

OE1) Effects of different NaNO_3 on the differential expression of HVPUFA genes in Marine Microalga *Isochrysis* sp

Sunirmal Sheet, Yang Soo Lee

Department of Forest Science and Technology, College of Agriculture and Life Sciences, Chonbuk National University

High Value Polyunsaturated Fatty Acids (HVPUFAs) are given high-priority in daily diet because of its crucial role in normal brain development as well as function for human health. So, in this study directly addressed the issue by focusing on the impacts of nutritional factors like nitrogen stress condition on algal biochemistry specifically related to HVPUFA production processes. The effects of nitrogen stress condition on biochemical composition and differential expression of different HVPUFA producing enzyme encoding genes were examined after growing the marine microalgae *Isochrysis* sp under different NaNO_3 concentration 100 mg/L, 300 mg/L, 25 mg/L. To analysis the impact of nitrogen depletion and repletion stress on algal growth, biochemical composition, photosynthetic rate and the differential expression of different HVPUFA producing enzyme encoding genes; the wet biomass, total lipid, chlorophyll content and gene expression were analyzed after 3rd, 5th, 7th and 10th day of treatment of nitrogen stress to alga. The highest lipid accumulation on 7th day under nitrogen starvation condition (25 mg/L) was confirmed by Nile red fluorescence dye method. But the chlorophyll content found to be maximal on 5th of treatment under 100 mg/ml concentration and the highest biomass content was observed on 7th day in 300 mg/ml concentration. After semi-quantitative PCR analysis of specific HVPUFA biosynthesis gene, results reveled that transcription level of target genes ($\Delta 4$ Des, $\Delta 5$ Des, $\Delta 6$ Des) has been up regulated in nitrogen depleted condition. Our results show that nitrogen depleted influence micro algal metabolism and HVPUFA productivity, which should be of great interest to scale up HVPUFA production by using microalga as a sustainable source after changing their metabolic functions.