



Purification and partial characterization of coxsackievirus B3 2A protease expressed in *Escherichia coli*

Na der Maghsoudi a*, Fariba Khodagholi a, Mahnaz Sadjadi b, Mehdi Zeinodini c, Marjan Sabbaghian d

^a *Neuroscience Research Center, Shahrood Beheshti University, M.C., Tehran, Iran*

^b *Department of Biology, Tofigh daru Corporation, Tehran, Iran*

^c *School of Basic Science, Tarbiat Modares University, Tehran, Iran*

^d *Institute of Biochemistry and Biophysics, The University of Tehran, Tehran, Iran*

ARTICLE INFO

Article history:

Received 29 March 2008

Received in revised form 11 July 2008

Accepted 29 May 2008

Available online 11 June 2008

Keywords:

2A protease

Coxsackievirus B3

Purification

ABSTRACT

Reported here is the overexpression, purification and partial characterization of recombinant coxsackievirus B3 2A protease (CVB3 2A^{pro}) from bacterial cells transformed with a plasmid containing the CVB3 2A^{pro} cDNA sequences. The structural investigation showed that the protein contains mostly β -strand elements and requires Zn^{2+} ions as a structural component which appeared to be highly conserved exogenously. The purified enzyme activity was optimal at 4 °C and had a short half-life at physiological temperature. This feature can be the result of the presence of a high content of β -structure and also hydrophobic residues in its structure.

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1. Introduction

Coxsackievirus B3 (CVB3) is considered as the most important infectious agent involved in viral heart muscle disease [1]. CVB3 may induce acute and chronic forms of human myocarditis, which can be a life-threatening disease with adverse acute and long-term clinical outcome [2]. In addition, persisting CVB3 genomes may lead to dilated cardiomyopathy [3,4]. Besides its clinically important adverse effects on the heart, CVB3 has also been implicated as an infectious agent involved in the pathogenesis of extracardiac diseases such as hepatitis [5], pancreatitis [6], and aseptic meningitis [7]. It has been shown that acute as well as persisting CVB3 infection of cardiac cells causes a direct cytopathic effect in both cultured human myocardial fibroblasts [8] and myocytes [9] and in various animal models [4,5,10]. In the intact myocardium, cleavage of dystrophin by coxsackievirus 2A protease (2A^{pro}) is considered an important mechanism for CVB3-induced cardiac injury [11]. Additionally, there is evidence for CVB3-mediated apoptotic cell death. On entry into the cell, coxsackievirus releases its messenger-like protein-stained RNA, which is subsequently translated into a

monocistronic polyprotein. The first step in subsequent polyprotein processing is cleavage by the viral 2A^{pro} [12]. This protease is also involved in cytopathic processes, mediated by either cleavage of dystrophin and/or shuttling of host cell translational mechanisms [11,13]. Thus, coxsackievirus 2A^{pro} comprises an important nonstructural viral gene essential for maturation and cytopathic processes and represents an ideal target for antiviral chemotherapy. For this aspect, the identification of the enzyme's structure serves as an important prerequisite for antiviral drug design.

To approach this goal, it is desirable to purify and characterize this enzyme, the purpose that has been followed in the present investigation and should prove useful for high-throughput screening of 2A^{pro} inhibitors.

2. Materials and methods

2.1. Materials

HeLa and Vero cells were purchased from National Cell Bank of Iran (NCBI CIIS). *E. coli* BL-21, BLR (0E3), BLR (DE3) pLysS, pET22b(+) vector were obtained from Novagen. RPMI, fetal calf serum and agarose were from Gibco and isopropanol chloroform was from Merck (Germany). Random Hexamer, Reverse Transcriptase, Tag polymerase, EcoRI, NdeI, T4 Ligase, ampicillin, tetracycline, were purchased from Roche, LB, Scharlau; KLH (Keyhole Limpet Hemocyanin) were from Sigma Chem (USA), polyvinylidene fluoride (PVDF) was obtained Fluka; peptides 17CA, 17CV, 20CS and 20Pn

Abbreviations: 2N^o, 2A protease; CD, circular dichroism; CVB3, coxsackievirus B3; DAB, diaminobenzidine; GuHCl, guanidinium hydrochloride; HRP, horse radish peroxidase; KLH, Keyhole Limpet Hemocyanin; PVDF, polyvinylidene fluoride; SDS, sodium dodecyl sulfate

* Corresponding author. Tel.: +98 21 22429768; fax: +98 21 22431624.

E-mail address: nmaghsoudi@sbm.u.ac.ir (N. Maghsoudi).

