Imaging single bacterial cells over multiple generations is crucial in deciphering dynamic, heterogeneous, and rare microbial responses, which would otherwise be missed from Population or single-cell snapshot studies. However, many classical experiments in microbiology have considered how cells change along the growth curve from exponential to stationary phase -- conditions that so far have been difficult to be replicated in single-cell imaging studies. Here, we have developed a platform that allows us to measure cell shape and growth rate as well as gene expression dynamics of individual bacterial cells under both constant and systematically changing conditions along bacterial growth-curves or in eco-systems, with unprecedented accuracy and throughput. It can routinely track $10^5$ parallel cell-lineages over $10^2$-$10^3$ consecutive generations, through multiple cycles of entering and exiting stationary phase, imaging cells several times per generation with enough resolution for automated segmentation and tracking of cells in each lineage. As a proof-of-principle we applied the platform to study aspects of stress responses of the model organisms *Escherichia coli* and *Bacillus subtilis*, which are separated by a billion years of evolution, and uncovered novel quantitative principles that connect the underlying molecular mechanisms to dynamics and physiology in single cells.