## Abstract Submitted for the MAR14 Meeting of The American Physical Society

On Growth and Form of the Zebrafish Gut Microbiome MATTHEW JEMIELITA, MICHAEL TAORMINA, Department of Physics, University of Oregon, ANNAH ROLIG, Institute of Molecular Biology, University of Oregon, ADAM BURNS, Institute of Ecology and Evolution, University of Oregon, JENNIFER HAMPTON, KAREN GUILLEMIN, Institute of Molecular Biology, University of Oregon, RAGHUVEER PARTHASARATHY, Department of Physics, Institute of Molecular Biology, and Material Science Institute; University of Oregon — The vertebrate gut is home to a diverse microbial community whose composition has a strong influence on the development and health of the host organism. Researchers can identify the members of the microbiota, yet little is known about the spatial and temporal dynamics of these microbial communities, including the mechanisms guiding their nucleation, growth, and interactions. We address these issues using the larval zebrafish (Danio rerio) as a model organism, which are raised microbe-free and then inoculated with controlled compositions of fluorophoreexpressing bacteria. Live imaging using light sheet fluorescence microscopy enables visualization of the gut's entire microbial population over the first 24 hours of colonization. Image analysis allows us to quantify microbial populations that range from a few individuals to tens of thousands of microbes, and analyze the structure and growth kinetics of gut bacterial communities. We find that genetically-identical microbes can show surprisingly different growth rates and colonization abilities depending on their order of arrival. This demonstrates that knowing only the constituents of the gut community is insufficient to determine their dynamics; rather, the history of colonization matters.

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