ELSEVIER

Mitochondrion 5 (2005) 363–388

Mitochondrion

www.elsevier.com/locate/mito

Review

Biogenesis of cytochrome *c* oxidase

Oleh Khalimonchuk, Gerhard Rödel*

Institut für Genetik, Technische Universität Dresden, 01062 Dresden, Germany

Received 8 August 2005; accepted 10 August 2005
Available online 29 September 2005

Abstract

Cytochrome *c* oxidase (COX), the terminal enzyme of electron transport chains in some prokaryotes and in mitochondria, has been characterized in detail over many years. Recently, a number of new data on structural and functional aspects as well as on COX biogenesis emerged. COX biogenesis includes a variety of steps starting from translation to the formation of the mature complex. Each step involves a set of specific factors that assist translation of subunits, their translocation across membranes, insertion of essential cofactors, assembly and final maturation of the enzyme. In this review, we focus on the organization and biogenesis of COX.
© 2005 Elsevier B.V. and Mitochondria Research Society. All rights reserved.

Keywords: Cytochrome *c* oxidase; Mitochondria; Assembly factors; Metallation

Contents

* Corresponding author. Tel.: +49 351 46336210; fax: +49 351 46337725.
E-mail address: gerhard.roedel@mailbox.tu-dresden.de (G. Rödel).

1567-7249/$ - see front matter © 2005 Elsevier B.V. and Mitochondria Research Society. All rights reserved.
doi:10.1016/j.mito.2005.08.002

1. Introduction

Cytochrome *c* oxidase (common abbreviations: CO, CcO, COX, or complex IV) is the terminal enzyme of electron transport chains in eukaryotes and some prokaryotes. It belongs to the family of heme-copper enzymes, and as all its members COX not only reduces dioxygen to water, but also acts as a proton pump (Pereira et al., 2001). Eukaryotic COX is a complex enzyme, which consists of 11–13 subunits depending on the organism. Prokaryotic homologues usually have a less complex organization. The core of the eukaryotic enzyme is formed by three subunits, which are encoded by mitochondrial (mt) DNA and translated on mt ribosomes. The three core subunits are highly conserved between different organisms. Their prokaryotic homologues constitute the functional enzyme. They contain a couple of redox-active metal centers which play a key role in the assembly steps and function of the enzyme. The low-spin heme *a* and a bimetallic site composed of high-spin heme a_3 and a copper ion (Cu_B) reside in subunit Cox1p. The latter two form the oxygen reduction site termed Cu_B center. The binuclear Cu_A center is coordinated by subunit Cox2p and—together with heme *a*—constitutes the entry site for electrons which are channeled through the respiratory chain to COX.

The other subunits are encoded by the nuclear genome. Compared with their mt counterparts they show relatively low levels of conservation. Nevertheless, most of them are indispensable for the proper assembly and function of the enzyme. The nuclear-encoded COX subunits appear not to originate from the genome of the ancestral endosymbiont. Neither in *Rickettsia prowazekii* nor in the primitive eukaryotic organisms *Reclinomonas americana* or *Giardia sp.* (Lang et al., 1997; Das et al., 2004) putative homologues are detected, suggesting that the nuclear COX genes evolved after the invasion of the endosymbiont.

Besides the above mentioned metal centers, COX contains magnesium, sodium and zinc ions. Only few data are available on the role of these metals for COX function.

Mitochondria evolved sophisticated mechanisms of simultaneously recruiting both nuclearly and mitochondrially encoded subunits, thus allowing the coordinated assembly of proteins and cofactors of different origins into one complex. COX formation requires multiple proteins which facilitate and assist its assembly. Their number exceeds by far that of the COX subunits which represent only a minor part of mt proteome (Sickmann et al., 2003). Although some of these assisting proteins are also involved in other processes, a large number of them is exclusively dealing with COX. Many of them are required for delivery, formation and insertion of the cofactors and metal ions. A less discovered group of proteins is engaged in chaperoning the subunits during delivery or in stabilizing immature COX pre-complexes.

Our knowledge of the COX assembly process is still limited despite of a bulk of data describing structural and functional features of this complicated process. The main aspects of this review will encompass the question of COX organization (including protein composition, organization of the Cu_A and Cu_B centers and of the other groups important for COX function), essential aspects of COX assembly, formation and insertion of the heme moieties, delivery of metal ions and formation of the

Download English Version:

https://daneshyari.com/en/article/10883276

Download Persian Version:

https://daneshyari.com/article/10883276

Daneshyari.com