

Media Release

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ESCMID Global 2026

Antibiotic resistance genes found in newborns within hours of birth, study shows

(Monday, 20 April 2026, Munich, Germany) Antibiotic resistance genes (ARGs) – segments of DNA that help bacteria survive the effects of antibiotics – can be present in newborns within the first hours of life, according to research presented at ESCMID Global 2026.¹

The study analysed meconium samples from 105 infants admitted to a neonatal intensive care unit (NICU) within the first 72 hours of life between July 2024 and July 2025. The study was part of a multidisciplinary research project led by Professor Elias Iosifidis at Aristotle University of Thessaloniki, involving pediatric infectious disease specialists, neonatologists and molecular microbiology researchers.

Meconium, the first stool passed by newborns, was traditionally thought to be sterile.² However, recent molecular studies have detected microbial genetic material in meconium samples,³ suggesting that the neonatal gut may be exposed to bacteria during pregnancy. This early microbial exposure has been proposed as a potential contributor to the development of antibiotic resistance. ARGs have been detected in meconium samples,⁴ and their presence at this early stage may facilitate the spread of resistance through horizontal gene transfer between bacteria. Based on this, researchers screened the samples for 56 different resistance genes associated with commonly used antibiotics.

“This is the largest study of its kind exploring the effect of hospital environment on the collection of ARGs in the neonatal gut,” lead author Dr Argyro Ftergioti said. “We analysed meconium samples within the first 72 hours of life to capture the earliest snapshot of microbial and genetic exposure in newborns. At this stage, the collection of resistance genes is mainly shaped by maternal transmission, delivery mode and very early hospital exposures.”

The most common genes detected were *oqxA* (in 98% of samples) and *qnrS* (96%), which have been associated with resistance to some commonly used antibiotics.⁵ The study also identified several genes encoding beta-lactamases, enzymes that break down widely used antibiotics.⁶ Among these, the most prevalent were *blaCTXM* (55%), *blaCMY* (51%) and *blaSHV* (39%). Genes linked to resistance to carbapenems, a last-line class of antibiotics,⁷ were detected in 21% of samples. Each sample contained a median of eight resistance genes.

“This finding suggests that a pattern of ARGs is already established at this stage. The neonatal gut harbours a diverse resistome, and the presence of clinically important ARGs so early in life is concerning,” Dr Ftergioti added.

“Although some ARGs were expected, their high prevalence across the majority of samples was striking – particularly for clinically critical genes offering carbapenem resistance.”

The study also identified associations between resistance genes and several maternal and neonatal factors. The presence of the *msrA* (macrolide-streptogramin resistance) gene was linked with maternal hospitalisation during pregnancy, while a higher number of resistance genes was associated with central venous catheter placement within the first 24 hours of life. Both findings likely reflect exposure to healthcare-associated microbes in hospital settings.

“Surprisingly, resuscitation shortly after birth was associated with fewer resistance genes. We would caution that this finding should be interpreted carefully, however, as it may reflect differences in early microbial exposure or other clinical factors,” Dr Ftergioti noted.

Overall, the findings suggest that both maternal transmissions and early exposure to the hospital environment may contribute to the establishment of ARGs in the neonatal gut.

“While further research is needed to understand how early carriage of resistance genes affects microbiome development and infection risk, these findings highlight the importance of surveillance, infection prevention and control in neonatal care,” concluded Dr Ftergioti.

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Notes to editors:

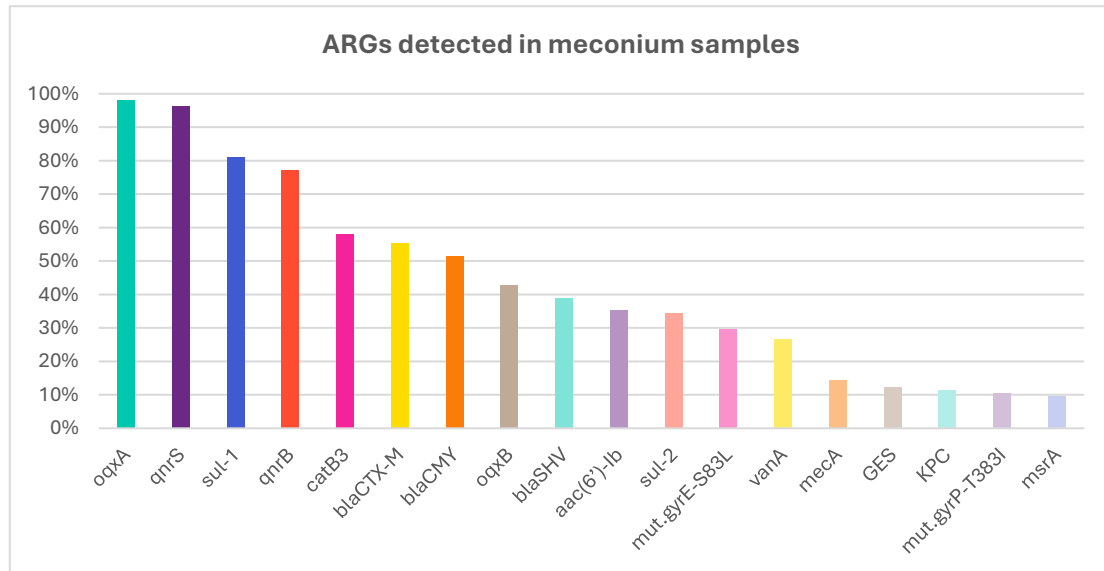
A reference to ESCMID Global must be included in all coverage and/or articles associated with this study.

This research was supported by a donation that enabled the implementation of advanced molecular technologies in neonatal infectious disease research.

For more information or to arrange an expert interview, please contact the ESCMID Press Office at: communication@escmid.org

Figure 1:

Prevalence of ARGs detected in meconium samples from newborns within the first 72 hours of life.



About the study author:

Argyro Ftergioti is a medical doctor qualified with a master’s degree in research methodology in health sciences. She is currently a PhD candidate at Aristotle University of Thessaloniki, where, under the supervision of Professor Elias Iosifidis who leads her research project, she explores disturbances in the resistome, microbiome and metabolome of neonates colonised by multidrug-resistant bacteria. Her primary scientific interest lies in paediatric infectious diseases, with a research focus on the epidemiology, pathophysiology, prevention and management of infections, particularly those caused by multidrug resistant bacteria and neonatal bacterial infections. In addition, she is actively engaged in the application of innovative omics approaches and advanced molecular technologies infectious diseases in neonates and critically ill children.

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Website: www.escmid.org/

References:

1. Ftergioti, A., Simitsopoulou, M., Kontou, A., et al. (2026). Antibiotic resistance genes in meconium of newborns very early after admission to neonatal intensive care unit. Oral presentation. *ESCMID Global 2026*.
2. Perez-Muñoz, M.E., Arrieta, MC., Ramer-Tait, A.E. et al. (2017). A critical assessment of the “sterile womb” and “in utero colonization” hypotheses: implications for research on the pioneer infant microbiome. *Microbiome* 5, 48.
3. Jiménez, E., Marín, M. L., Martín, R., et al. (2008). Is meconium from healthy newborns actually sterile? *Research in Microbiology*, 159(3), 187–193.
4. Gosalbes, M. J., Vallès, Y., Jiménez-Hernández, N., et al. (2016). High frequencies of antibiotic resistance genes in infants' meconium and early fecal samples. *Journal of developmental origins of health and disease*, 7(1), 35–44.
5. Rodríguez-Villodres, Á., Galiana-Cabrera, A., Torres Fink, I., et al. (2023). Evaluation of the MDR Direct Flow Chip Kit for the Detection of Multiple Antimicrobial Resistance Determinants. *Microbial drug resistance (Larchmont, N.Y.)*, 29(8), 381–385.
6. Tooke, C.L., Hinchliffe, P., Bragginton, E.C. et al. (2019). β -Lactamases and β -Lactamase Inhibitors in the 21st Century. *Journal of Molecular Biology*, 431(18):3472-3500.
7. Meletis, G. (2016). Carbapenem resistance: overview of the problem and future perspectives. *Therapeutic Advances in Infectious Disease*, 3(1):15-21.