

Alternative antibiotic regimens improve palatability and welfare in mice for gut bacterial depletion

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The problem

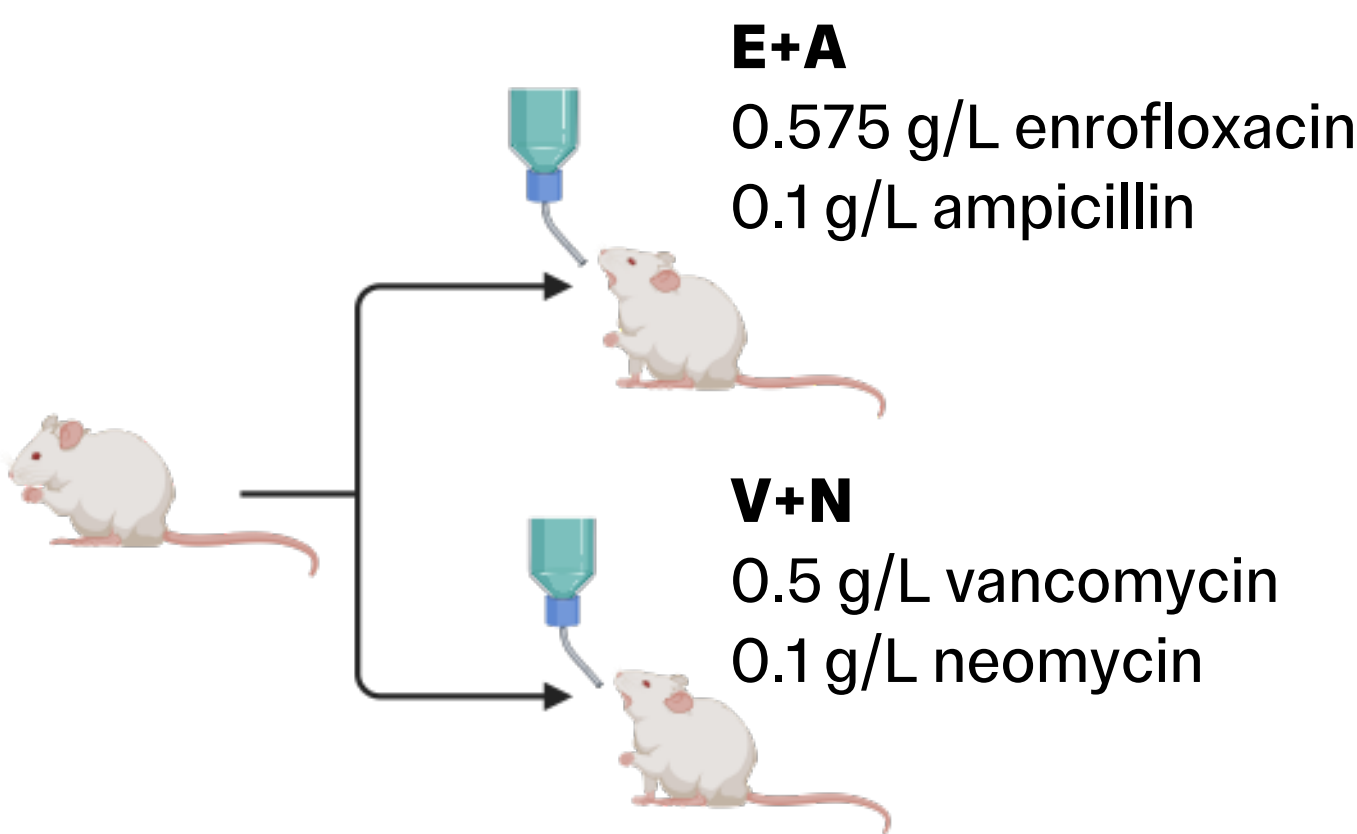
Antibiotic cocktails are widely used to deplete gut bacteria in mouse models. A commonly used regimen, **AMVN** (ampicillin, metronidazole, vancomycin and neomycin), is typically administered via drinking water¹. However, we (Fig. 1) and others^{2,3} show that this approach reduces water intake, leading to dehydration and significant body weight loss.

While oral gavage (OG) can maintain dosing, repeated handling may induce stress and carry procedural risks, **highlighting the need for refined antibiotic strategies that balance efficacy and animal welfare.**

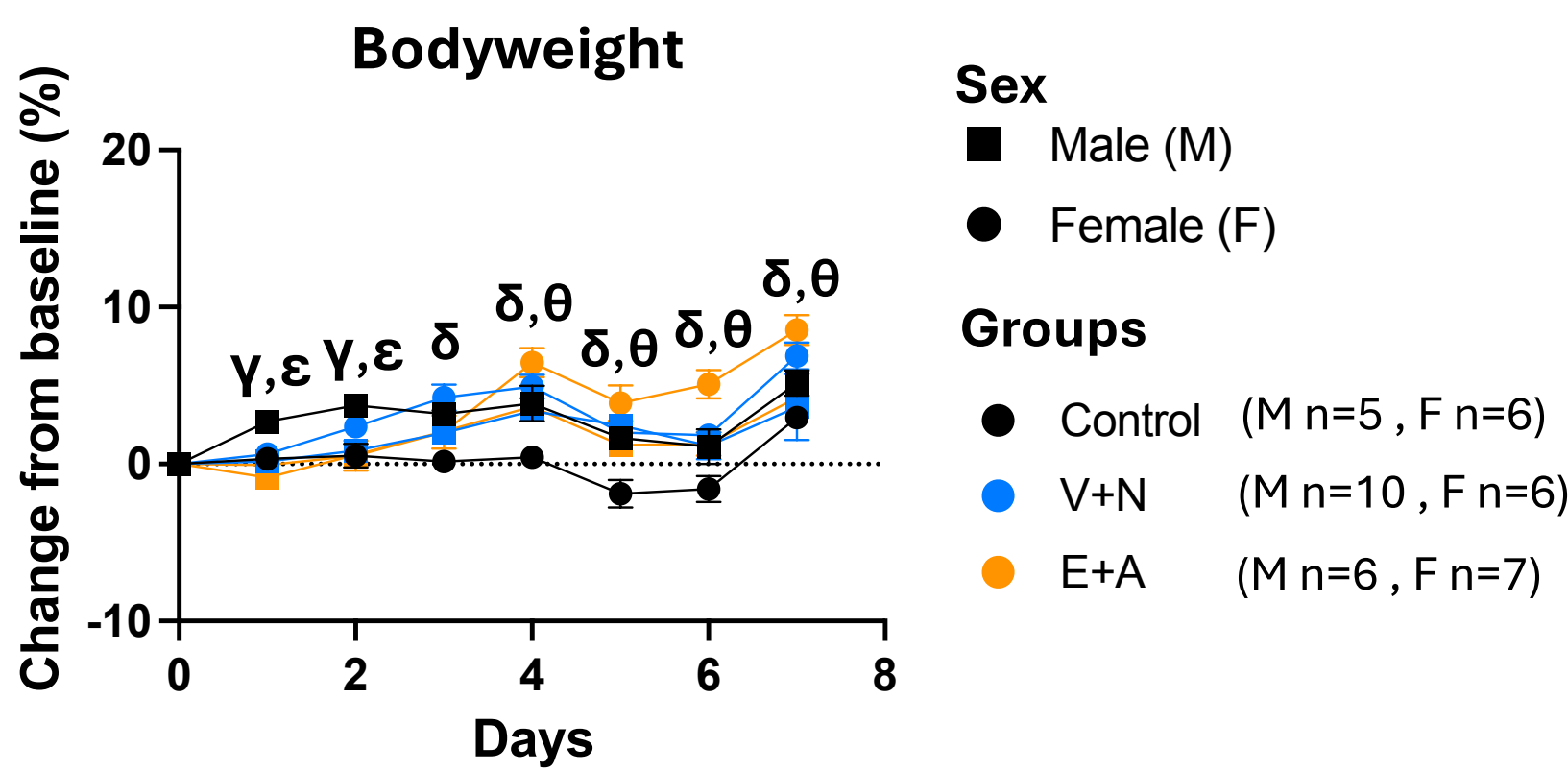


Body weight changes in Fabp1Cre;Apc^{15lox/+} mice during AMVN treatment reveal initial weight loss followed by recovery after refinement to oral gavage (OG). α and β denote significant differences between AMVN-treated and control mice in females and males, respectively.

The refinement



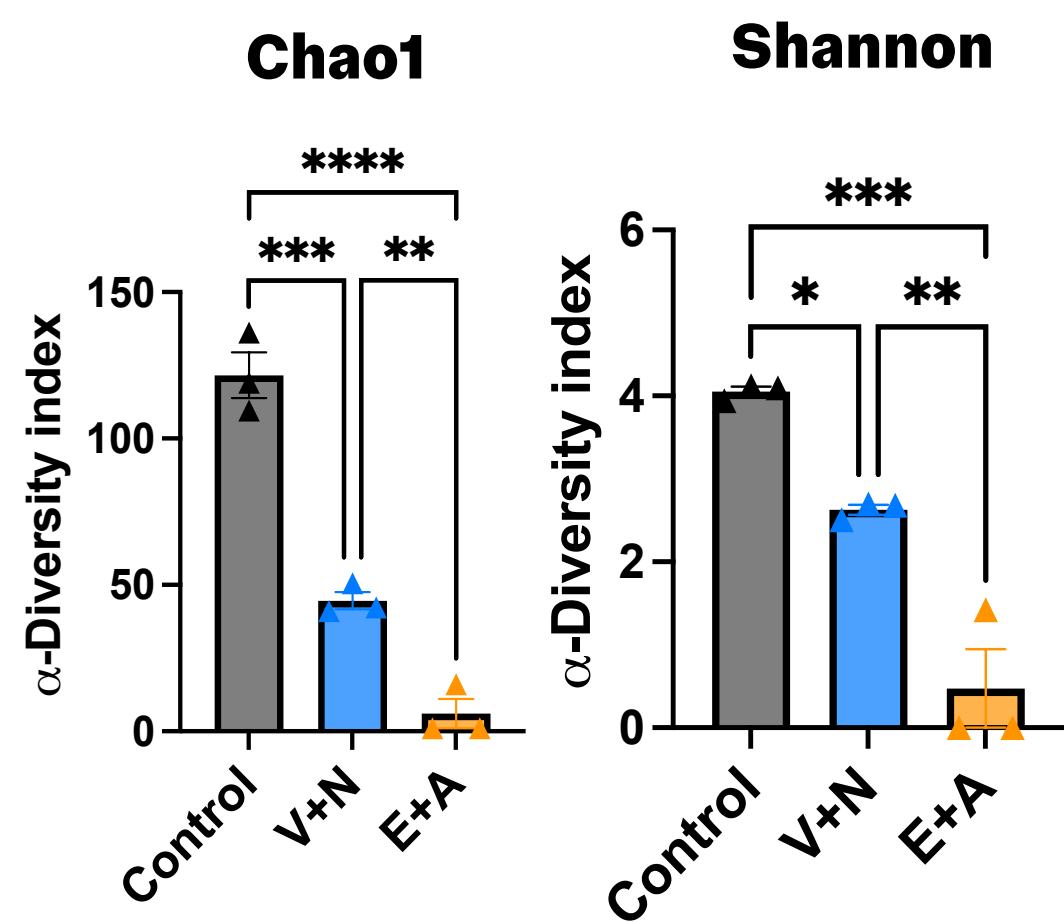
Refining antibiotic selection improves palatability and maintains healthy body weight.



Refined antibiotic regimens (V+N and E+A) are well tolerated and maintain stable body weight, with increased body weight observed in some groups compared to controls. γ and ε denote significant differences in V+N- or E+A-treated male mice compared to controls, while δ and θ denote these differences in females.

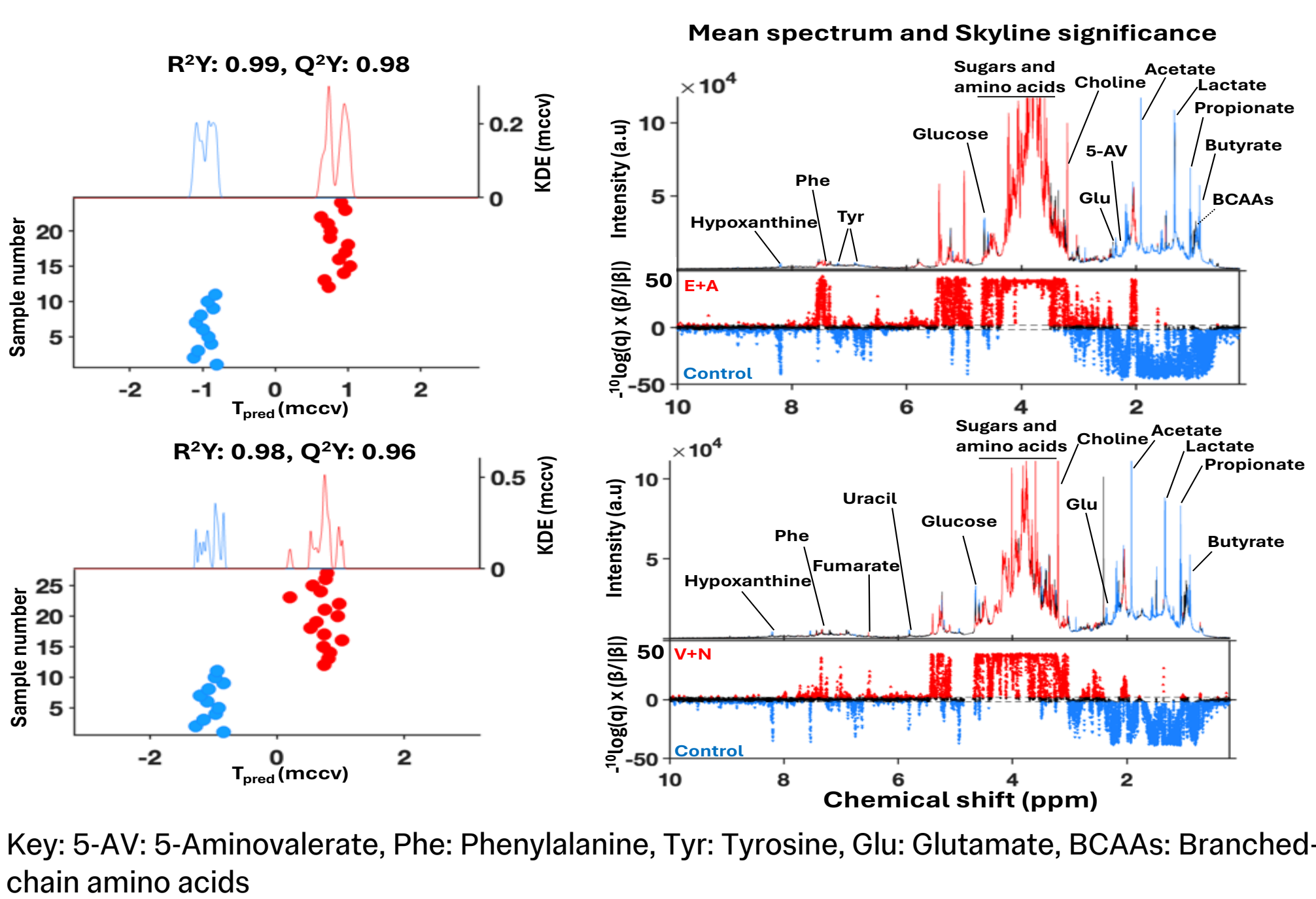
Biological Outcomes After Refinement

1. Gut Bacterial Depletion



Refined antibiotic regimens significantly reduced gut bacterial alpha diversity compared to controls, with a more pronounced reduction observed following E+A treatment relative to V+N, demonstrating that refinement **preserves effective bacterial depletion.**

2. Bacterial Function: Metabolic Depletion



¹H NMR-based faecal metabolomic profiling, analysed by CAPLS modelling⁴ and adjusted for sex, revealed clear metabolic separation between control and refined antibiotic-treated groups, indicating **preserved metabolic depletion following refinement.**

References

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4. Posma, J. M. *et al. J Proteome Res* **17**, 1586-1595 (2018).

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