Abstract 30 – Paper ID: 042

Environmental Ampicillin Pollution Disrupts Gut Microbiome Composition and Host Immunity in *Drosophila melanogaster*

Asem Sanjit Singh[1,2], Ch. Brajakishor Singh[2], Upendra Nongthomba[1]

[1]Developmental and Biomedical Genetics Laboratory, Department of Developmental Biology and Genetics,
Indian Institute of Science, Bengaluru–560012, India
[2]BRIC–Institute of Bioresources and Sustainable Development, Takyelpat, Institutional Area,
Imphal–795001, Manipur, India

Email: sanjitasem21@gmail.com

Abstract

The problem of environmental pollution by antibiotic residues, and ampicillin, is gaining growing concern throughout the world because of the long-term impacts on the ecology and a possible disruption of the interaction of host microbes. Antibiotics are vital in the treatment of infections is that an enduring presence of antibiotics in the water and soil ecologies causes chronic exposure of non-target organisms to low dose antibiotics. The present study tries to understand the effect of environmentally relevant concentrations of ampicillin on the structure of the gut microbiota, including their functional potential and host physiology. 16S rRNA amplicon sequencing showed that antibiotic exposed flies are strongly dysbiotic in their gut. Large bacterial phyla (Proteobacteria, Firmicutes, Bacteroidota, Actinobacteria, Verrucomicrobiota and Planctomycetata) were subject to great change. Intervention of ampicillin led to the drastic reduction of the major symbionts, including Proteobacteria and Firmicutes and the growth in relative abundance of Bacteroidota and Chloroflexi. On the genus level fourteen taxa such as *Wolbachia*, *Lactobacillus*, *Bacillus*, *Pseudomonas*, *Vibrio*, *Clostridium* and *Staphylococcus* had significant increases ($p \geq 0.05$). Among the most notable changes, the significant decrease of *Acetobacter* which is an essential part of the commensal nutrient metabolism and the simultaneous increase in the number of the *Wolbachia* lineages, particularly *Wolbachia pipientis*, were noteworthy. Functional prediction analysis revealed improvement of microbial abilities of the ampicillin-treated groups in terms of nucleotide biosynthesis, metabolism, and enzymatic activities. Host physiological measurements also showed a decreased production of antimicrobial peptides (AMP) and impaired innate immune factors representing a disturbed immune homeostasis of gut in response to antibiotic stress. Generally, the present study demonstrates the low but consistent effects of environmental pollution of ampicillin at low levels on the microbial ecology of the gut and host immunity. Results justify the importance of the increased control of the release of antibiotics and increasing the number of checks on the pollution of the environment with antibiotics.

Keywords: Ampicillin pollution, Gut microbiome, *Drosophila melanogaster*, Dysbiosis, Host immunity

---

Published by AIJR Publisher in "Abstracts of International Conference on Advances in Multidisciplinary Sciences and Engineering 2026" (ICAMSE 2026), January 21-23, 2026. Organized by the Department of Basic Sciences, Manipur Technical University, Imphal, Manipur, India.
ISBN: 978-81-989164-2-6; DOI: 10.21467/abstracts.8.1