E201 Characterization and Expression of Ornithine Decarboxylase gene by Oxidative Stress in *Chlamydomonas reinhardtii*

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A cDNA for ornithine decarboxylase, a key enzyme in putrescine and polyamine biosynthesis, has been isolated from unicellular green alga, *C. reinhardtii.* Reverse transcription-PCR employing degenerate oligonucleotide primers representing conserved motifs from other eukaryotic ODCs was used to isolate the ODC cDNA. The sequence contains an open reading frame of 1413bp encoding a polypeptide of 470 amino acid, with an estimated molecular mass of 51.5kD and exhibits high similarity to other eukaryotic ODCs within the conserved region. Expression of the ODC *in vitro* transcription/translation system and demonstration of ODC activity confirmed that ODC cDNA encodes an active ODC enzyme. Southern blot analysis of genomic DNA stands for a single gene encoding ODC based on the restriction map of the pCrODC. Exposure to an oxidative stress by the addition of H_2O_2, cumen hydroperoxide, paraquat resulted in a greater increase of CrODC activity and higher *CrODC* transcripts levels in *Chlamydomonas reinhardtii*

E202 Glucose Determination by Using Korean-Radish Peroxidase

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Glucose concentration was measured by using glucose oxidase- peroxidase coupling method. The chromogen used in this work was *o*-tolidine or 4-aminoantipyrine/diethylaniline(4AA/DEA) and the colored products were measured at 630 nm by using SCINCO UVS-2100. The optimal pHs for enzymatic glucose determination with *o*-tolidine and 4AA/DEA were determined to be 5.5. Korean-Radish peroxidase purified from Korean radish root(Raphanus sativus L.) was used as a coupling enzyme instead of commercial horseradish peroxidase. Various optimal reaction conditions were also determined. Notably Korean-Radish peroxidase could replace well horseradish peroxidase for enzymatic determination of glucose concentration when *o*-tolidine or 4AA/DEA was used as the chromogens.
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