



Determining Antimicrobial Resistance in the Gut Microbiome Leveraging the Versatility of Microfluidics-Based qPCR

Objective

The gut microbiome is known to play a significant role in human health but can be severely affected by antibiotic treatments. These disturbances can not only result in short-term effects, but also create long-term health issues from infancy to adulthood. Researchers at the University Medical Center Utrecht set out to evaluate the ecological effects of infants treated with broad-spectrum antibiotics by assessing the microbiome for antimicrobial resistance (AMR), with the goal of suggesting the least offensive treatment approaches for infants with suspected early-onset neonatal sepsis (sEONS).

Utilization of Standard BioTools™ products

- Biomark™ system
- 96.96 Dynamic Array™ IFCs (integrated fluidic circuits)

Background

- The gut microbiome is important for overall health, especially at early stages of life.
- Disturbances in gut microbial communities can result in infant disease as well as long-term adult health issues.
- Treatment by antibiotic regimens too often uses the motto “when in doubt, there’s no harm in treating.” This approach is being questioned as more studies show the effects of broad-spectrum antibiotics on gut microbiome development and selection of AMR, especially when administered in the first week of life.

Key takeaways

- The study showed major effects of broad-spectrum antibiotics on microbial diversity, community composition and AMR gene elections.
- The impacts of antibiotics were still measurable at 12 months of life.
- Microfluidics-based qPCR identified distinct and relevant shifts in AMR gene profiles, using a panel of 31 clinically relevant AMR genes.

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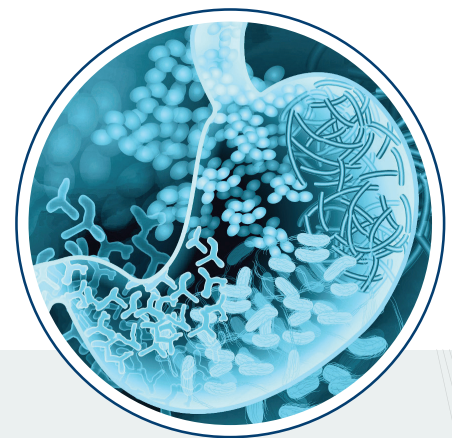


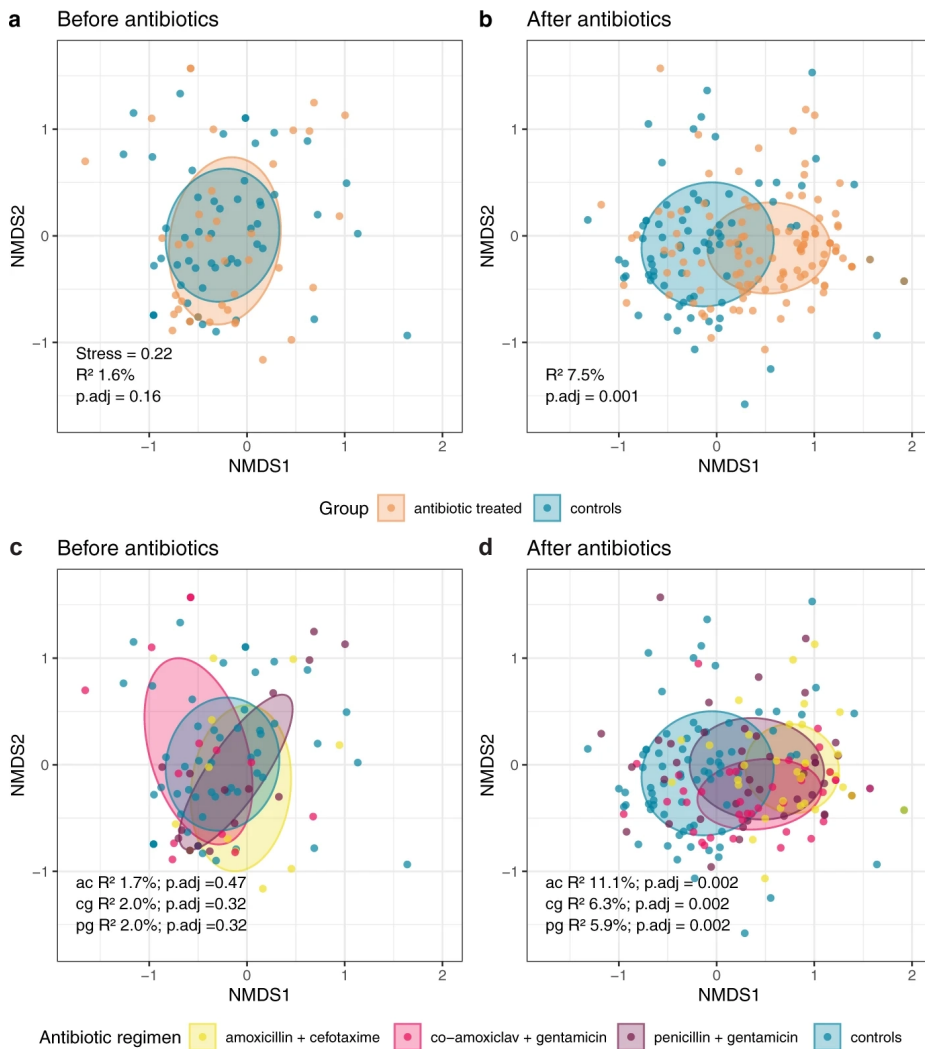
Image credit: Darryl Leja, NHGRI (CC BY 2.0)

Results

In the AMR gene profiles, significant differences were found

- at multiple time points between antibiotic-treated infants and controls;
- between the separate regimens compared with controls.

Antibiotic-treated infants show temporarily reduced gut microbial diversity and major and prolonged ecological perturbations in their gut microbiome.



Conclusions

The study revealed significant long-term effects of broad-spectrum antibiotic treatment for sEONS. Based on the treatments studied, the authors suggest a preferred approach would be to prescribe penicillin and gentamicin, as this regimen causes the fewest ecological side effects.

Methods

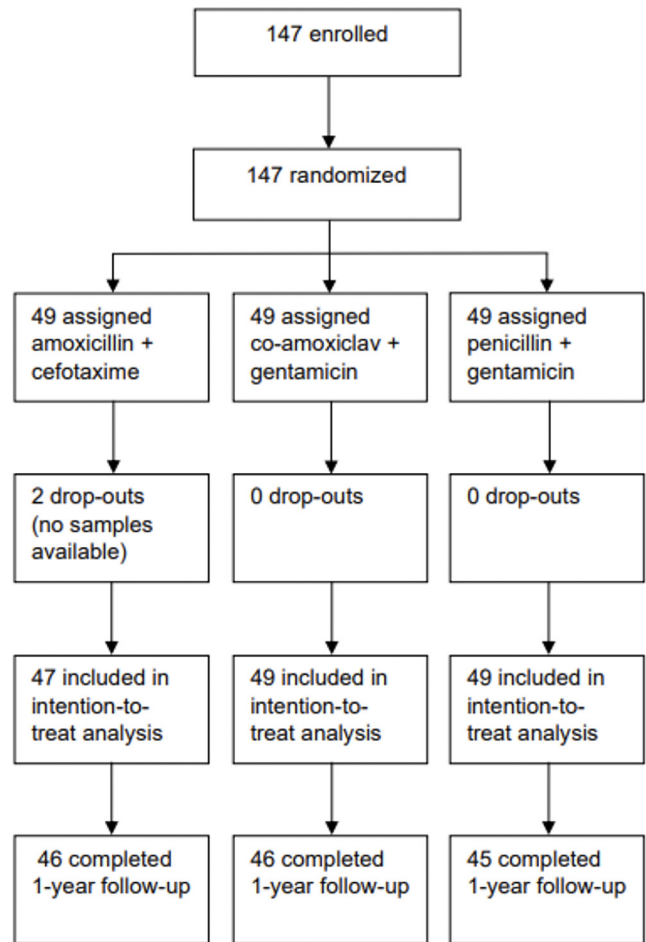
Biomark system, IFC Controller HX, 96.96 Dynamic Array IFCs

Samples:

- Rectal swabs and feces collected before treatment and at 1 and 6 days, followed by 1, 4 and 12 months of age
- Bacterial DNA isolated with a mag™ mini DNA Isolation Kit

AMR detection:

- 16S rRNA metagenomic shotgun sequencing
- EvaGreen® detection assays were from a previously validated panel that consisted of 31 AMR gene targets and one 16S rRNA target.



Reference

1. Reyman, M. et al. "Effects of early-life antibiotics on the developing infant gut microbiome and resistome: a randomized trial." *Nature Communications* 13 (2022): 893.

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CORPORATE HEADQUARTERS

2 Tower Place, Suite 2000
South San Francisco, CA 94080 USA
Toll-free: 866 359 4354 in the US and Canada
Fax: 650 871 7152
standardbio.com

SALES

North America | +1 650 266 6170 | info-us@standardbio.com
Europe/Middle East/Africa/Russia | +33 1 60 92 42 40 | info-europe@standardbio.com
Latin America | +1 650 266 6170 | info-latinamerica@standardbio.com
Japan | +81 3 3662 2150 | info-japan@standardbio.com
China (excluding Hong Kong/Macau) | +86 21 3255 8368 | info-china@standardbio.com
All other Asia-Pacific countries/India/Australia | +1 650 266 6170 | info-asia@standardbio.com

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