Analysis of lipid biosynthesis protein family and phospholipid strucutal variations

Michihiro Tanaka[1] Yuki Moriya[1] Susumu Goto[1] Minoru Kanehisa[1,2]

[1] Bioinformatics Center, Institute for Chemical Research, Kyoto University, Uji, Kyoto 611-0011, Japan
[2] Human Genome Center, Institute of Medical Science, University of Tokyo, Minato-ku, Tokyo 108-8639, Japan

Major structural lipids in cellular membrane systems are glycerophospholipids, which play key roles as suppliers of the first and second messengers in the signal transduction and molecular recognition processes. The distribution of lipid components is different among different organelles and cells. The distribution is controlled by two pathways in lipid metabolism: *de novo* and remodeling pathways. Glycerophospholipids including arachidonic and stearic acids are mostly produced in the remodeling pathway, where lipid chains are reconstructed from those synthesized in the *de novo* pathway.

Recently lysophospholipid acyltransferases have been isolated as key enzymes in the remodeling pathway and the substrate specificity has been investigated in terms of the chemical substructures of glycerophospholipids, such as the type of head groups and the length of aliphatic chains. These experimental studies have reported for specific organisms and only two representative sequence motifs are known for acyltransferases: a general pattern and the pattern for membrane-bound *O*-acyltransferase (MBOAT). Here we attempt to correlate the sequence patterns and the substrate specificity of lysophospholipid acyltransferases in 89 eukaryotic genomes, in order to understand the roles of this enzyme family and underlying glycerophospholipid structural variations. Using the phylogenetic and domain analyses, the lysophospholipid acyltransferase family was divided into 18 subfamilies. Furthermore, we examined the occurrence of identified subfamilies in eukaryotic genomes, and found the expansion of these subfamilies in vertebrates. These findings may provide clues to understanding structural variations and distributions of glycerophospholipids in different organisms.