

Characterization of the Self-Association of Human Interferon- α 2b, Albinterferon- α 2b, and Pegasys

YIMING LI,¹ WALTER F. STAFFORD,² MARK HESSELBERG,¹ DAVID HAYES,² ZHUCHUN WU,¹ MICHAEL BYRNE¹

¹Human Genome Sciences, Inc., Rockville, Maryland 20850

²Boston Biomedical Research Institute, Watertown, Massachusetts 02472

Received 17 May 2011; revised 8 August 2011; accepted 16 August 2011

Published online 4 October 2011 in Wiley Online Library (wileyonlinelibrary.com). DOI 10.1002/jps.22751

ABSTRACT: The self-association of human interferon- α 2b (hIFN- α 2b), albinterferon- α 2b (a recombinant protein with human serum albumin and hIFN- α 2b peptides fused together in a single polypeptide chain), and Pegasys (PEGylated hIFN- α 2a) was characterized by analytical ultracentrifugation analyses. By examining the apparent sedimentation coefficient distribution profiles of each protein at different concentrations, it was concluded that the above three proteins are self-associating in albinterferon- α 2b formulation buffer. By model fitting of sedimentation data using SEDANAL software, the stoichiometry and equilibrium constants of the self-association of these proteins were characterized. The self-association of hIFN- α 2b results in the formation of stable dimers, fast-reversible tetramers, octamers, and hexadecamers. In contrast, although both albinterferon- α 2b and Pegasys are self-associated, their self-association stoichiometries are significantly different from that of hIFN- α 2b. The self-association of albinterferon- α 2b results in the formation of reversible dimers and trimers, whereas the self-association of Pegasys gives only reversible dimers. The self-association behaviors of hIFN- α 2b and albinterferon- α 2b involves attractive electrostatic forces, which can be suppressed to a negligible level in low pH (pH 4.0–4.5) and high salt concentration (400 mM NaCl) buffer, allowing quantification of their size variant contents by sedimentation velocity analysis. © 2011 Wiley Periodicals, Inc. and the American Pharmacists Association *J Pharm Sci* 101:68–80, 2012

Keywords: analytical ultracentrifugation; biopharmaceuticals characterization; macromolecular prodrugs; physicochemical properties; physical characterization; proteins

INTRODUCTION

Interferons (IFNs) are a family of pleiotropic cytokines with antiviral, antiproliferation, antitumor, and immunomodulatory properties.¹ Recombinant human interferon (hIFN)- α 2a and hIFN- α 2b were the first two IFNs licensed by the US Food and Drug Administration for treatment of hairy cell leukemia. Subsequently, these IFNs were approved for clinical use for a variety of viral and cancer indications.² Owing to their rapid clearance from the body, frequent dosing (daily or three times weekly) of these two IFNs over an extended period (6–12 months or more) is necessary for some indications such as hepatitis

B and C.³ To prolong the serum half-life, PEGylated forms of these two IFNs were developed. PEGylated hIFN- α 2a (Pegasys), manufactured by Hoffmann La Roche, Inc. (Basel, Switzerland), is a covalent conjugate of hIFN- α 2a with a single 40 kDa branched bis-monomethoxy-polyethylene glycol (PEG) chain.^{4–6} PEGylated hIFN- α 2b (Pegintron), manufactured by Schering Corporation (now Merck & Co.) (Kenilworth, New Jersey), is a covalent conjugate of hIFN- α 2b with a linear 12 kDa PEG chain.⁷ Both products have a half-life much longer than their unmodified counterparts.⁸ A different approach to improve the pharmacokinetic properties of IFNs was adopted by Human Genome Sciences, Inc. This approach is based on the expression of the recombinant “gene” formed by fusing DNA sequences encoding human serum albumin (HSA) and hIFN- α 2b. The fusion protein manufactured in this manner is referred to as albinterferon- α 2b. The clinical trial data showed that albinterferon- α 2b has a half-life significantly longer than PEGylated IFNs.^{9–11}

Correspondence to: Yiming Li (Telephone: +301-398-5254; LiYi@Medimmune.com), Walter F. Stafford (Telephone: +617-658-7808; Stafford@bbri.org)

Yiming Li and David Hayes' present address is Analytical Biochemistry, MedImmune, LLC., Gaithersburg, Maryland 20878.

Journal of Pharmaceutical Sciences, Vol. 101, 68–80 (2012)

© 2011 Wiley Periodicals, Inc. and the American Pharmacists Association

Self-association of a protein pharmaceutical may impact its stability, biological function, and bioavailability.^{12–16} Moreover, there is a concern that self-association may favor the formation of stable, long lived aggregates, which might cause immunogenicity.¹⁷ Therefore, characterizing the self-association of a drug protein is important for drug development. Although the structures and biological functions of various IFN- α species have been extensively studied, the self-association of various forms of IFN- α in aqueous environment has not been characterized. In this paper, the work on characterizing the self-association of albinterferon- α 2b in comparison with hIFN- α 2b and Pegasys is reported.

EXPERIMENTAL

Materials

Albinterferon- α 2b, hIFN- α 2b, HSA, albinterferon- α 2b formulation buffer, and Pegasys formulation buffer were manufactured in-house in Human Genome Sciences, Inc. Pegasys was from Hoffmann La Roche, Inc.

Albinterferon- α 2b formulation buffer composition: 10 mM sodium phosphate, 200 mM mannitol, 60 mM trehalose, 0.01% polysorbate 80, pH 7.2.

Pegasys formulation buffer composition: 8 g/L of NaCl, 0.05 g/L of polysorbate 80, 10 g/L of benzyl alcohol, 2.62 g/L of sodium acetate trihydrate, 0.0462 g/L acetic acid, pH 6.0.

Preparation of Pegasys

Pegasys sample (8 \times 0.6 mL) in its own formulation buffer (containing polysorbate 80) was subjected to cation-exchange chromatography as given below. The sample (8 \times 0.6 mL) was buffer exchanged into 20 mM sodium acetate (pH 4.5) and concentrated to approximately 950 μ L by ultrafiltration with an Amicon Ultra-4 30 kDa centrifugal filter device (Millipore, Billerica, Massachusetts). Chromatography of the buffer-exchanged Pegasys was performed using a Gold HPLC System (Beckman Coulter, Fullerton, California) with a 4.0 \times 250 mm Propac WCX-10 column (Dionex, Sunnyvale, California). The chromatography was performed at a flow rate of 1 mL/min. For each of the four injections, the column was equilibrated with mobile phase A (25 mM sodium acetate, pH 4.5). After sample application, the column was washed 10 min with mobile phase A. Pegasys was eluted from the column with a 30 mL gradient of 0%–90% mobile phase B (mobile phase A containing 400 mM NaCl). The eluted Pegasys was pooled, concentrated, and buffer exchanged to the buffer for ultracentrifugation.

Sample Preparation for Ultracentrifugation

All four proteins, HSA, IFN- α 2b, albinterferon- α 2b, and Pegasys (purified by cation-exchange chromatography), were dialyzed against the buffers used for

ultracentrifugation. Concentrations of the dialyzed proteins were determined by measuring sample absorbance at 280 nm using an 8453 diode-array spectrophotometer (Agilent, Santa Clara, California). After protein concentration determination, the sample proteins were diluted to desired concentrations with dialysate.

Analytical Ultracentrifugation

Sedimentation velocity (SV) and sedimentation equilibrium (SE) were performed in a ProteomeLabTM-XLA protein characterization system analytical ultracentrifuge (Beckman Coulter, Brea, CA). Except for the SV run of Pegasys in a low concentration range (0.019, 0.056, and 0.167 mg/mL), the SV runs of all the proteins were monitored with absorbance scans at 280 nm. The SV run of Pegasys in low concentrations was monitored with absorbance scans at 220 nm for higher signal/noise ratio. To keep the loading absorbance values within the suitable range for SV run, a cell assembled with a 3-mm centerpiece was used for the samples with high protein concentrations. These samples include HSA at 3 mg/mL, albinterferon- α 2b at 3 and 2.7 mg/mL, hIFN- α 2b at 1.2 mg/mL, and Pegasys at 0.167 mg/mL (for run monitored by 220 nm scans) and at 1.5 mg/mL (for run monitored by 280 nm scans). All other samples were loaded into cells with a 12-mm centerpiece. For cells with a 12-mm centerpiece, 440 μ L of reference buffer was loaded into the reference sectors and 430–435 μ L of sample was loaded into the sample sectors. For cells with a 3-mm centerpiece, 110 μ L of reference buffer was loaded into the reference sector and 108 μ L of sample was loaded into the sample sector. Test scans at a rotor speed of 3000 rpm were performed to ensure proper loading without leaking before an SV run was performed. All SV runs were performed at 20°C. The rotor speed and protein concentrations for SV analysis were varied for different proteins and will be given in the *Results and Discussion* section.

Sedimentation equilibrium runs of albinterferon- α 2b and hIFN- α 2b were performed at 20°C, at three loading concentrations (0.3, 0.9, and 2.7 mg/mL for albinterferon- α 2b; 0.2, 0.6, and 1.2 mg/mL for IFN- α 2b) and three rotor speeds (8000, 12,000, and 16,000 rpm).

Determination of the Physicochemical Parameters for Data Analysis and Model Fitting

The densities of the buffers were measured using a DMA 5000 density meter (Anton Paar, Graz, Austria). The viscosities of the buffers at 20°C were measured using an Ostwald viscosimeter (VWR, West Chester, Pennsylvania). The ϵ_{280} (absorbance extinction coefficient at 280 nm) value of albinterferon- α 2b was

Download English Version:

<https://daneshyari.com/en/article/2485395>

Download Persian Version:

<https://daneshyari.com/article/2485395>

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