Technical Decision Making with Higher Order Structure Data: Higher Order Structure Characterization During Protein Therapeutic Candidate Screening

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ABSTRACT: Protein therapeutics differ considerably from small molecule drugs because of the presence of higher order structure (HOS), post-translational modifications, inherent molecular heterogeneity, and unique stability profiles. At early stages of development, multiple molecular candidates are often produced for the same biological target. In order to select the most promising molecule for further development, studies are carried out to compare and rank order the candidates in terms of their manufacturability, purity, and stability profiles. This note reports a case study on the use of selected HOS characterization methods for candidate selection and the role of HOS data in identifying potential challenges that may be avoided by selecting the optimal molecular entity for continued development. © 2015 Wiley Periodicals, Inc. and the American Pharmacists Association J Pharm Sci 104:1533–1538, 2015

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INTRODUCTION

Higher order structure (HOS) characterization is employed to study the structure–function relationship and stability of proteins.[1,2] Many biophysical techniques including circular dichroism (CD), FTIR, fluorescence spectroscopies, and differential scanning calorimetry (DSC) have been used widely to study protein HOS.[3–10] Changes in the HOS of proteins have been implicated in their decreased stability and potency.[11,12] During protein therapeutics development, a potential product will go through many processing and storage steps (e.g., extreme pH, elevated temperature) exerting stresses that may lead to changes in protein structure. To ensure the selection of the optimal molecule for commercialization, candidate screening is carried out by biopharmaceutical companies.[13–15] Characterization of HOS, along with other analyses, provides enhanced insight into structure and stability, which can often differentiate one candidate from another.

The study reported here is one of a series of case studies arising from an HOS Consortium, which was organized to study how HOS methods and data are currently used in the biopharmaceutical industry to make technical decisions during development of biologics. In this short note, we discuss the use of HOS methods in the context of selecting one protein molecule from two potential candidates that bind to the same biological target, a specific and very relevant industrial application of HOS characterization. We show that HOS methods may be used in concert with other analytical methods to make a technical decision about a candidate's likelihood for success during development.

The degree of rigor required to characterize the chemical and physical structures of therapeutic products changes during the course of development. At early stages of product development, the amount of data and extent of analysis applied to characterize biopharmaceutical products is typically small compared with the data requirement later in development. By the time a product is sufficiently advanced to apply for marketing authorization, it must be comprehensively characterized. Phase appropriate characterization also applies to making decisions during development. Thus, for the purpose of candidate selection, as described in this case study, only a limited amount of HOS data were collected as deemed sufficient to make the decision.

Antibodies X and Y are IgG 2 mAbs against the same target, and they exhibit similar biological activities. The HOSs and relative stabilities of the two molecules were characterized for an initial assessment of manufacturability and overall product quality. The effect of pH on the conformation and thermal stability of the two candidates was assessed at pH 3 and at pH 7 by several biophysical methods including near UV CD, FTIR, fluorescence spectroscopy, and DSC. In addition, the size distribution of each candidate mAb was measured by dynamic light scattering (DLS) because significant differences in self-association of mAbs had been previously observed at pH 2–8 in studies of other antibodies.[16–18] The reversibility of pH-induced changes was analyzed by dialyzing the protein into phosphate-buffered saline (PBS) following 2-h incubation at ambient temperature in pH 3 solution. The storage stability of the molecules at their formulation pH of 5, and a temperature of 37°C, was assessed by size-exclusion HPLC (SE-HPLC). The pH of 3, 5, and 7 were chosen to mimic actual conditions of production and storage.

MATERIALS AND METHODS

Materials

mAbs X and Y were produced at Amgen (Thousand Oaks, California) with purities of at least 99% by SE-HPLC. The decision for lead candidate selection was based on HOS and stability

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data collected for both mAbs at protein concentrations ranging from 0.5 to 70 mg/mL depending on the condition and method as detailed here. For the pH study, the two samples (at 10.6 and 18.2 mg/mL, respectively) in 10 mM sodium acetate buffer at pH 5 were diluted to about 0.5 mg/mL in 20 mM sodium citrate, 140 mM NaCl, at pH 3 (C3N) and separately into PBS buffer at pH 7 to about 0.5 mg/mL.

To study the reversibility of HOS changes, samples (2 mL) of each of the antibodies (X and Y), diluted into C3N at 0.5 mg/mL protein concentration, were incubated at room temperature for 2 h, and then dialyzed against 3 L of PBS using dialysis cassettes overnight without further buffer exchange. The dialyzed samples were stored at 4°C until analysis. The changes in buffer conditions and pH were selected to mimic the viral inactivation and neutralization processing steps which the antibodies undergo during purification.

Methods

Near UV CD spectra were obtained on a Jasco J-715 spectropolarimeter (Oklahoma City, Oklahoma) at ambient temperature. Mabs X and Y were each analyzed at a concentration of about 0.5 mg/mL, using cuvettes with a path length of 1 cm (340–240 nm); each spectrum was an average of 10 scans, and a single spectrum of each sample was collected. The spectra are normalized by the protein concentration and reported as mean residue ellipticity.

Spectral similarities of CD spectra were calculated using Thermo Fischer Scientific (Waltham, Massachusetts) OMINC QC compare software. The QC Compare function correlates the spectral features of two spectra in a specified wavelength region to determine the similarity between them. The result is a value between 0% and 100%, which indicates how closely the spectra match each other (100% for identical spectra). Because of the natural variability in the CD technique, as discussed in Reference3, replicate measures of the same sample typically have a similarity of 95% or higher.

Size variant distributions of the candidate samples were determined using a Malvern Zetasizer Nano ZS instrument (Westborough, Massachusetts) at 20°C using a low volume glass cuvette (50 μL). The viscosity (1.0041 cP) and refractive index (1.330) were used for calculating the size distribution of the proteins. All samples were measured at a concentration of about 0.5 mg/mL. Dispersion Technology Software (DTS) v5.03 was used for data collection and analysis. More than 10 runs of 10 s each were performed for each measurement. At least duplicate measurements were performed for each sample. For data processing, general purpose with normal resolution mode was used. The averaged intensity-weighted (*Z*-average) hydrodynamic diameter and polydispersity index (PDI) were reported.

The DSC experiments were performed using a MicroCal VP-Capillary DSC system (GE Healthcare Bio-Sciences, Pittsburgh, Pennsylvania), and data analysis was conducted using MicroCal Origin software version 7. Samples were heated at a rate of 60°C/h with a 15 min pre-scan and a 10 s filtering period. The built-in baseline correction function was used after subtracting the corresponding buffer scan. After baseline correction, the apparent thermal transition midpoints of each sample were determined by the built-in T_m determination function in the software. As with the CD and DLS measurements, the protein concentration was approximately 0.5 mg/mL for all DSC scans.

The final purified mAb X and Y proteins were prepared at 70 mg/mL and pH 5. The antibody samples were vialed and incubated at 37°C for up to 4 weeks, and the stability was assessed by SE-HPLC to monitor the loss of monomer and formation of high-molecular-weight species (HMWS). An Agilent 1100 HPLC system was used to collect the SE-HPLC data. The samples were injected on a Tosoh Bioscience TSK-GEL G3000SW$_{xl}$ column (5 μm, 7.8 × 300 mm^2) and eluted isocratically using a mobile phase of 150 mM sodium phosphate, 300 mM sodium chloride, pH 6.8 at a flow rate of 0.5 mL/min at ambient temperature. Absorbance was measured at 215 nm. The chromatogram was divided into regions representing the protein monomer, HMWS and low-molecular-weight species. The regions were individually integrated, and their respective areas were reported relative to the total area of the three regions.

Although other biochemical and biophysical methods were used in the candidate selection studies, including FTIR and fluorescence spectroscopies, only results from near UV CD, DLS, DSC, and SE-HPLC are reported here, as they were most sensitive to the irreversible changes in conformation and self-association of mAbs X and Y. (FTIR spectra are shown as supplement information.)

RESULTS AND DISCUSSION

Conformation

Circular dichroism spectra in the near UV region can be used to study tertiary structure.[3] The near UV CD spectra of mAbs X and Y in C3N and PBS are shown in Figure 1. The CD spectra of mAbs X and Y at pH 5 were not collected based on our previous experiences on multiple mAbs that show no differences in their CD spectra between pH 5 and 7. Although there may be exceptions, mAbs are generally folded at pH 5–7, and in this case *in vitro* potency data confirmed that the proteins were biologically active, and hence properly folded, at pH 5. Because of the differences in the primary sequences of the two mAbs, their near UV CD spectra differ from each other in both buffers. However, both proteins contain signals at 291–293 and 286–289 nm attributable to tryptophan, fine structure between 270 and 285 nm attributable to tyrosine and tryptophan, and features between 250 and 270 nm attributable to phenylalanine and tyrosine, superimposed on the broad negative disulfide signal from 250 to 280 nm. At pH 3, the spectra of both candidates show a loss in the intensity of the disulfide signal and changes in peak intensity and position at 291–293 and 286–289 nm because of the changes in the tryptophan signal. This indicates that both proteins undergo a significant loss of tertiary structure at pH 3.

In order to compare the spectral changes quantitatively, the overall similarity between a sample spectrum and a control spectrum was calculated.[3,19] The similarity of the near UV CD spectrum of mAb X in C3N compared with its spectrum in PBS is 51%, whereas that of mAb Y in C3N to PBS is 43%. Given the spectral similarity precision of CD measurements from a multisite and instrument study is 5%,[3] the difference in spectral similarity of 51% for mAb X compared with 43% for mAb Y is significant, suggesting that the near UV CD spectral changes are less pronounced for mAb X and hence its tertiary structure is slightly more stable at pH 3 compared with that of mAb Y.

The spectra of both candidates incubated in C3N for 2 h and then dialyzed into PBS are also shown in Figure 1. The

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