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Using microfluidics to understand stress signaling in individual bacterial cells

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To ensure their survival, all living organisms—including bacteria—must be able to sense environmental stressors and mount an effective response. Certain species, including our model bacterium *Bacillus subtilis* and the pathogen *Listeria monocytogenes*, sense environmental stress via large 'stressosome' complexes that include multiple stress-sensor variants among their 80 protein constituents. Why use such stress-sensing molecular machines in combination with sensor variants? We seek a greater understanding of how stressosomes sense and integrate different input signals to produce different stress responses that help cells survive diverse environmental insults. To gain insight into stressosome function, we employ a microfluidic platform that permits us to examine stress response patterns at the single-cell level over tens or hundreds of generations with precise control of environmental conditions. In response to ethanol stress, a wild-type strain containing multiple stress sensors and strains containing each sensor in isolation showed distinct long-term response patterns. For example, one sensor closely matched the rapid and transient wild-type response, whereas another showed a slower but sustained average response composed of pulsatile activation events in single cells. We are presently asking whether stressors other than ethanol elicit distinct response patterns and whether different response patterns confer different degrees of fitness on stressed cell populations.