Conditions for Chemotactic Behaviors both in Single Bacterium and in Interacting Aggregation

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***Short Abstract* — We have numerically studied bacterial chemotaxis introducing a particle model with intracellular adaptive dynamics and state-depending tumbling rate. In a single bacterium chemotaxis, we showed a condition between timescales of tumbling and intracellular dynamics, which states that the time scale of tumbling frequency must be smaller than that of adaptation and greater than that of sensing. We also studied the aggregation behavior of chemotactic particles interacting through signal chemical secretion and found the self-consistent condition for stable aggregation.**

***Keywords* — chemotaxis, chemotactic aggregation, numerical simulation.**

I. Single bacterium chemotaxis

Chemotaxis is ubiquitously observed in bacteria and other microorganisms[1,2]. In particular, bacteria sense and move toward a region with a higher concentration of an attractive chemical, by changing the rate of tumbling for random walk. We have numerically studied a model consisting of elements with intracellular adaptive dynamics, random walks with a state-dependent turnover rate to examine the validity of the condition for chemotaxis that was originally proposed by Oosawa and Nakaoka[1]. It states that the time scale of tumbling frequency must be smaller than that of adaptation and greater than that of sensing and that each time scale of sensing, tumbling and adaptation should be laid at regular interval in log scale in this order. It is demonstrated that this condition is valid for a variety of environments and for both short- and long-term behavior by suitable renormalization of the parameters for timescales[3,4].

II. Chemotactic aggregation

Next we studied collective aggregation of organisms through inter-cellular interactions with the aid of signaling molecules. In fact, bacteria show chemotaxis toward an attractant which they themselves secreted, and form a clusters by aggregation, within a much shorter time scale than colony formation[5,6].

By extending the previous single cell model, we have introduced and simulated an interacting cell model with internal adaptive dynamics to change the tumbling rate and interaction through secretion of an attractant chemical, which diffuses and is degraded[7]. The cells are found to aggregate stably when the attractant forms a concentric gradient high enough to be detected by them, within a cluster they form. The self-consistent condition for aggregation is determined by the time scales of tumbling, adaptation and sensing, as well as the diffusion constant and degradation rate of the attractant. Depending on these parameters, we have classified the phases for aggregation behavior of bacteria into stable cluster formation(aggregation), partial aggregation, and a homogeneous distribution. In the partial aggregation phase, cells aggregate to form a cluster for some time span, but then this cluster collapses so that cells are broadly scattered until they aggregate again. Intermittent aggregation and collapse is repeated. The phase diagram is obtained numerically and analyzed both from continuous reaction diffusion equation by Keller-Segel[8], and stochastic chemotactic dynamics.

Moreover, we have shown that the cluster size is independent of the density of bacteria forming the cluster when a stable cluster is formed, as is consistent with recent experimental one[5].

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