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Author(s)	Nakaoka, Shinji; Katsuyama, Chie; Takeuchi, Yasuhiro et al.
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Mathematical study on microbial coexistence mediated by syntrophic association

Shinji Nakaoka

JSPS PD Research Fellowship for Young Scientists
Graduate School of Mathematical Sciences, The University of Tokyo
with Chie Katsuyama, Yasuhiro Takeuchi and Kenji Katoh

Bacterial populations play a major role in a mineralization of organic compounds. Metabolically related bacterial populations occur within a given space. Some bacterial populations correlate strongly with each other in the expression of function, such an association is regarded as a microbial consortium. It is often the case that more than two species are synergistically involved in the degradation of organic compounds by syntrophic association in a consortium, suggesting that the degradation is mediated effectively by multiple species, rather than a single species.

Experiments were performed to figure out the character of xenobiotics degrading bacterial species, *Sphingomonas* sp. TFEE and *Burkholderia* sp. MN1 isolated from soil microcosm. It was revealed that *Sphingomonas* sp. TFEE is capable of degrading a xenobiotics, fenitrothion, to 3-methyl-4-nitrophenol (3M4N) but not utilizing 3M4N as a sole carbon and energy source. By contrast, *Burkholderia* sp. MN1 grows based on the metabolite of fenitrothion, 3M4N, while it cannot degrade fenitrothion. Methylhydroquinone (MHQ), the intermediate of 3M4N, is utilized by both species. Based on these experimental observations, we developed a mathematical model that represents the syntrophic association composed of *Sphingomonas* sp. TFEE and *Burkholderia* sp. MN1. The variables S_0 , S_1 and S_2 denote the concentrations of fenitrothion, 3M4N and MHQ, respectively. The population densities of *Sphingomonas* sp. TFEE and

Burkholderia sp. MN1 are denoted by x_1 and x_2 . The model is given by

$$\begin{aligned}
\frac{dS_0}{dt} &= \lambda - d_0 S_0 - \beta S_0 x_1 \\
\frac{dS_1}{dt} &= -d_1 S_1 + \beta S_0 x_1 - f_2(S_1) \frac{x_2}{\eta_2} \\
\frac{dS_2}{dt} &= -d_2 S_2 + \gamma f_2(S_1) \frac{x_2}{\eta_2} - f_1(S_2) \frac{x_1}{\eta_1} - f_2(S_2) \frac{x_2}{\eta_2} \\
\frac{dx_1}{dt} &= x_1 (f_1(S_2) - \mu_1) \\
\frac{dx_2}{dt} &= x_2 ((1 - \gamma) f_2(S_1) + f_2(S_2) - \mu_2)
\end{aligned} \tag{Eq}$$

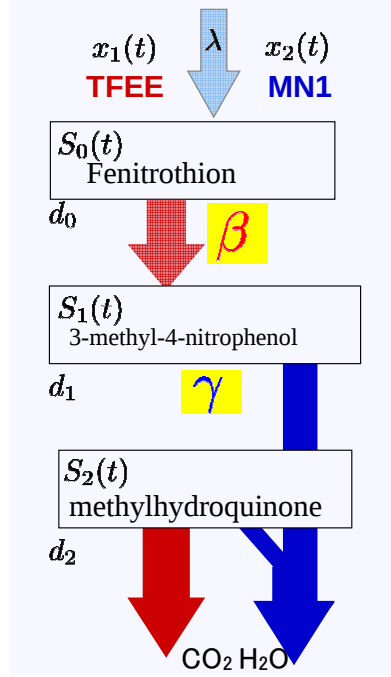


Figure 1: Scheme of fenitrothion degradation by two bacteria.

There are possibly three equilibria. *Null-degradation* equilibrium $E_F = (\frac{\lambda}{d_0}, 0, 0, 0, 0)$ always exists. All substrates and bacteria except fenitrothion have been diminished at this equilibrium. Sustainable degradation of fenitrothion requires the existence of at least one stable positive equilibrium. We analytically derived necessary and sufficient conditions for the existence of positive equilibria [1]. Under these conditions, two positive equilibria generically exist. *Syntrophic union* equilibrium $E_S :=$

$(S_0^+, S_1^*, S_2^*, x_1^+, x_2^+)$ is a stable equilibrium, representing the coexistence of two bacteria. Unstable equilibrium $E_U := (S_0^-, S_1^*, S_2^*, x_1^-, x_2^-)$ divides the region into two parts, namely, *associative* region and *dissociative* region (Fig. 2). On the associative region, all solutions tend to syntrophic equilibrium E_S , while on the dissociative region, all solutions tend to degradation-free equilibrium E_F . In this way, bistability between E_F and E_S is the common feature.

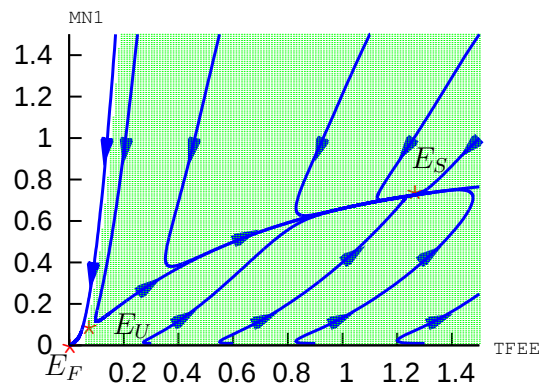


Figure 2: Dynamics of the syntrophic association. Both E_S and E_F are stable.

We further found that these two bacteria are characterized by mutual complementation; two species have complementary qualities to degrade pesticide completely. The degradative ability of one species facilitates the degradative activity of the other species and vice versa.

References

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- [2] S. Nakaoka and Y. Takeuchi, Mathematical study on sharing metabolism, *RIMS Kokyuroku Bessatsu* **B3** (2007) 193–205.