

Researchers identify workings of L-form bacteria

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Researchers at the Johns Hopkins Bloomberg School of Public Health have for the first time identified the genetic mechanisms involved in the formation and survival of L-form bacteria. Their findings are described in a study published October 6 in the journal *PLoS ONE*.

L-form bacteria, which were first discovered in the 1930s, are morphological variants of classical bacteria that lack a cell wall. Under specialized growth conditions L-form bacteria are capable of forming a typical "fried egg" colony, which resembles a fried egg rather than the smooth appearance of a classic bacteria colony. These bacteria are believed to form in response to cell wall stress from certain antibiotics or the body's immune attack, and are suspected to be associated with antibiotic-resistant and persistent infections, as well as certain diseases.

"Our study provides new insight about the molecular basis of L-form bacteria, which was not previously known," said Ying Zhang, MD, PhD, senior author of the study and professor in the Bloomberg School's W. Harry Feinstone Department of [Molecular Microbiology](#) and Immunology. "These findings establish the framework for future research on how the identified genes and pathways interact leading to L-forms. They also have important implications for understanding the emergence of [antibiotic resistance](#) and bacterial persistence and for developing new drugs and vaccines targeting such persistent L-form bacteria for improved [infection control](#)."

According to Zhang, L-form bacteria are difficult to study because their

biology and the circumstances favoring the transition of classical bacteria into L-forms are not fully understood. In addition, specialized culture conditions are required for study. Most research on L-form bacteria was largely abandoned in the 1980s before modern molecular tools could be applied, but renewed interest in L-form bacteria has recently emerged.

For the study, Zhang and colleagues William Glover, a graduate student at the Bloomberg School, and Yanqin Yang, a senior program analyst with the Johns Hopkins School of Medicine, conducted a genome-wide gene expression analysis of L-form colonies of *E. coli* bacteria. They identified interesting stress genes and pathways that overlap with persisters and biofilm bacteria. Furthermore, the authors carried out mutant screens and identified three groups of mutants with varying degrees of defect in L-form [bacteria](#) formation or survival compared to classic colonies of *E. coli*. Mutants that showed complete lack of L-form growth belonged to pathways related to cell envelope stress, DNA repair, iron regulation and outer membrane biogenesis. The mutants could be restored to L-form growth by their respective wild type genes, confirming their role in L-form formation or survival.

Source: Johns Hopkins University Bloomberg School of Public Health ([news](#) : [web](#))

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