Nucleotide sequence of the cDNA encoding subunit VIIe of cytochrome c oxidase from the slime mold *Dictyostelium discoideum*

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Cytochrome c oxidase is the terminal enzyme of the respiratory chain of eukaryotes and many aerobic bacteria (1). In the slime mold *Dictyostelium discoideum* the enzyme is composed of three large subunits encoded in the mitochondrial DNA and four additional polypeptides of nuclear origin. As recently demonstrated, the smallest nuclear-encoded subunit is present with two isoforms whose alternative expression is modulated by oxygen (2). In this respect, the slime mold oxidase can be a useful model for studying a typical feature of the more complex mammalian enzyme, where at least three of the ten nuclear subunits are present with tissue-specific isoforms (3).

Here, we present the cDNA sequence for the *D. discoideum* oxidase subunit form, termed VIIe, present under normal oxygen tension. The cDNA was cloned from a lambda gt11 expression library, by using a subunit-specific polyclonal antibody. The antibody was purified by affinity chromatography from the antiserum obtained by injecting a rabbit with the subunit isolated by SDS-PAGE. The 354 bp cDNA cloned contains an open reading frame coding for a protein of 52 amino acids. The amino terminus of the deduced amino acid sequence matches the sequence of the mature protein (underlined in the figure) thus suggesting the absence of a cleavable signal peptide. In

confirmation of a previous observation based on preliminary protein sequencing data (4), this polypeptide appears to be homologous to subunit VIIa and subunit VIc of yeast and bovine cytochrome c oxidase, respectively.

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EcoRI linker -TTTTTTTTTTTTTTTCGCATACATACACTTCAATCACATAAAATAAATAAA (53)

ATG TCC CAC GCA TTA CCA GCT CTC ATT AAA ATG CAT ATC ACC AAA GAT ATT (104)
Met Ser His Ala Leu Pro Ala Leu Ile Lys Met His Ile Thr Lys Asp Ile
      (1)                               (10)

GGT TAT GGT CTC CTT TTA GGT ATC ATC CCA GGT GTT TGG TTC AAA TAT CAA (155)
Gly Tyr Gly Leu Leu Leu Gly Ile Ile Pro Gly Val Trp Phe Lys Tyr Gln
      (20)                               (30)

ATT GGC CAA TCT ATC CAA AAA AGA GAA GAT TTT TAC GCT GCC TAT GAT AAG (206)
Ile Gly Gln Ser Ile Gln Lys Arg Glu Asp Phe Tyr Ala Ala Tyr Asp Lys
      (40)                               (50)

AGA AAT TAA ATAGTAACATTAAATATAAAGTAAATTAAAATAAAAGTTGTAAAGTTCAATAATA (269)
Arg Asn *

TTAAGAAAAAAACCAACAACATAAAGAAATTTATATATAAAAAAAATAAAATAAAAAACAATG (336)

TCAATATAACAAATAAAA- EcoRI linker (354)

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