

N-terminal region of α -synuclein is essential for the fatty acid-induced oligomerization of the molecules

Hiroki Karube¹, Masahiro Sakamoto¹, Shigeki Arawaka*, Susumu Hara, Hiroyasu Sato, Chang-Hong Ren, Saori Goto, Shingo Koyama, Manabu Wada, Toru Kawanami, Keiji Kurita, Takeo Kato

Department of Neurology, Hematology, Metabolism, Endocrinology and Diabetology, Faculty of Medicine, Yamagata University, 2-2-2 Iida-Nishi, Yamagata 990-9585, Japan

Received 18 September 2008; revised 30 September 2008; accepted 2 October 2008

Available online 9 October 2008

Edited by Barry Halliwell

Abstract Exposure of α -synuclein (α S), a major component of Lewy bodies in Parkinson's disease, to polyunsaturated fatty acids (PUFAs) triggers the formation of soluble α S oligomers. Here, we demonstrate that PUFA binds recombinant α S protein through its N-terminal region (residues 2–60). In HEK293 cells, α S mutants lacking the N-terminal region failed to form oligomers in the presence of PUFA. The PUFA-induced α S oligomerization was accelerated by C-terminal truncation or Ser129 phosphorylation of α S; however, this effect was abolished by deletion of the N-terminus. The results indicate that the N-terminus of α S is essential for the PUFA-induced α S oligomerization. © 2008 Federation of European Biochemical Societies. Published by Elsevier B.V. All rights reserved.

Keywords: Parkinson's disease; α -Synuclein; Oligomerization; Fatty acid; Truncation; Phosphorylation

1. Introduction

Parkinson's disease (PD) is characterized by the progressive degeneration of dopaminergic neurons in the substantia nigra and the presence of intracytoplasmic filamentous inclusions called Lewy bodies (LBs) and Lewy neurites (LNs). Identification of missense mutations in the α -Synuclein (α S) gene (A30P, A53T, and E46K) [1–3] and the multiplication [4] of the locus in autosomal-dominant familial PD indicates a direct link of α S to the pathogenesis of familial PD. α S is also thought to play a critical role in sporadic cases of PD, because fibrillized α S is a major component of LBs and LNs [5]. In vitro experiments have shown that α S readily oligomerizes into fibrils that share ultrastructural features of fibrils in LBs [6]. Furthermore, overexpression of human wild-type [7] or A53T [8,9] α S in transgenic mice results in motor impairment with the develop-

ment of α S inclusions. Feany and colleagues have also reported that overexpression of wild-type, A30P or A53T- α S in *Drosophila* shows loss of dopaminergic neurons with an increase in filamentous α S inclusions [10]. Accumulated evidence suggests that the oligomerization of α S into fibrils affects the toxicity of the molecule [11]. Previous studies have demonstrated that the oligomerization of α S is accelerated by oxidation and nitration of α S [12], phosphorylation of α S at Ser129 [13,14], C-terminal truncation of α S [15] or binding of phospholipids to α S [16]. However, the exact biochemical mechanisms for the formation of pathological α S oligomers remain to be elucidated.

Sharon et al. reported that the N-terminus (residues 2–19) and the C-terminus (residues 123–140) of α S have homology to the fatty acid (FA)-binding motif of fatty acid-binding protein (FABP) [17]. They also showed that recombinant α S directly binds to FA in a stoichiometric manner, and that soluble, lipid-associated monomers and oligomers of α S are present in transgenic mouse brains expressing wild-type or A53T- α S [17,18]. On the basis of the facts, they concluded that α S has the properties of FABP [17,18]. They further demonstrated that exposure of monomeric α S to polyunsaturated fatty acids (PUFAs) promotes the formation of soluble α S oligomers in cultured mesencephalic cells [18]. In the brains of PD and dementia with Lewy bodies, the amount of soluble, lipid-associated α S oligomers increased [18]. Since the soluble α S oligomers seem to be precursors of fibrils [11], the findings suggest that the binding of α S to PUFA is one of the key events in the process for conversion from soluble monomers to pathological oligomers of α S.

The present study was carried out to determine the α S region responsible for the binding to FA by using a series of α S deletion mutants, and to assess a role of the binding of α S to PUFA in the oligomerization of α S. The results show that the binding of α S to PUFA in its N-terminal region is essential for the PUFA-induced oligomerization of α S.

2. Materials and methods

2.1. Plasmid construction

Wild-type human α S (Wt- α S) cDNA and human G protein-coupled receptor kinase 5 (GRK5) cDNA were cloned into the pcDNA3.1 vector (Invitrogen) [14]. α S deletion mutant cDNAs and α S familial PD-linked mutant (A30T, E46K and A53T) cDNAs were generated by the two-step PCR mutagenesis method. Nucleotide sequences of all constructs were confirmed.

*Corresponding author. Fax: +81 23 628 5318.

E-mail address: arawaka@med.id.yamagata-u.ac.jp (S. Arawaka).

¹These authors contributed equally to this work.

Abbreviations: PD, Parkinson's disease; α S, alpha-synuclein; LB, Lewy body; LN, Lewy neurite; FA, fatty acid; PUFA, polyunsaturated fatty acid; FABP, fatty acid-binding protein; OA, Oleic acid; ALA, α -linolenic acid; GRK, G protein-coupled receptor kinase; NAC, non-amyloid β -protein component

2.2. Expression and purification of recombinant α S

Wild-type and deletion mutants of human α S cDNAs were cloned into the pGEX-4T-1 vector (GE Healthcare) to generate glutathione S-transferase fusion protein. The fusion proteins were expressed in *Escherichia coli*. Recombinant α S was purified from the fusion protein by the method described previously [14].

2.3. Oleic acid (OA)-binding assay

OA-binding assay was carried out as previously described with slight modifications [17,19]. Hydroxyalkoxypropyl-Dextran type IV (known as Lipidex 1000, Sigma) was known to bind to free FA at 0–4 °C and FA-bound proteins at 37 °C [19]. To collect FA-unbound proteins, recombinant α S proteins purified from *E. coli* were incubated for 30 min with 5% Lipidex 1000 at 37 °C. After centrifugation at 20000 \times g for 5 min, the supernatant containing FA-unbound α S was recovered and stored at –80 °C. To determine the binding of α S to OA, 5 μ M α S protein was incubated with various amounts of [¹⁴C] OA (Moravak Biochemicals, 54 mCi/mmol) in 100 μ l of phosphate-buffered saline (PBS; 100 mM phosphate, pH 7.4, 150 mM NaCl) for 1 h at room temperature. The mixture was kept on ice for 10 min, and 10 μ l of 50% (v/v) Lipidex 1000 was added. The mixture was incubated for 10 min on ice. After centrifugation at 15000 \times g for 5 min, protein-bound [¹⁴C] OA in the supernatant was measured by scintillation counting.

2.4. In vitro oligomerization of α S

One micromolar recombinant α S proteins in PBS were incubated at 37 °C for 12 h with or without α -linolenic acid (ALA, Sigma) of indicated concentrations [14]. Samples (100 ng protein) were analyzed by immunoblotting using anti- α S monoclonal antibody (Syn-1, which recognizes residues 91–99 of human α S; BD Transduction Laboratories) [20].

2.5. Cell culture and transfection

Human embryonic kidney (HEK) 293 cells were maintained in Dulbecco's modified Eagle's medium (Invitrogen) supplemented with 10% fetal bovine serum. HEK293 cells were transfected with α S cDNAs using Lipofectamine Plus reagents (Invitrogen), according to the manufacturer's protocol.

2.6. PUFA-induced α S oligomerization in the cells

For the PUFA-induced α S oligomerization, the transfectants were recovered at 32 h after transfection, and the cells were further incubated with serum-free medium containing 500 μ M ALA and 100 μ M FA-free bovine serum albumin (BSA, Sigma) for 16 h [14,18].

2.7. PUFA-induced oligomerization of phosphorylated α S in the cells

HEK293 cells were transiently co-transfected with GRK5 cDNA and either wild-type or mutant α S cDNA [14]. Twenty-four hours after the transfection, 20 nM okadaic acid (Wako) was added to the culture and the cells were incubated for 16 h. The cells were further incubated for 9 h in fresh serum-free medium containing ALA/BSA complexes and okadaic acid and the cell lysates were analyzed by immunoblotting [14].

2.8. Protein fractionation and immunoblotting

Transfectants of HEK293 cells were suspended in homogenization buffer [20 mM HEPES, pH 7.4, 1 mM MgCl₂, 0.32 M sucrose, 43 mM 2-mercaptoethanol, 1 \times protease inhibitor cocktail (RocheDiagnostics), 20 mM NaF, 1 mM Na₃VO₄] and were disrupted by brief sonication [14,17]. Samples were sequentially centrifuged at 8000 \times g for 15 min and at 370000 \times g for 1 h. The resultant supernatant was recovered and stored as the cytosol fraction. The post-370000 \times g pellet was disrupted by sonication in homogenization buffer containing 1% Nonidet P-40, 1% sodium deoxycholate and 0.1% SDS, and the homogenates were incubated on ice for 30 min. After centrifugation at 12000 \times g for 30 min, the supernatant was stored as the pellet fraction. Since the detection of lipid-associated α S oligomers by immunoblotting requires delipidation procedures, we treated the cytosol fractions at 60 °C for 16 h for delipidation prior to gel-loading. The effect of the delipidation for detection of α S oligomers was described previously [14,17,18].

Protein samples were denatured by boiling for 5 min in Laemmli's sample buffer containing 2.5% 2-mercaptoethanol. Immunoblotting was performed as described previously [14]. The transferred membrane was probed with the antibodies as follows: α S specific, Syn-1, LB509 (monoclonal IgG, which recognizes residues 115–122 of α S; Zymed) [21] and 211 (monoclonal IgG, which recognizes residues 121–125 of α S; Sigma) [22]; phosphorylated α S at Ser129 specific, psyn#64 (monoclonal IgG; Wako) [23]; β -actin (Sigma); or superoxide dismutase 1 (SOD1, Stressgen). Bands were visualized by enhanced chemiluminescence (ECL) or ECL plus (GE Healthcare). Relative intensities of detected bands were scanned and quantified with NIH Image J, version 1.33 or Quantity one (Bio-Rad) software.

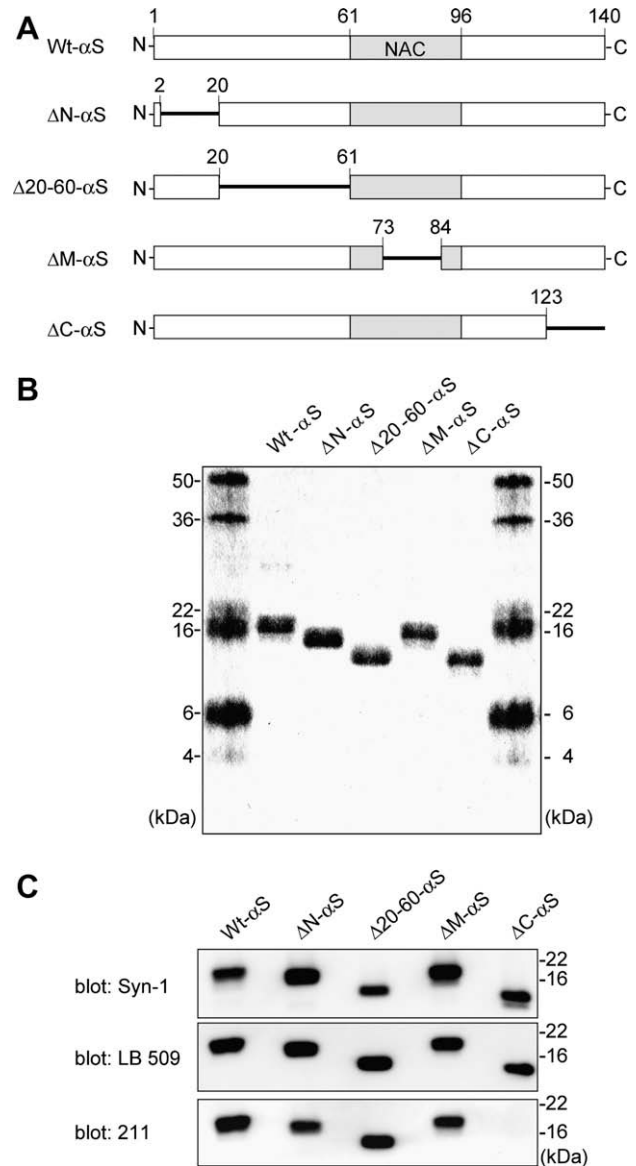


Fig. 1. α S deletion mutants. (A) Schematic diagrams of wild-type α S (Wt- α S) and α S deletion mutants. (B) The purity and electrophoretic pattern of recombinant α S mutants. Recombinant proteins (2 μ g) were analyzed by SDS-PAGE using 15% polyacrylamide gel. The gel was stained with Coomassie brilliant blue R-250. (C) Recombinant α S proteins (100 ng) were loaded to the 12.5% polyacrylamide gel and analyzed by immunoblotting using three different monoclonal antibodies. Monoclonal antibodies Syn-1, LB509 and 211 recognize residues 91–95, 115–122 and 121–125, respectively.

Download English Version:

<https://daneshyari.com/en/article/2049861>

Download Persian Version:

<https://daneshyari.com/article/2049861>

[Daneshyari.com](https://daneshyari.com)