Boletín
Divulgativo
DE LA FACULTAD DE CIENCIAS AGRARIAS

Boletín
Divulgativo

Editorial

Queridos lectores,

A lo largo del año 2021, el planeta ha enfrentado lo que hoy se conoce como uno de los mayores desafíos globales en el ámbito de la salud pública mundial: la pandemia de COVID-19. Mientras luchamos por contener la propagación del virus y encontrar soluciones efectivas, es fundamental no perder de vista otra amenaza concomitante, creciente y silenciosa: la resistencia a los antimicrobianos. El volumen 4 del Boletín Divulgativo de la Facultad de Ciencias Agrarias de la Fundación Universitaria Agraria de Colombia (UNIAGRARIA), aborda esta importante temática desde el ámbito de la salud y producción animal, considerando el impacto que tiene nuestro ejercicio profesional sobre la salud pública local, regional y mundial, desde el enfoque de Una Salud (*One Health*). La resistencia a los antimicrobianos es un problema grave que afecta a la salud humana, animal y ambiental en todo el mundo. Con la pandemia de COVID-19, el uso excesivo e inadecuado de antimicrobianos ha aumentado significativamente, acelerando el desarrollo de bacterias resistentes a los medicamentos. Además, el uso indiscriminado de antibióticos en la medicina veterinaria ha contribuido en gran medida a la aparición de cepas resistentes de bacterias, incrementando el riesgo para la salud de nuestros animales y, por ende, la nuestra.

En este momento crítico, mientras enfrentamos la postpandemia de COVID-19, no podemos relegar el desafío persistente que supone la resistencia a los antimicrobianos. Como profesionales de la salud, debemos comprometernos y concientizar sobre el uso responsable de antimicrobianos, siguiendo las pautas de prescripción adecuadas y educando a los tenedores de nuestros pacientes sobre la importancia de completar y suministrar los tratamientos de acuerdo con las indicaciones del médico veterinario. Es esencial actuar con

determinación, responsabilidad y unidad para proteger la eficacia y eficiencia de estos medicamentos vitales, así como garantizar un futuro más saludable para todos, contemplando el enfoque de Una Salud (*One Health*).

Diana Yamile Gallego Villa y Yenny Catherine Pinilla López, Equipo Editorial de la Facultad de Ciencias Agrarias – UNIAGRARIA

OPS (2022). Resistencia Antimicrobiana en Producción Animal [Ilustración]. Organización Panamericana de la Salud.

https://www.paho.org/es/panaftosa/resistencia-antimicrobiana-produccion-animal

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Contenido

Emergencia de la resistencia antimicrobiana: amenaza latente y consecuencias de la pandemia

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La resistencia a los antibióticos es reconocida como una de las grandes preocupaciones en la salud pública y ha persistido desde hace varias décadas. Este fenómeno afecta especialmente a aquellos antimicrobianos que se usan como última opción terapéutica. A pesar de los numerosos esfuerzos de los gobiernos y organizaciones, estos no han sido suficientes para mitigar una de las mayores amenazas de nuestra época, la cual también se relaciona estrechamente con los Objetivos de Desarrollo Sostenible (ODS). La Resistencia a los Antimicrobianos (RAM), presenta un comportamiento comparable con un síndrome, debido a las diversas causas que desencadenan este problema, lo que dificulta la lucha contra estas células procariotas.

Además de las bacterias con resistencia intrínseca, la adquisición de genes de resistencia a los antibióticos de última elección agrava el problema. Este recrudecimiento está ligado a prácticas como la automedicación, la formulación o uso incorrecto de los antimicrobianos, la disponibilidad de pocas moléculas que resultan efectivas y la contaminación del medio ambiente con bacterias que transfieren genes de resistencia de manera horizontal.

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Asimismo, los residuos de antibióticos usados tanto en la industria terapéutica como en la farmacéutica, favorecen la diseminación de resistencia a través de plásmidos.

Imagen 1. (Fuente propia).

La disponibilidad reducida de moléculas potenciales para eliminar bacterias de importancia a nivel oportunista y nosocomial, ya sean multi-droga resistentes (MDR) o pan-resistentes, afecta directamente a naciones en vías de desarrollo, a los países con enfermedades endémicas y, sobre todo, a los sistemas de salud donde el rubro destinado para dichas áreas es reducido. El panorama se complica aún más con la pandemia de COVID-19, que trajo consigo grandes desafíos y retrocesos, especialmente en la investigación de enfermedades transmisibles por vectores y en las transmisiones

horizontales de genes de resistencia. La mayoría de los esfuerzos se enfocaron en el comportamiento de la enfermedad viral, lo que resultó en un aumento en las tasas de resistencia de varios antibióticos prioritarios utilizados para infecciones oportunistas producidas por bacterias gramnegativas, como los carbapenémicos, e incluso en bacterias grampositivas, que fueron utilizados masivamente durante esta emergencia.

Desde la perspectiva Una Salud (*One Health*), se presentan varios retos para abordar de forma holística este objetivo prioritario a nivel mundial. Se estima que para el año 2030 las opciones terapéuticas frente a estos microrganismos serán casi nulas. Además, varias de las líneas de desarrollo de moléculas efectivas para eliminar este tipo de microrganismos se reducen a escasas opciones. Según un informe desarrollado por la Organización Mundial de la Salud (OMS), en medio de uno de los panoramas más desafiantes del siglo, de entre decenas de opciones plausibles para patógenos primarios, solo seis fueron clasificadas como innovadoras (OMS, 2021). Dicho esto, estamos en una carrera contra el tiempo, ya que las bacterias han resultado ser más "audaces y rápidas" que los esfuerzos humanos dirigidos al desarrollo de antibacterianos. Según datos de del Sistema de Vigilancia de la Resistencia a los Antimicrobianos y de su Uso (GLASS) de 2020, se incluyen patógenos MDR como *Escherichia coli, Acinetobacter spp., Klebsiella pneumoniae, Salmonella spp., Shiguella spp., Staphylococcus aureus y Streptococcus pneumoniae* (OMS, 2020), los cuales tienen importancia clínica no solo en la medicina humana sino también en la medicina veterinaria.

Sin embargo, es crucial reconocer los esfuerzos que están realizando los miembros de la alianza tripartita (OMS-OMSA-FAO) (Organización Mundial de Sanidad Animal y Organización de las Naciones Unidas para la Agricultura y la Alimentación). Esta alianza, dentro del Plan de Acción Mundial, tiene como objetivo reducir las tasas de resistencias involucrando aspectos económicos, político-sociales y la colaboración de profesionales de varias disciplinas dentro del enfoque Una Salud (*One Health*).

A esta situación se suma el empleo de antibióticos como la colistina (antibiótico de última elección en infecciones por bacterias resistentes a los carbapenémicos), que ha sido usado en medicina veterinaria y zootecnia por muchos años, contribuyendo al problema. Sin embargo, se han tomado medidas de impacto global para mitigar la diseminación de la resistencia a la colistina a través del gen mcr y sus variantes. Colombia fue pionera en Sudamérica en 2015, ya que prohibió la importación, fabricación, registro, comercialización y uso de aditivos que contengan polimixina E (colistina) y polimixina B, como promotores de crecimiento en especies animales productoras de alimentos para el consumo humano (ICA, 2015), seguido por otros países de la región.

Por tal razón, si no se toman medidas decisivas ahora, nos enfrentamos a un futuro en que las resistencias bacterianas a los antibióticos podrían convertirse en la próxima pandemia y una potencial amenaza mortal. El compromiso de los profesionales involucrados en el enfoque Una Salud (*One Health*) es fundamental para unir esfuerzos en beneficio de la salud humana, de las futuras generaciones, y de la salud animal y del medio ambiente.

2. Artículos y publicaciones de interés
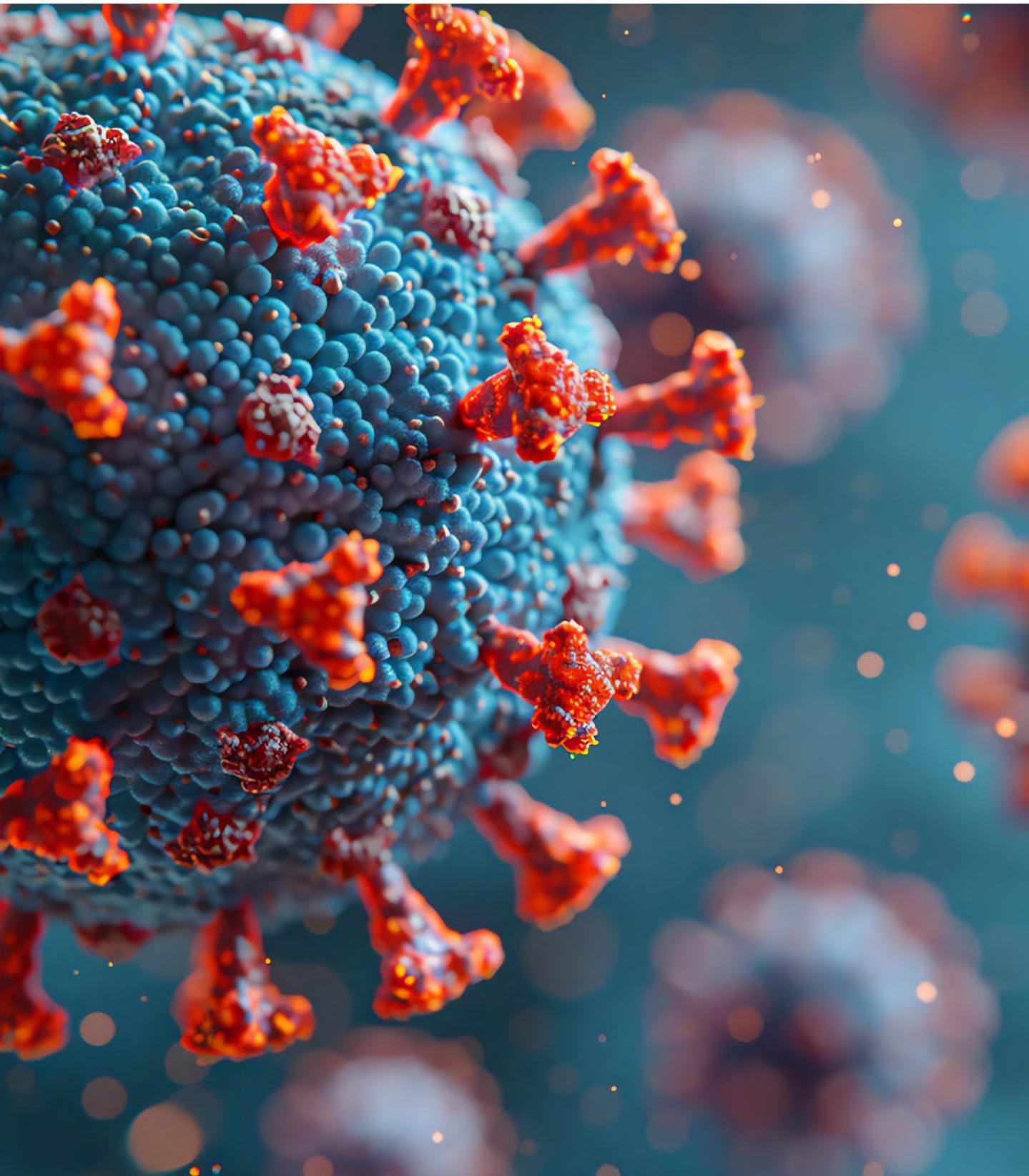
University of Bristol (2021). *Helen Lambert wins a BSAC award to study the implications of COVID-19 for AMR in China and other LMIC settings* [Ilustración]. University of Bristol

https://www.bristol.ac.uk/blackwell/news/2021/helen-lambert-bsac-award-amr-covid-19.html
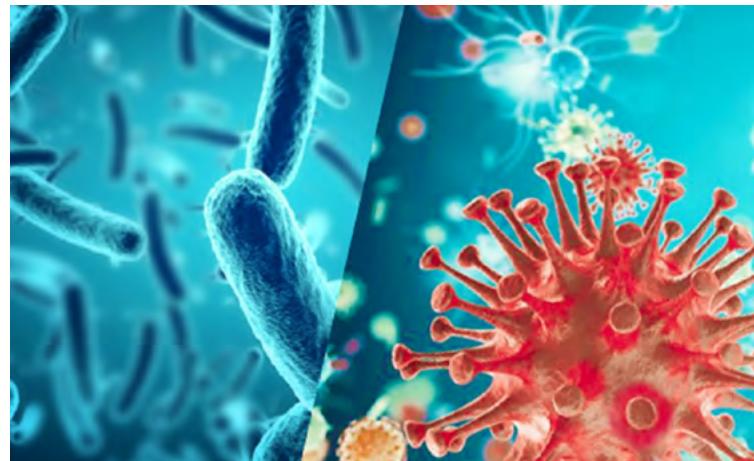
Bacterial and fungal growth in sputum cultures from 165 COVID-19 pneumonia patients requiring intubation: evidence for antimicrobial resistance development and analysis of risk factors

Context: The coronavirus SARS-CoV-2 causes COVID-19, an illness that can progress to severe pneumonia. Empiric antibacterial treatment is often used, though the frequency of bacterial coinfection and superinfection is debated. There are also concerns regarding the selection of bacterial antimicrobial resistance due to these treatments.

We evaluated sputum bacterial and fungal growth from 165 intubated COVID-19 pneumonia patients. Our objectives were to determine frequency of culture positivity, identify risk factors for positive cultures, assess the outcomes of these cultures, and examine the timing of antimicrobial resistance development.

Methods: Retrospective reviews were conducted of COVID-19 pneumonia patients requiring intubation, who were admitted to a 1058-bed, four-community hospital system on the East Coast of the United States from March 1 to May 1, 2020. The length of stay (LOS) was expressed as mean (standard deviation); 95% confidence interval (95% CI) was computed for overall mortality rate using the exact binomial method, and overall mortality was compared across each level of a potential risk factor using a Chi-Square Test of Independence. All tests were two-sided, and significance level was set to 0.05.

Results: The results demonstrated that the average patient age was 68.7 years and

LOS was 19.9 days. A total of 83 patients (50.3% of total) originated from home, 10 from group homes (6.1% of total), and 72 from nursing facilities (43.6% of total). Mortality was 62.4%, highest for nursing home residents (80.6%). Findings from 253 sputum cultures overall did not suggest acute bacterial or fungal infection in 73 (45%) of 165 individuals sampled within 24 hours of intubation. Cultures ≥1 week following intubation did grow potential pathogens in 72 (64.9%) of 111 cases with 70.8% consistent with late pneumonia, and 29.2% suggesting colonization. Twelve (10.8% of total) of these late post-intubation cultures revealed worsened antimicrobial resistance, predominantly in *Pseudomonas, Enterobacter, and Staphylococcus aureus.*

Conclusions: In severe COVID-19 pneumonia, a radiographic ground glass interstitial pattern and lack of purulent sputum, prior to/around the time of intubation, correlated with no culture growth or recovery of normal oral fora±yeast. Discontinuation of empiric antibacterial should be considered in these patients, aided by other clinical findings, history of prior antimicrobials, laboratory testing, and overall clinical course. Continuing long-term hospitalization and antibiotic use are associated with sputum cultures reflective of hospital-acquired microbes and increasing antimicrobial resistance.

Liu, H. H., Yaron, D., Piraino, A. S., & Kapelusznik, L. (2021). Bacterial and fungal growth in sputum cultures from 165 COVID-19 pneumonia patients requiring intubation: evidence for antimicrobial resistance development and analysis of risk factors. A*nn Clin Microbiol Antimicrob*, 20, 69.

https://doi.org/10.1186/s12941-021-00472-5

Antimicrobial susceptibility patterns of respiratory gram-negative bacterial isolates from COVID-19 patients in Switzerland

Context: Bacterial superinfections associated with COVID-19 are common in ventilated ICU patients and significantly impact morbidity and mortality. However, the role of antimicrobial resistance in the manifestation of bacterial infections in these patients has yet to be fully elucidated.

Methods: We collected 70 Gram-negative bacterial strains, isolated from the lower respiratory tract of ventilated COVID-19 patients in Zurich, Switzerland, between March and May 2020. Species identification was performed using MALDI-TOF, antibiotic susceptibility profiles were determined by EUCAST disk diffusion and, CLSI broth microdilution assays. Selected *Pseudomonas aeruginosa* isolates were analyzed by whole-genome sequencing.

Results: *Pseudomonas aeruginosa* (46%) and *Enterobacterales* (36%) comprised the two largest etiologic groups. Drug resistance in *P. aeruginosa* isolates was high for piperacillin/tazobactam (65.6%), cefepime (56.3%), ceftazidime (46.9%) and meropenem (50.0%).

Enterobacterales isolates showed slightly lower levels of resistance to piperacillin/tazobactam (32%), ceftriaxone (32%), and ceftazidime (36%). All *P. aeruginosa* isolates and 96% of *Enterobacterales* isolates were susceptible to aminoglycosides, with apramycin found to provide best-in-class coverage. Genotypic analysis of consecutive *P. aeruginosa* isolates in one patient revealed a frameshift mutation in the transcriptional regulator NalC that coincided with a phenotypic shift in susceptibility to β-lactams and quinolones.

Conclusions: Considerable levels of antimicrobial resistance may have contributed to the manifestation of bacterial superinfections in ventilated COVID-19 patients and may, in some cases, mandate consecutive adaptation of antibiotic therapy. High susceptibility to amikacin and apramycin suggests that aminoglycosides may remain an effective second-line treatment of ventilator-associated bacterial pneumonia, provided efficacious drug exposure in lungs can be achieved.

Gysin, M., Acevedo, C. T., Haldimann, K., Bodendoerfer, E., Imkamp, F., Bulut, K., Karl-Buehler, P., Brugger S. D., & Hobbie S. N. (2021). Antimicrobial Susceptibility Patterns of Respiratory Gram-Negative Bacterial Isolates from COVID-19 Patients in Switzerland. *Ann Clin Microbiol Antimicrob,* 20, 64.

https://doi.org/10.1186/s12941-021-00468-1

A general public study on preferences and welfare impacts of antimicrobial resistance in the United Kingdom

Context: Antibiotics have led to considerable increases in life expectancy. However, over time, antimicrobial resistance has accelerated and is now a significant global public health concern. Understanding societal preferences for antibiotic use and gauging the willingness to pay for future research are crucial steps in addressing this issue.

Objective: To investigate preferences for different strategies to optimize antibiotic use and to understand the willingness to pay for future research in antimicrobial resistance and antimicrobial drug development.

Methods: A discrete-choice experiment was administered to a sample of the UK general population. Respondents were asked to make nine choices, each offering three options—two hypothetical "doctor and antibiotics" and one "no doctor—no antibiotics"—defined by five attributes: treatment, days needed to recover, risk of bacterial infection in need of antibiotics, risk of common side effects, and risk of antimicrobial resistance by 2050. Data were analyzed using random parameters logit models. A double-bounded contingent valuation was included in the survey to explore the willingness to pay for policies to contain antimicrobial resistance.

Results: Among the 2579 respondents who completed the survey, 1151 always selected "no doctor-no antibiotics" and 57

never varied their choices. Therefore, 1371 responses were used in the analysis. The risk of antimicrobial resistance by 2050 was the most important attribute and the "treatment" was the least important one, although this was sensitive to a higher risk of bacterial infection. The aggregate annual willingness to pay for containing antimicrobial resistance was approximately £8.35 billion (~£5–£10 billion).

Conclusions: The antimicrobial resistance risk is relevant and important to the general public. The high willingness to pay suggests that large investments in policies or interventions to combat antimicrobial resistance are justified.

Dorgali, M. V., Longo, A., Vass, C. Shields, G., Harrison, R., Scarpa R., & Boeri, M. (2022). A General Public Study on Preferences and Welfare Impacts of Antimicrobial Resistance in the United Kingdom. *PharmacoEconomics*, 40, 65–76.

https://doi.org/10.1007/s40273-021-01076-9

Global research publications on irrational use of antimicrobials: a call for more research to contain antimicrobial resistance

Context: The irrational use of antimicrobials is highly prevalent and a major driving factor for antimicrobial resistance (AMR). Research on this issue is crucial for developing policies and regulations to combat and contain AMR. The present study aims to provide an overview of research publications on the irrational use of antimicrobials at the national and global levels.

Methods: Publications on irrational use of antimicrobials were extracted from Scopus using a wide range of relevant keywords for the study period from 1980 to 2020.

Results: In total, 656 publications on irrational use of antimicrobials were found. The bulk of publications in this field were about irrational use in humans. A limited number of publications were found on the irrational use of antimicrobials in the context of veterinary and the environment. The number of publications, contributing countries, and the mean number of authors per article increased with time, most notably in the last decade. Authors from 105 different countries contributed to the retrieved articles, with 22 countries (21.0%) having participated in 10 or more publications. The United States led with 140 (21.6%) articles, followed distantly by China (n = 49, 7.5%), India (n = 45, 6.9%), and the United Kingdom (n = 45, 6.9%). Countries in the South-East Asian region (n = 69, 10.5%) and the African region (n = 42, 6.4%) made the smallest contribution. The list of most frequent author keywords included "antimicrobial stewardship" and "community pharmacies". The research themes focused on the hospital-based rational use of antimicrobials and the self-medication practices with antimicrobials in the community. In total, 420 different journals participated in publishing the retrieved documents. The PLOS One journal (17, 2.6%) ranked first. The

retrieved articles received an average of 15.6 citations per article and an h-index of 52. The most frequent antimicrobials encountered in the retrieved literature were penicillin, cephalosporin, and fluoroquinolones, while the most frequently encountered pathogens were S. aureus and *P. aeruginosa*.

Conclusion: There is a need for research on the irrational use of antimicrobials across all countries and regions to develop effective policies for containing antimicrobial resistance (AMR). Specifically, research focusing on the irrational use of antimicrobials in veterinary contexts is crucial.

Sweileh, W. M. (2021). Global research publications on irrational use of antimicrobials: call for more research to contain antimicrobial resistance. *Global Health*, 17, 94.

https://doi.org/10.1186/s12992-021-00754-9

Combined effects of composting and antibiotic administration on cattle manure–borne antibiotic resistance genes

Context: Research is needed to delineate the relative and combined effects of different antibiotic administration and manure management practices, in either amplifying or attenuating the potential for antibiotic resistance to spread.

Methods: We carried out a comprehensive parallel examination of the effects of small-scale (> 55 °C × 3 days) static and turned composting of manures from dairy and beef cattle. The manures were collected during standard antibiotic administration (cephapirin/pirlimycin or sulfamethazine/chlortetracycline/tylosin, respectively) and from untreated cattle. We assessed the impact on resistomes (total antibiotic resistance genes (ARGs) determined via shotgun metagenomic sequencing), bacterial microbiota, and indicator ARGs quantified via quantitative polymerase chain reaction. To gain insight into the role of the thermophilic phase, compost was also externally heated to > 55 °C for 15 days.

Results: The progression of composting over time and succession of the corresponding bacterial microbiota was the primary drivers of resistome composition in all small-scale composts (ANOSIM; R = 0.424, P = 0.001, respectively). Reduction in relative abundance (16S rRNA gene normalized) of total ARGs in finished compost (day 42) versus day 0 was noted across all conditions (ANOSIM; R = 0.728, P = 0.001), except when externally heated. Sul1, intI1, beta-lactam ARGs, and plasmid-associated genes increased in all finished composts as compared with the initial condition. External heating proved to be more effective in reducing certain clinically relevant ARGs (blaOXA, blaCARB), fecal coliforms, and resistome risk scores, which take into account putative pathogen annotations. When manure was collected during antibiotic administration, the taxonomic composition of the compost differed distinctly according to nonmetric multidimensional scaling analysis. Additionally, the tet(W) gene

decayed at different rates depending on the type of manure and antibiotic treatment: it decayed faster in dairy manure treated with antibiotics and slower in beef manure under the same conditions.

Conclusions: This comprehensive integrated study revealed that composting had a dominant effect on corresponding resistome composition, while little difference was noted as a function of collecting manure during antibiotic administration. Reduction in total ARGs, tet(W), and resistome risk suggested that composting reduced some potential for antibiotic resistance to spread, but the increase and persistence of other indicators of antibiotic resistance were concerning. Results indicate that composting guidelines intended for pathogen reduction do not necessarily provide a comprehensive barrier to ARGs or their mobility prior to land application and additional mitigation measures should be considered.

Keenum, I., Williams, R. K., Ray, P., Garner, E. D., Knowlton, K. F., & Pruden, A. (2021). Combined effects of composting and antibiotic administration on cattle manure–borne antibiotic resistance genes. *Microbiome* 9, 81.

https://doi.org/10.1186/s40168-021-01006-z

Knowledge, attitudes and practices of animal farm owners/workers on antibiotic use and resistance in amhara region, northwestern Ethiopia

Context: The inappropriate use of antibiotics in animals and humans contributes to the emergence and spread of antibiotic-resistant bacteria, posing a significant threat to human health. Although extensive use of these antibiotics could contribute to the development of drug resistance, information on the knowledge, attitude and practice of antimicrobial resistance and use among animal farm owners/workers in northwestern Ethiopia is rare. The objective of the present study was to assess knowledge, attitudes and practices of animal farm owner/workers towards antibiotic resistance and use in Amhara regional state in northwestern Ethiopia.

Methods: A cross-sectional study was conducted in selected cities of Amhara regional state from January to February 2020. Data was collected from 91 participants using a structured questionnaire and it was later analyzed using SPSSS version 23.

Results: The results showed that 96.7% of respondents administered antibiotics to their livestock from different sources. Most of the respondents bought their antibiotics from private pharmacies, without prescription. The most frequently mentioned antibiotic used to treat animal diseases was tetracycline (76.9%), followed by ampicillin (72.5%). Although, 90.1% of the animal farm owners heard about antibiotics and antibiotic

resistance from different sources, they did not know the factors contributing to the transmission of resistant bacteria to humans and the impact of antibiotic resistance on human and animals' health. Using the mean score 4.44 ± 0.15 as the cut-off, half of the animal farm owners/workers had good knowledge about antimicrobial resistance and use. In addition, 52.5% of animal farm owners/workers had positive attitudes towards wise antibiotic use and resistance with a mean score of 28.4 ± 0.5. However, 52.75% participants had poor practices, with the mean score of practice 4.95 ± 0.17. Better knowledge, positive attitudes and better practices on antibiotic use and resistance were associated with farm owners/workers who engaged in higher education.

Conclusions: Although 76.9% of respondents perceived poor awareness of antimicrobial resistance as a very important factor contributing to increasing antibiotic resistance, the majority of respondents viewed the use of complementary treatments as a crucial strategy to reduce antibiotic use and resistance. The current study disclosed that there is low level of awareness among animal farm owners about the correct use of antibiotics and resistance. It is necessary to raise awareness, develop and implement interventions to reduce antimicrobial use and antibiotic resistance in the study area.

Geta, K. & Kibret, M. (2021). Knowledge, attitudes and practices of animal farm owners/workers on antibiotic use and resistance in Amhara region, Northwestern Ethiopia. *Sci Rep*, 11, 21211.
https://doi.org/10.1038/s41598-021-00617-8

Antibiotic resistance of fecal carriage of *Escherichia coli* from pig farms in China: a meta-analysis

context: Fecal carriage of bacteria is a major source of antibiotic resistance genes (ARGs) and a public health risk, but the antibiotic resistance of *Escherichia coli* (*E. coli*) in Chinese pig farms remains a major gap in the available literature.

Methods: Our goal was to conduct a meta-analysis of studies reporting antibiotic resistance of fecal carriage of *E. coli* from pig farms in China, calculating the pooled resistance rates and summarizing factors associated with it. We searched PubMed and Web of Science for studies published in English up to February 28, 2021. We also searched bibliographic indices and corresponded with the authors. We chose ciprofloxacin, gentamicin, tetracycline, ampicillin, and florfenicol from five major types of antibiotics to comprehensively evaluate the resistance rate of *E. coli*. We used a random-effects model and Freeman-Tukey double arcsine transformation to calculate the resistance rate and 95% confidence interval. Among the 120 retrieved manuscripts, 16 studies (1985 *E. coli* isolates) were deemed eligible for our analysis.

Results: The combined resistance rate of *E. coli* from feces was 58.8% (95% CI: 45.3–

71.7%) to ciprofloxacin, 54.3% (95% CI: 35.3–72.6%) to gentamicin, 91.0% (95% CI: 83.1–96.7%) to tetracycline, 81.4% (95% CI: 62.0–95.1%) to ampicillin, and 65.4% (95% CI: 33.9–90.9%) to florfenicol.

Conclusions: In conclusion, fecal carriage of *E. coli* in Chinese pig farms shows high resistance to ciprofloxacin, gentamicin, tetracycline, ampicillin, and florfenicol. Subgroup analysis showed that the resistance of *E. coli* to antibiotics was closely related to the sample size and the health condition of the pigs. Specifically, ESBL-producing

E. coli has a higher ratio of resistance to other antibiotics. Future collection of antibiotic resistance data and other relevant information on pig farms should be more precise and based on local surveys.

Li, M., Li, Z., Zhong, Q., Liu, J., Han, G., Li, Y., & Li, C. (2022). Antibiotic resistance of fecal carriage of Escherichia coli from pig farms in China: a meta-analysis. *Environ Sci Pollut Res* 29, 22989–23000.

https://doi.org/10.1007/s11356-021-17339-z

Oral prodrug of remdesivir parent GS-441524 is efficacious against SARS-COV-2 in ferrets

Remdesivir is an antiviral approved for COVID-19 treatment, but its wider use is limited by intravenous delivery. An orally bioavailable remdesivir analog may boost therapeutic benefit by facilitating early administration to non-hospitalized patients. This study characterizes the anti-SARS-CoV-2 efficacy of GS-621763, an oral prodrug of remdesivir parent nucleoside GS-441524. Both GS-621763 and GS-441524, inhibit SARS-CoV-2, including variants of concern (VOC) in cell culture and human airway epithelium organoids. Oral GS-621763 is efficiently converted to plasma metabolite GS-441524, and in lungs to the triphosphate metabolite identical to that generated by remdesivir, demonstrating a consistent mechanism of activity. Twice-daily oral administration of 10 mg/kg GS-621763 reduces SARS-CoV-2 burden to near-undetectable levels in ferrets. When dosed therapeutically against

VOC, P.1 gamma γ, oral GS-621763 blocks virus replication and prevents transmission to untreated contact animals. These results demonstrate therapeutic efficacy of a much-needed orally bioavailable analog of remdesivir in a relevant animal model of SARS-CoV-2 infection.

Cox, R. M., Wolf, J. D., Lieber, C. M., Sourimant, J., Lin, M. J., Babusis, D., DuPont, V., Chan, J., Barret, K. T., Lye, D., Kalla, R., Chun, K., Mackman, R. L., Ye, C., Cihlar, T., Martinez-Sobrido, L., Greninger, A. L., Bilello, J. P., & Plempler, R. K. (2021). Oral prodrug of remdesivir parent GS-441524 is efficacious against SARS-CoV-2 in ferrets. *Nat Commun*, 12, 6415.

https://doi.org/10.1038/s41467-021-26760-4

Reversion of antibiotic resistance in multidrug-resistant pathogens using non-antibiotic pharmaceutical benzydamine

Antimicrobial resistance has been a growing concern that gradually undermines our tradition treatment regimens. The fact that few antibacterial drugs with new scaffolds or targets have been approved in the past two decades aggravates this crisis. Repurposing drugs as potent antibiotic adjuvants offers a cost-effective strategy to mitigate the development of resistance and to tackle increasing infections by multidrug-resistant (MDR) bacteria. Herein, we found that benzydamine, a widely used non-steroidal anti-inflammatory drug, remarkably potentiated broad-spectrum antibiotic-tetracyclines activity against a panel of clinically important pathogens, including MRSA, VRE, MCRPEC and tet(X)-positive Gram-negative bacteria. Mechanistic studies showed that benzydamine dissipated membrane potential ($\Delta\Psi$) in both Gram-positive and Gram-negative bacteria, which in turn upregulated the transmembrane proton gradient (ΔpH) and promoted the uptake of tetracyclines. Additionally, benzydamine exacerbated the oxidative stress by triggering the production of ROS and suppressing GAD system-mediated oxidative defensive. This mode of action explains the great bactericidal activity of the doxycycline-benzydamine combination against different metabolic states of bacteria including persister cells. As a proof-of-concept, the in vivo efficacy of this drug combination was evidenced in multiple animal infection models. These findings indicate that benzydamine is a potential tetracyclines adjuvant to address life-threatening infections by MDR bacteria.

Liu, Y., Tong, Z., Shi, J., Jia, Y., Deng, T., Wang, Z. (2021). Reversion of antibiotic resistance in multidrug-resistant pathogens using non-antibiotic pharmaceutical benzydamine. *Commun Biol* 4, 1328.

https://doi.org/10.1038/s42003-021-02854-z

A synthetic antibiotic class overcoming bacterial multidrug resistance

The dearth of new medicines effective against antibiotic-resistant bacteria presents a growing global public health concern. For more than five decades, the search for new antibiotics has relied heavily on the chemical modification of natural products (semisynthesis), a method ill-equipped to combat rapidly evolving resistance threats. Semisynthetic modifications within polyfunctional antibiotics are typically limited in scope, usually increase molecular weight, and rarely allow for

alterations to the underlying scaffold. When properly designed, fully synthetic routes can easily address these shortcomings. Here we report the structure-guided design and component-based synthesis of a rigid oxepanoproline scaffold which, when linked to the aminooctose residue of clindamycin, produces an antibiotic of exceptional potency and spectrum of activity, which we name iboxamycin. This antibiotic is effective against ESKAPE pathogens, including strains expressing Erm and Cfr ribosomal RNA methyltransferase enzymes, products of genes that confer resistance to all clinically relevant antibiotics targeting the large ribosomal subunit, namely macrolides, lincosamides, phenicols, oxazolidinones, pleuromutilins and streptogramins. X-ray crystallographic studies of iboxamycin in complex with the native bacterial ribosome, as well as with the Erm-methylated ribosome, uncover the structural basis for this enhanced activity, including a displacement of the nucleotide upon antibiotic binding. Iboxamycin is orally bioavailable, safe and effective in treating both Gram-positive and Gram-negative bacterial infections in mice, attesting to the capacity for chemical synthesis to provide new antibiotics in an era of increasing resistance.

Mitcheltree, M. J., Pisipati, A., Syroegin, E. A., Silvestre, K. J., Klepacki, D., Mason, J. D., Terwilliger, D. W., Testolin, G., Pote, A. R., Why, K. J. Y., Ladley, R. P., Chatman, K., Mankin, A. S., Polikanov, Y. S., & Myers, A. G. (2021). A synthetic antibiotic class overcoming bacterial multidrug resistance. *Nature*, 599, 507–512.

https://doi.org/10.1038/s41586-021-04045-6

Antibiotic-resistant bacteria, antibiotic resistance genes, and antibiotic residues in wastewater from a poultry slaughterhouse after conventional and advanced treatments

Slaughterhouse wastewater is considered a reservoir for antibiotic-resistant bacteria and antibiotic residues, which are not sufficiently removed by conventional treatment processes. This study focuses on the occurrence of ESKAPE bacteria (Enterococcus spp., S. aureus, K. pneumoniae, A. baumannii, P. aeruginosa, Enterobacter spp.), ESBL (extended-spectrum β-lactamase)-producing *E. coli*, antibiotic resistance genes (ARGs) and antibiotic residues in wastewater from a poultry slaughterhouse. The efficacy of conventional and advanced treatments, such as ozonation, in the in-house wastewater treatment plant was also evaluated for their removal efficiency. Target culturable bacteria were detected only in the influent and effluent after conventional treatment. High abundances of genes (e.g., blaTEM, blaCTX-M-15, blaCTX-M-32, blaOXA-48, blaCMY and mcr-1) of up to 1.48×10^6 copies/100 mL were detected in raw influent.

All of them were already significantly reduced by 1–4.2 log units after conventional treatment. Following ozonation, mcr-1 and blaCTX-M-32 were further reduced below the limit of detection. Antibiotic residues were detected in 55.6% (n = 10/18) of the wastewater samples. Despite the significant reduction through conventional and advanced treatments, effluents still exhibited high concentrations of some ARGs (e.g., sul1, ermB and blaOXA-48), ranging from 1.75×10^2 to 3.44×10^3 copies/100 mL. Thus, a combination of oxidative, adsorptive and membrane-based technologies should be considered.

Savin, M., Alexander, J., Bierbaum, G., Hammerl, J. A., Hembach, N., Schwartz, T., Schumithausen, R. M., Sib, E., Voigt, A., & Kreyenschmidt, J. (2021). Antibiotic-resistant bacteria, antibiotic resistance genes, and antibiotic residues in wastewater from a poultry slaughterhouse after conventional and advanced treatments. *Sci Rep*, 11, 16622.

https://doi.org/10.1038/s41598-021-96169-y

A trimethoprim derivative impedes antibiotic resistance evolution

The antibiotic trimethoprim (TMP) is used to treat a variety of Escherichia coli infections, but its efficacy is limited by the rapid emergence of TMP-resistant bacteria. Previous laboratory evolution experiments have identified resistance-conferring mutations in the gene encoding the TMP target, bacterial dihydrofolate reductase (DHFR), in particular the L28R mutation. Here, we show that 4'-desmethyltrimethoprim (4'-DTMP) inhibits both DHFR and its L28R variant and selects against the emergence of TMP-resistant bacteria that carry the L28R mutation in laboratory experiments. Furthermore, antibiotic-sensitive *E. coli* populations acquire antibiotic resistance at a substantially slower rate when grown in the presence of 4'-DTMP, than in the presence of TMP. We find that 4'-DTMP impedes evolution of resistance by selecting against resistant genotypes with the L28R mutation and diverting genetic trajectories to other resistance-conferring DHFR mutations with catalytic deficiencies. Our results demonstrate how a detailed characterization of resistance-conferring mutations in a target enzyme can help identify potential drugs against antibiotic-resistant bacteria, which may ultimately increase long-term efficacy of antimicrobial therapies by modulating evolutionary trajectories that lead to resistance.

Manna, M.S., Tamer, Y.T., Gaszek, I., Poulides, N., Ahmed, A., Wang, X., Toprak, C. R., Woodward, D. R., Koh, A. Y., Williams, N. S., Borek, D., Rana-Atilgan, A., Hulleman, J. D., Atilgan, C., Tambar, U. & Toprak, E. (2021). A trimethoprim derivative impedes antibiotic resistance evolution. *Nat Commun* 12, 2949.

https://doi.org/10.1038/s41467-021-23191-z

Ciprofloxacin induced antibiotic resistance in *Salmonella Typhimurium* mutants and genome analysis

Antibiotic resistance of Salmonella species is well reported, with ciprofloxacin being the frontline antibiotic for salmonellosis. The repeated exposure to ciprofloxacin leads to resistant strains. After 20 cycles of antibiotic exposure, resistant bacterial clones were evaluated. The colony size of the mutants was small and had an extended lag phase compared to parent strain. The whole genome sequencing showed 40,513 mutations across the genome. A small percentage (5.2%) of mutations was non-synonymous. Four-fold more transitions were observed than transversions and the ratio of < 1 transition vs. transversion showed a positive selection for antibiotic resistant trait. Mutation distribution across the genome was uniform. The native plasmid was an exception, and 2 mutations were observed on 90 kb plasmid. The important genes like dnaE, gyrA, iroC, metH and rpoB involved in antibiotic resistance had point mutations. The genome analysis revealed most of the metabolic pathways were affected.

Kakatkar, A. S., Das, A. & Shashidhar, R. (2021). Ciprofloxacin induced antibiotic resistance in Salmonella Typhimurium Mutants and Genome Analysis. Arch Microbiol, 203, 6131–6142.

https://doi.org/10.1007/s00203-021-02577-z

Ai-based mobile application to fight antibiotic resistance

Antimicrobial resistance is a major global health threat, and its development is promoted by antibiotic misuse. While disk diffusion antibiotic susceptibility testing (AST, also called antibiogram) is broadly used to test for antibiotic resistance in bacterial infections, it faces strong criticism because of inter-operator variability and the complexity of interpretative reading. Automatic reading systems address these issues but are not always adapted or available to resource-limited settings. We present an artificial intelligence (AI)-based, offline smartphone application for antibiogram analysis. The app captures images with the phone's camera, and the user is guided throughout the analysis on the same device by a user-friendly graphical interface. An embedded expert system validates the coherence of the antibiogram data and provides interpreted results. The fully automatic measurement procedure of our application's reading system achieves an overall agreement of 90% on susceptibility categorization against a hospital-standard automatic system, and 98% against manual measurement (gold standard), with reduced inter-operator variability. The application's performance showed that the

automatic reading of antibiotic resistance testing is entirely feasible on a smartphone. Moreover, our application is suited for resource-limited settings, and therefore has the potential to significantly increase patients' access to AST worldwide.

Pascucci, M., Royer, G., Adamek, J., Mail, A. A., Aristizabal, D., Blanche, L., Bezzarga, A., Boniface-Chang, G., Brunner, A., Curel C,. Dulac-Arnold, G., Fakhri, R. M., Malou, N., Nordon, C., Runge, V., Samson, F., Sebastian, E., Soukieh, D., Vert, J. P., … Madoui, M. A. (2021). AI-based mobile application to fight antibiotic resistance. *Nat Commun,* 12, 1173.

https://doi.org/10.1038/s41467-021-21187-3

Latent tuberculosis co-infection is associated with heightened levels of humoral, cytokine and acute phase responses in seropositive SARS-COV-2 infection

Context: Latent Tuberculosis infection (LTBI) is believed to modulate immune responses and alter disease severity in SARS-CoV-2 co-infection. However, no data exist on the effect of LTBI on the immune responses in SARS-CoV-2 co-infected individuals.

Methods: We examined the SARS-CoV-2 specific antibody responses, plasma cytokines, chemokines, acute phase proteins and growth factor levels in LTBI positive and negative individuals with SARS-CoV-2 infection.

Results: Our results demonstrated that individuals with LTBI (LTBI+) and seropositive for SARS-CoV-2 infection were associated with elevated SARS-CoV-2 specific IgM, IgG and IgA antibodies, as well as enhanced neutralization activity compared to those negative for LTBI (LTBI-) individuals. In addition, our results also showcase that LTBI+ individuals exhibited significantly higher plasma levels of IFNγ, IL-2, TNFα, IL-1α, IL-1β, IL-6, IL-12, IL-15, IL-17, IL-3, GM-CSF, IL-10, IL-25, IL-33, CCL3 and CXCL10, compared to LTBI- individuals. Finally, it was evidenced that LTBI+ individuals exhibit significantly higher levels of C-reactive protein, alpha-2 macroglobulin, VEGF and TGFα compared to LTBI- individuals.

Conclusions: Our data demonstrates that LTBI+ individuals seropositive for SARS-CoV-2 infection exhibit heightened levels of humoral, cytokine and acute phase responses compared to LTBI- individuals. Thus, LTBI is associated with modulation of antibody and cytokine responses as well as systemic inflammation in individuals seropositive for SARS-CoV-2 infection.

Rajamanickam, A., Pavan-Kumar, N., Padmapriyadarsini, C., Nancy, A., Selvaraj, N., Karunanithi, K., Munisankar, S., Shrinivasa B. M., Renji, R. M., Ambu T.C.,

Venkataramani, V., Babu, S. (2021). Latent tuberculosis co-infection is associated with heightened levels of humoral, cytokine and acute phase responses in seropositive SARS-CoV-2 infection, *Journal of Infection* 12.

https://doi.org/10.1016/j.jinf.2021.07.029

Inadequate use of antibiotics in the COVID-19 era: effectiveness of antibiotic therapy

Since December 2019, the COVID-19 pandemic has changed the concept of medicine. This work aims to analyze the use of antibiotics in patients admitted to the hospital due to SARS-CoV-2 infection.

The methodology of this work relies on analyzing the use and effectiveness of antibiotics in hospitalized patients with COVID-19, based on data from the SEMI-COVID-19 registry, an initiative to generate knowledge about this disease using data from electronic medical records. Our primary endpoint was all-cause in-hospital mortality according to antibiotic use. The secondary endpoint was the effect of macrolides on mortality. Of 13,932 patients, antibiotics were used in 12,238. The overall death rate was 20.7% and higher among those taking antibiotics (87.8%). Higher mortality was observed with use of all antibiotics (OR 1.40, 95% CI 1.21–1.62; p < .001) except macrolides, which had a higher survival rate (OR 0.70, 95% CI 0.64–0.76; p < .001). The decision to start antibiotics was influenced by presence of increased inflammatory markers and any kind of infiltrate on an x-ray. Patients receiving antibiotics required respiratory support and were transferred to intensive care units more often.

To conclude, bacterial co-infection was uncommon among COVID-19 patients, yet use of antibiotics was high. There is insufficient evidence to support widespread use of empiric antibiotics in these patients. Most may not require empiric treatment and if they do, there is promising evidence regarding azithromycin as a potential COVID-19 treatment.

Bendala-Estrada, A.D., Calderón-Parra, J., Fernández-Carracedo, E., Muiño-Míguez, A., Ramos-Martínez, A., Muñez-Rubio, E., Rubio-Rivas, M., Agudo, P., Arnalich-Fernández, F., Estrada-Perez, V., Taboada-Martínez, M. L., Crestelo-Vieitez, A., Pesqueira-Fontan, P. M., Bustamante, M., Freire, S. J., Oriol-Bermúdez, I., Artero, A., Olalla-Sierra, J., Areses-Manrique, M., …, Núñez-Cortés, J. M. (2021). Inadequate use of antibiotics in the covid-19 era: effectiveness of antibiotic therapy. *BMC Infect Dis*, 21, 1144.

https://doi.org/10.1186/s12879-021-06821-1

Using essential oils to overcome bacterial biofilm formation and their antimicrobial resistance

The increase of resistant bacteria puts a huge pressure on the antimicrobials in current use. Antimicrobial resistance (AMR), driven by years of antibiotic misuse and overuse, has led to a substantial global financial burden. New policies must be developed for antimicrobial use and to sustain research efforts aimed at mitigating AMR. It is essential to target the most harmful bacteria and focus on their resistance mechanisms to develop effective antimicrobials. Essential oils (EOs), which occur naturally in plants, have long been used as antimicrobials, though most remain under-researched. This review explores EOs as an alternative to antimicrobials, investigating their ability to decrease or inhibit biofilm formation, and assess their ability to contribute to AMR control. Low concentrations of EOs can inhibit Gram-positive and Gram-negative pathogenic bacteria. Some EOs have demonstrated strong anti-biofilm activities. If EOs are successful against biofilm formation, particularly in bacteria developing AMR, they could be incorporated into new antimicrobials. Therefore, it is necessary to investigate the potential of these EOs, particularly for surface disinfection, and against bacteria found in food, clinical, and non-clinical environments.

3. Proyectos de investigación activos desarrollados por la Facultad de Ciencias Agrarias - UNIAGRARIA

Proyectos liderados por los docentes en la facultad de Ciencias Agrarias en el 2021:

Análisis metagenómico comparativo de la alteración de la microbiota dérmica en renacuajos de la rana sabanera (*Dendropsophus molitor*) expuestos a Roundup Activo®

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Nieto-Escribano E, Infante-González J[2]

La especie Dendropsophus molitor, conocida comúnmente como rana sabanera, es un miembro de la clase Amphibia, específicamente del orden Anura. Esta clase ha sido impactada por la actividad humana, particularmente por la agricultura y el cultivo ilícito en Colombia, debido al uso de herramientas como herbicidas a base de glifosato, entre los cuales se destaca el Roundup activo®. Las investigaciones han revelado los efectos adversos de estas sustancias en los organismos que las encuentran, siendo los anfibios, junto con su microbiota dérmica, uno de los grupos más afectados. Esta microbiota juega un papel crucial en el mantenimiento y composición de la mucosa dérmica, esencial para la respiración adecuada y la protección contra patógenos. El objetivo de este estudio es analizar el impacto de diferentes tiempos y concentraciones de exposición al herbicida Roundup activo® en la microbiota dérmica de los renacuajos de la rana sabanera. Con este fin, se expondrán los renacuajos a diversas concentraciones y duraciones de exposición al Roundup activo®, extrayendo y purificando luego el ADN de las muestras dérmicas obtenidas. Posteriormente, se secuenciará el gen 16s ARNr para identificar las comunidades microbianas presentes, empleando técnicas de filtración, agrupación y asignación taxonómica de las secuencias obtenidas. Finalmente, se analizarán estas comunidades microbianas para evaluar su diversidad y determinar si la exposición a diferentes concentraciones y tiempos de Roundup activo® tiene un efecto significativo en la microbiota de los individuos en estudio. Se anticipa que las poblaciones de rana sabanera expuestas a concentraciones elevadas de Roundup Activo® muestren diferencias significativas en densidad y diversidad microbiana en comparación con la población control.

Imagen 2. Rana sabanera (fuente: Jorge Oliveros Rojas).

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Animal welfare evaluation at slaughterhouses for pigs at the "Eje Cafetero" region in Colombia

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Viviana María Velásquez A. [b],
María Nelly Cajiao P. [b],
Juan David Córdoba P. [b]

During the electronarcosis and bleeding processes in pig slaughterhouses, certain factors hinder achieving adequate slaughter conditions, a critical phase in which animal welfare must be guaranteed. This study aimed to evaluate and compare the effectiveness of electronarcosis for desensitization alongside two bleeding methods (horizontal and vertical directions). Dependent variables were measured as indicators of animal welfare (absence of the corneal reflex, lack of reflex of sensitivity to painful stimuli, attempts to reinstatement or posture recovery and

Table 7. Chi-square Of Pearson (value) - alternative hypothesis (Source: author data).

Alternative hypothesis	Relationship	Chi-square of Pearson (value)	Asymptotic sig. (2 sides)	Contingency coefficient
H1 *A	Handling * reinstatement	184.713	0.000	0.331
H1 *B	Amperage * reinstatement	9.308	0.010	0.79
H1 *C	Time insensitization * reinstatement	211.043	0.000	0.351
	Time insensitization – bleeding * corneal reflex	136.875	0.000	0.289
	Time insensitization – bleeding * reinstatement	123.874	0.000	0.276

Table 1. Chi-square of Pearson (value). Own elaboration

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vocalization), following stunning and bleeding processes at four slaughterhouses of national category in the "Eje Cafetero", Colombia (Table 1). The methodological approach included binomial distribution, descriptive statistics, hypothesis testing and statistical significance. The results showed that the efficiency of the desensitization procedures and type of bleeding direction depends on multiple aspects, including the tranquility of the animals during their handling, the correct position of the desensitization clamps, the amperage used and the time between desensitization and bleeding. Therefore, potential preventive and corrective measures include continuous training and supervision of personnel performing procedures, the necessity of immobilizing pigs before desensitization, ongoing monitoring of procedural variables, and ensuring proper vascular cutting to ensure the animals' death before entering the scalding machine.

DAVID FERNANDO BALAGUERA

Aunque hemos superado los desafíos más difíciles de la pandemia en el marco de la salud, aún enfrentamos un gran reto con la educación virtual. Como docentes, debemos realizar grandes esfuerzos para guiar a nuestros estudiantes a través de las herramientas digitales y asegurar que puedan continuar su proceso de aprendizaje en su formación profesional. En el área de la fisiología ha sido posible continuar con didácticas como lo son los laboratorios virtuales, creación de biomodelos y exploración de estudios investigativos aplicados a la medicina. En la investigación sobre el uso de los biomodelos didácticos en las ciencias veterinarias, hemos publicado un capítulo en el libro *Bioética, bienestar y la experimentación con animales* publicado por ASFAMEVEZ, así como un artículo de investigación en la revista Ciencias Veterinarias de Costa Rica. Este trabajo se realizó en conjunto con diferentes docentes de nuestra facultad.

ISABEL SOFÍA SANDOVAL BOLAÑO

Recientemente, tuvimos la oportunidad de publicar un estudio en la revista del Instituto Nacional de Salud sobre la historia de infección de la bacteria zoonótica *Brucella canis* en un albergue para animales de compañía en Bogotá. Además, presentamos los resultados de un segundo estudio sobre esta misma bacteria en caninos de compañía asintomáticos durante el marco del XVII Encuentro Científico del Instituto Nacional de Salud. También orientamos a dos estudiantes para que presentaran una ponencia en el V Encuentro de Semilleros de Investigación: investigación formativa en los retos del entorno. Finalmente, acompañamos a algunos estudiantes de medicina veterinaria a través del plan padrino y continuamos con el proyecto de aula enfocado en la elaboración y defensa de pósteres científicos. Este proyecto tiene el objetivo de fortalecer las habilidades comunicativas y la comprensión de la ciencia entre los estudiantes.

NICOLÁS HERNÁNDEZ GALLO

A pesar de ser su segundo año de funcionamiento, la Especialización en Salud Pública Veterinaria ha destacado nuevamente en 2021 como un referente de excelencia académica y compromiso con la salud animal y humana en Colombia. Con un enfoque holístico, multidisciplinario y transdisciplinario "Una Salud" (*One Health*), el programa ha ofrecido una amplia gama de actividades que han fortalecido la formación de sus estudiantes y han contribuido al desarrollo del campo de la salud pública veterinaria en el país.

Una de las principales actividades realizadas durante el año fue el ciclo de charlas *One Health*, donde destacados expertos nacionales e internacionales compartieron sus conocimientos y experiencias en temas relevantes para Una Salud. Estas conferencias abordaron desde la epidemiología de enfermedades que han roto la barrera inter-especie hasta la gestión del bienestar animal para control

de efectos adversos en poblaciones animales y humanas, incluyendo el enfoque de género como apoyo a la salud pública.

Además, la Especialización en Salud Pública Veterinaria promovió activamente la participación de sus estudiantes en investigaciones científicas y proyectos aplicados. A través de convenios con instituciones gubernamentales y organizaciones no gubernamentales, los estudiantes han tenido la oportunidad de realizar consultorías y prácticas profesionales en diferentes áreas de la salud pública veterinaria, adquiriendo experiencia práctica y contribuyendo al avance del conocimiento en el campo.

En resumen, el año 2021 fue un período de gran actividad y logros para la Especialización en Salud Pública Veterinaria. A través de sus diversas actividades académicas, científicas y de extensión, el programa continuó consolidándose como un líder en la formación de profesionales comprometidos con la promoción de la salud animal y humana en Colombia.

CAMILA CARVAJAL LANCHEROS

"La salud pública nos motiva a salir de nuestra zona de confort, a enfrentarnos a diferentes retos y a tener la valentía de poner cara a lo desconocido"

Como la primera egresada del programa de Salud Pública Veterinaria de La Fundación Universitaria Agraria de Colombia, me siento orgullosa de los aprendizajes obtenidos, de los retos superados y de la calidad humana y profesional del equipo administrativo y docente, quienes desde su conocimiento y experiencia forjan la pasión por esta maravillosa área.

El programa de Medicina Veterinaria, del cual me gradué, tiene un enfoque diferencial en salud pública que despertó mi interés desde el pregrado. Desde entonces, he sentido una profunda vocación para el servicio a las personas, comunidades y territorios, además de la curiosidad por la higiene, inspección y seguridad alimentaria. Dado lo anterior, ingresé al programa de especialización con muchas expectativas y una gran sed de conocimiento, decisión que sin duda fue una de las mejores que he tomado, pues el plan de estudios y la ruta formativa superaron mis expectativas iniciales.

Haber realizado este posgrado me ha permitido conocer territorios como el departamento del Guainía, comprendiendo y enfrentando la realidad de las problemáticas de la salud pública del país. De esta manera he podido aportar desde mi conocimiento a la prevención de enfermedades y promoción de la salud con diferentes estrategias como educación en salud, comunicación, gestión, trabajo interdisciplinario, transectorial y actividades de inspección, vigilancia y control.

Espero que, en algunos años, podamos formar una extensa red de colegas especialistas en salud pública veterinaria, todos encaminados al mismo objetivo: *One Health*.

5. Eventos de interés a realizarse en el año 2022

IV Congreso Internacional de Ciencias Agrarias y Ambientales (CICAA) 2022

Se llevará a cabo los días 9, 10 y 11 de noviembre de 2022.

El evento, "Cuarto Congreso Internacional de Ciencias Agrarias y Ambientales: Una mirada integral a la Seguridad Alimentaria en el contexto mundial (CICAA) 2022", será un escenario de dialogo académico centrado en investigaciones sobre seguridad alimentaria. Los temas abordarán

experiencias relacionadas con el cambio climático, sistemas sostenibles de producción agrarios, mercados verdes, gestión ambiental, extensión y desarrollo rural, conservación y el aprovechamiento sostenible de la biodiversidad. Contará con la asistencia de expertos internacionales y nacionales, a fin de dar una visión global de los desafíos y las implicaciones que esta temática genera.

La Universidad Pedagógica y Tecnológica de Colombia, a través del Grupo de Investigación en Medicina Veterinaria y Zootecnia (GIDIMEVETZ), junto con la Fundación Universitaria Juan de Castellanos, realizarán el VII Seminario Internacional y VIII Nacional de Investigadores en Salud y Producción Animal, SENISPA. En el 2022, el evento bienal ofrecerá una oportunidad para socializar y dialogar con la comunidad investigativa en las áreas de las Ciencias Agropecuarias y las Ciencias Biológicas y Ambientales sobre el impacto académico e investigativo en nuestra sociedad.

CONGRESO VEPA COLOMBIA 2022
Medicina Veterinaria
Cuidando el Planeta

27, 28 Y 29 DE JULIO
CENTRO DE CONVENCIONES
CARTAGENA DE INDIAS

2022

CENTRO DE CONVENCIONES
CARTAGENA DE INDIAS

6. Publicidad

Clínica Veterinaria UNIAGRARIA

Centro de Investigación y Desarrollo Tecnológico (CIDT)

Boletín Divulgativo – Facultad de Ciencias Agrarias

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