA. Website:** http://conferences.asm.org/index.php/upcoming-conferences/asm-conference-on-antibacterial-development

Impact of antibiotic treatment on infant gut microbiome revealed

A comprehensive analysis of changes in the intestinal microbial population during the first three years of life has revealed some of the impacts of factors such as mode of birth, vaginal versus cesarean section and antibiotic exposure, including the effects of multiple antibiotic treatments.

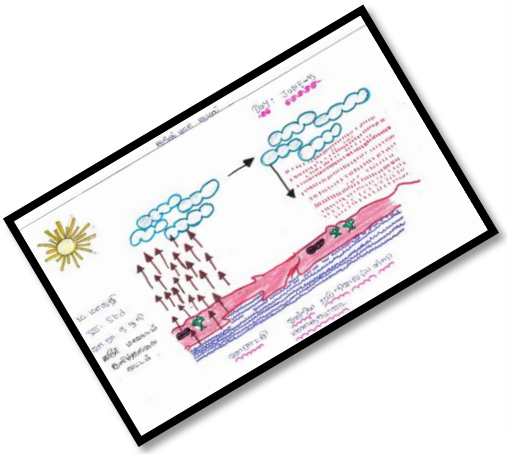


"One of the key motivations of microbiome research is that the microbial population of early childhood appears to be critical to human health, in that decreased diversity of the gut microbiome has been implicated in a number of allergic and autoimmune diseases," says Ramnik Xavier, MD, PhD, chief of the MGH Gastrointestinal Unit and an institute member at the Broad. "Not only did our study analyze the gut microbiome at a high resolution that allowed us to identify both microbial species and strains, but by following our study participants over time we also were able to uncover findings that would not have been revealed by single samples from each patient".

"We need to have biosafety features that allow you to ensure that when you've made something it's not going to escape from the lab, or if it does it won't be able to prosper," Ellington told *New Scientist*. "In the presence of antibiotics and the absence of the [artificial] amino acid, there's very little way for our circuitry to leave the lab." The researchers published their results this week (January 18) in *Nature Chemical Biology*.

Source: www.sciencedaily.com

Art of children – World Environment Day



UNIVERSITY OF MADRAS

ENVIRONMENTAL INFORMATION SYSTEM (ENVIS) CENTRE

(Funded by: Ministry of Environment, Forest & Climate Change, Govt. of India)

DEPARTMENT OF ZOOLOGY

"Fight against the Illegal Trade in Wildlife"

UNEP

WORLD ENVIRONMENT DAY - JUNE 5, 2016

GO WILD FOR LIFE