Partitioning error of transcription factors at cell division

Popular science summary

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Negative feedback is common in all kinds of biological processes and can enhance a system's stability to internal and external perturbations. However, at the single molecule level, control loops always rely on random productions and decays of individual molecules and involve delays due to assembly and transport. Transcription factors (TFs) involved in regulating gene expression in cells is a good example of this event.

Many transcription factors in bacteria are present in less than 10 copies per cell. Inaccuracy in partitioning of these molecules at cell division leads to a large stochastic variation in the copy number between daughter cells. Stochastic variation causes severe consequences in metabolism and physiology. In this study, we have focused on the copy number variation of TFs in the light of previously published theoretical models for noise in cell division. We made a computer simulation in accordance with a recent experiment which was done to observe LacI (lactose operon repressor) molecule distribution at cell division in *Escherichia coli*. The experiment was performed in two different chemical conditions, with or without IPTG (Isopropyl β-D-1-thiogalactopyranoside).

The model includes a coupled process of gene expression and partitioning of protein molecules. Parameters were fitted from experimental data. We have simulated three different models: the equal distribution, binomial distribution and the distribution caused by chromosome hitchhiking mechanism. Modeling the distribution of LacI over a very long cell lineage reveals the extent of noise related to the three different distribution principles. The main insight that we gained from the simulation result, cells must have some underlined mechanisms distributing the molecules more evenly than the random way. Chromosome hitchhiking mechanism is one of the probable candidates for TFs distribution in an even manner.

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