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Soft Materials Actuated by Transcriptional Logic

1-2 pm PST Monday August 9th, 2021
Zoom link is provided via email, or
contact dyss@uw.edu

Bio

Growing up in the California desert I was equally drawn to the arts and the sciences, but ultimately was most inspired to pursue scientific research as a creative endeavor. I received my B.S. in chemical engineering from UC Santa Barbara and am currently pursuing my Ph.D. in chemical engineering at the University of Texas at Austin in the Keitz Group. I am the recipient of an NSF Graduate Research Fellowship, a Best Mentor Prize from the NSF Research Experience for Teachers Program, and the Arthur Nowick Teaching Award from the Materials Research Society. I am also an outspoken member of the LGBTQ+ engineering community, volunteering in student organizations and creating an undergraduate research program aimed at promoting this underrepresented population. In my free time, I enjoy live music, skiing, playing tennis, and generally being outdoors with friends.

Abstract

Keywords: living materials, synthetic biology, genetic logic

Qualities exhibited by living systems, including self-regulation, self-healing, morphology control, and environmental responsiveness are highly attractive from a material design perspective. Collectively, these properties arise from the capability of cells to perform computation using genetic, transcriptional, and proteomic machinery. However, traditional cellular materials, such as biofilms and tissues, are generally less robust and more difficult to engineer than synthetic materials. Next-generation materials must bridge the computational and sensing abilities of natural systems with the precision of synthetic systems. These designs will require re-programming metabolic activity to control synthetic material properties. Towards these goals, engineered living materials (ELMs) are a class of materials that incorporate living cells and employ biological functions to control material properties. Our group recently showed that leveraging extracellular electron transfer (EET) from the bacterium Shewanella oneidensis enables control over redox- active metal catalysts to polymerize and cross-link synthetic ELMs viaatom-transfer radical polymerization[1,2,3] (Fig. 1a,b). By coupling material synthesis to EET gene expression, we highlight how the design rules of synthetic biology can be applied to material properties, such as hydrogel mechanics. Cross- linking by genetic knockouts demonstrates that hydrogel formation is closely coupled to the expression of specific EET genes, and a Buffer gate architecture (single-input; single-output) enables quantitative control over storage modulus in response to inducer concentration. A standard gene expression model, the Hill Function, yields quantitative prediction of hydrogel storage modulus. Furthermore, genetic Boolean logic (e.g. OR, AND) controlling EET gene expression enables design of materials that sense-and-respond to combinatorial inputs. In a process emulating tissue formation, these hydrogels sense dilute and poorly differentiated input signals by using S. oneidensis as distributed actuators within a synthetic polymer network. They then respond by cross-linking, and resultant hydrogel mechanical properties are a function of input signal identity and concentration (Fig. 1c,d). Finally, we validate the general applicability of EET- controlled material synthesis by cross-linking fully synthetic polymer networks using thiole-ene and CuAAC click chemistries directed by S. oneidensis. Living control over these non-living chemistries will significantly expand the synthetic capability of microorganisms and enable unprecedented ELM designs. These materials will continue to find application as soft actuators, tissue mimetics, and 3D printing architectures.
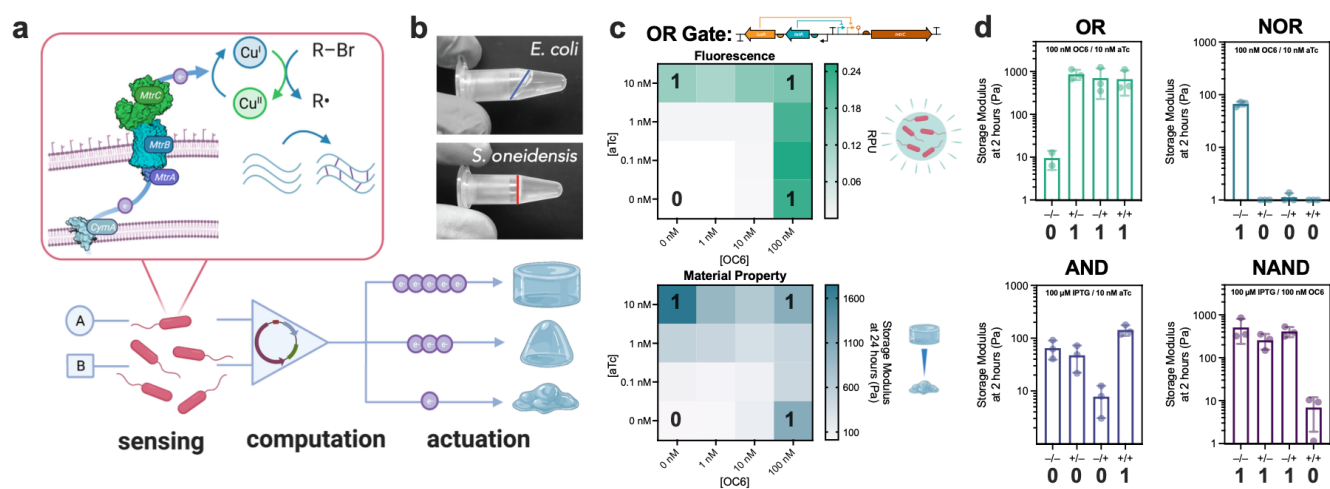
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Figure 1. Computational synthetic materials actuated by transcriptional logic controlling EET. (a) Cartoon depicting computational ELMs, wherein EET controls synthetic cross-linking through radical polymerization. (b) Gels do not form unless EET metabolism is active. (c) Heat maps showing genetic OR gate controlling fluorescence (top) or hydrogel storage modulus (bottom) in response to nM concentrations of two inputs (small molecules aTc and OC6). (d) Various genetic Boolean architectures controlling storage modulus in response to two-input combinations (aTc, OC6, or IPTG).

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