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### **Getting into shape: the physics of bacterial morphology<sup>1</sup>**

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Bacterial cells come in a wide variety of shapes and sizes, with the peptidoglycan cell wall as the primary stress-bearing structure that dictates cell shape. In recent years, cell shape has been shown to play a critical role in regulating many important biological functions including attachment, dispersal, motility, polar differentiation, predation, and cellular differentiation. Though many molecular details of the composition and assembly of the cell wall components are known, how the peptidoglycan network organizes to give the cell shape during normal growth, and how it reorganizes in response to damage or environmental forces have been relatively unexplored. We introduce a quantitative mechanical model of the bacterial cell wall that predicts the response of cell shape to peptidoglycan damage in the rod-shaped Gram-negative bacterium *Escherichia coli*. To test these predictions, we use time-lapse imaging experiments to show that damage often manifests as a bulge on the sidewall, coupled to large-scale bending of the cylindrical cell wall around the bulge. The direction of bending confirms the hypothesis of a longitudinal orientation of peptides and a circumferential orientation of glycan strands in the peptidoglycan layer. Our simulations based on our physical model also suggest a surprising robustness of cell shape to damage, allowing cells to grow and maintain their shape even under conditions that limit crosslinking. Finally, we show that many common bacterial cell shapes can be realized within the model via simple spatial patterning of peptidoglycan defects, suggesting that subtle patterning changes could underlie the great diversity of shapes observed in the bacterial kingdom.

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