

## The recombinant delta4 Fatty Acid Desaturases from *Thraustochytrium aureum* ATCC 26185 and BK1, Involved in the Biosynthesis of Docosahexanoic Acid Heterologous Expression in *E. coli* and Yeast

Hyo-Jeong Oh, Tae-Ho Chung, Geun-Joong Kim, Byung-Ki Hur and Keum-Hwa Choi

Institute of Biotechnological Industry, College of Engineering, Inha University

TEL: 82-32-860-2767, FAX :82-32-875-0827

*Thraustochytrium* is a unicellular marine eukaryotic microorganism and unusually produces long chain polyunsaturated fatty acids such as DHA and docosapentanoic acid (DPA) 22:5(n-6). DHA (docosahexanoic acid) is a fatty acid of the (n-3) series, according to the location of the last double bond at the methyl end. The *Fad4* and putative *Tad4*, coding for delta4 fatty acid desaturases from *Thraustochytrium aureum* ATCC 26185 and BK1, respectively were amplified by PCR and cloned into pMAL protein expression vector. The function of *Fad4* and putative *Tad4* was identified as the enzyme which involved in the biosynthesis of docosahexanoic acid (DHA) by fatty acid profiles. In the present study, when the *Fad4* or putative *Tad4* from *Thraustochytrium aureum* was expressed in *E. coli* and yeast at the lower temperature, the fatty acid composition was changed, resulting in the production of DHA and other long-chain unsaturated fatty acids. These results would be the valuable raw data for large scale DHA production and ongoing investigations of DHA synthetic pathway in lower eukaryotes.

### References

1. Xiao Qiu, Haiping Hong, and Samuel L. Mackenzie (2001), Identification of a delta4 fatty acid desaturase from *Thraustochytrium* sp. involved in the biosynthesis of DHS by Heterologous expression in *Saccharomyces cerevisiae* and *Brassica juncea*, *J. Biological Chemistry* **276**, 31561-31566.
2. Xiao Qiu (2003), Bioynthesis of docosahexanoic acid (DHA, 22:6, 7,10,13,16,19):two distinct pathways, *Prostaglandins, Leukotriens and Essential Fatty Acids* **68**, 181-186.