In silico construction of metabolic network from the complete sequence of *M. pneumoniae* genome

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Genome project gives us a lot of information to deal with and analyze. However in general, these approaches are limited by the lack of kinetic information on the metabolism. The ultimate goals of the systematic approaches are the establishment of dynamic model that behaves similar to the cell or microorganism. Basic studies of *M. pneumoniae* were hampered by the difficulties in cell culture and genetic manipulation. Therefore, *in silico* metabolic modeling can give clues to the metabolism and physiology of this strain. In this study, we analyzed the genome sequence of *M. pneumoniae* and developed a static metabolic model. This microorganism has a genome size of about 816 Kbp and has less than 700 ORFs. In this model, a graph concept was applied to generate the pathway. The enzymatic reactions with stoichiometric coefficients were collected from the metabolic databases. The reactions were categorized into groups by functions. Reactions in the functional group were synthesized into local metabolic pathway. Starting from a selected reaction, all reactions were added to the local pathway. Reactions, which did not have any relations with other reactions, were remained alone. To generate completed pathway, all groups were analyzed to find the possibilities of connectivity. The model shows that *M. pneumoniae* does not have many components involved in energy generation and biosynthesis compared with other microorganisms and this is consistent with previous study. The absent components mean they exist in other microorganisms. In our case, the number and size of functional group was relatively small and the complexity of connections between groups was not so high.

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