線虫 *Caenorhabditis elegans* のペルオキシソームの同定と その独特な蛋白質について

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The peroxisome of the nematode *Caenorhabditis elegans*: Identification and its unique proteins

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Peroxisome is a single membrane organelle that is ubiquitous in eukaryotic cells. Peroxisomes is the site of such metabolic activities as detoxification of hydrogen peroxide, a by-product generated from oxidative reactions, β-oxidation of fatty acids, synthesis of cholesterol and bile acids, and so on. The peroxisomes of the nematode *Caenorhabditis elegans* were not detectable by cytochemical staining using 3,3'-diaminobenzidine (DAB), a commonly used method for mammalian peroxisomes. This method depends on the peroxidase activity of catalase, which is the universal marker enzyme of peroxisomes. The inability to detect peroxisomes by the standard DAB staining in *C. elegans* strangely suggested the absence of peroxisomal catalase. However, open reading frames (ORFs) of *C. elegans* predict a catalase that carries a probable peroxisomal targeting signal 1. The author purified the catalase to near homogeneity from the homogenate of *C. elegans* cells. The purified enzyme (220 kDa) was tetrameric, similar to many catalases from various sources, but exhibited unique pH optimum (pH 4.0) for peroxidase activity; the corresponding pH for bovine catalase was 9.2. The low pH optimum explains why the peroxisomes were undetectable when the standard alkaline DAB-staining method was used. Now it is possible to identify *C. elegans* peroxisomes immunologically.

In peroxisomes there is the family of a unique protein termed sterol carrier protein 2 (SCP2), the physiological role of which is thus far unclear. It exists both as an independent protein and as a fusion protein. One of the mammalian fusion proteins is SCPx, which has a thiolase domain that acts on CoA thioesters with an α-methyl side chain (e.g. the intermediates of bile acid synthesis). A *C. elegans* protein P-44 shows an amino acid sequence similar to the thiolase domain of SCPx, has substrate specificity similar to SCPx, but lacks the SCP2 domain. The author located P-44 in the matrix of *C. elegans* peroxisomes by immunocytological means and revealed that it is expressed mainly in intestinal cells at larval stages. No SCP2 fusion of P-44 was found in *C. elegans* peroxisomes. However, among putative ORFs predicted from the completed *C. elegans* genome se-

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quence there were other SCP2 family fusions (e.g. m03a8.1) and an independent form of SCP2 family (zk892.2). Their predicted sequences suggest they are peroxisomal proteins. The author cloned the cDNA of zk892.2, expressed the encoded protein in bacterial cells, purified it to near homogeneity, and raised mouse antisera against it. The zk892.2 protein was co-expressed with P-44 in peroxisomes of intestinal cells and exhibited a weak but significant lipid-transfer activity. Therefore zk982.2 is an ortholog of SCP2 and, together with P-44 and SCP2 family fusions, provides us with an opportunity to study the cellular role of SCP2 family proteins.