

Oral presentation

Navigational control of bacteria: the design of a synthetic chemotactic biological system

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Background

Synthetic Biology is a rapidly developing field, which sees engineering principles applied to natural biological systems with a view to re-engineer them for useful purposes. This study focused on chemotaxis, the natural directed motion of a micro-organism toward environmental conditions it deems attractive, with an aim of demonstrating external navigational control over *E. coli* bacteria. The concept has potential long-term applications in a range of fields, including biological and environmental sensors, drug discovery and the maintenance or enhancement of human health.

Method

The periplasmic maltose-binding protein (MBP) is essential for maltose transport and taxis. It was placed under external control via synthetic plasmids containing 2 different IPTG-based promoters coupled to the MBP-encoding *malE* and *malE31* [1] genes. These were transformed into three engineered $\Delta malE$ *E. coli* strains allowing for both permanent and temporary reactivation of maltose chemotaxis. The stochastic simulator StochSim [2] was adapted from the standard aspartate model to consider the associated maltose regulon.

Results

The re-engineering of the natural chemotaxis system was successfully demonstrated on both the macro and micro scale using swimming and agarose plug assays. It was shown maltose chemotaxis could be initiated and

repressed by an external signal. Stochsim was successfully adapted to model the maltose system, with simulation data for the adaptation and dependence on MBP shown to closely match experimental data [3].

Conclusion

A novel approach demonstrated the feasible control of the sensory system and resultant motile behaviour of synthetically engineered *E. coli* cells. This provides an appropriate tool for generating experimental data that in turn may feed the computational modelling of chemotaxis. This allows a better understanding of the natural system and how one might go about specifically engineering that system for a useful cause.

References

1. Sandén AM, Boström M, Markland K, Larsson G: **Solubility and proteolysis of the Zb-MalE and Zb-MalE31 proteins during overproduction in *Escherichia coli*.** *Biotechnol Bioeng* 2005, **90**:239-247.
2. Morton-Firth CJ, Shimizu TS, Bray D: **A free-energy-based stochastic simulation of the tar receptor complex.** *J Mol Biol* 1999, **286**:1059-1074.
3. Manson MD, Boos W, Bassford PJ Jr, Rasmussen BA: **Dependence of maltose transport and chemotaxis on the amount of maltose-binding protein.** *J Biol Chem* 1985, **260**:9727-9733.