

Overview of Analytical Methods for Characterizing the Charge Heterogeneity of Antibody-Drug Conjugates



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Abstract: Antibody-drug conjugates (ADCs) are ideal candidates for selective therapy. ADCs display considerable heterogeneity resulting from various modifications. One of the molecular characteristics of ADCs is charge heterogeneity. Several analytical methods could be used to characterize the charge heterogeneity of ADC including ion exchange chromatography (IEC), isoelectric focusing (IEF), and capillary electrophoresis (CE). This work aimed to give insights into the different analytical techniques used to determine pI and the charge distribution profile of ADCs.

Keywords: Antibody, conjugates, charge, heterogeneity.

I. INTRODUCTION

Cancer is the second leading cause of death worldwide. This dangerous disease is the focus of the pharmaceutical industry. Surgery and radiation therapy are often employed when the tumor is located in a certain tissue. In cases of metastasis, chemotherapy is used [1]-[5].

Most anti-cancer drugs have non-specific toxicity due to the lack of discrimination between healthy and tumor tissue. These cytotoxic drugs have a narrow therapeutic window, which limits their effectiveness and can lead to serious side effects. In addition, prolonged treatment can lead to tumors developing resistance to anticancer drugs. Consequently, it is necessary to aim cytotoxic drugs toward cancer cells [1]-[5].

Targeted prodrugs permit a more selective treatment. The ideal candidates for these prodrugs are antibody-drug conjugates (ADCs).

ADCs are monoclonal antibodies (mAbs) linked to cell-killing drugs. With high binding specificity for tumor-specific antigens, mAbs can target cell-killing payloads in tumor cells. Tumor-specific antigens, unique or overexpressed, can be found in various human tumor cells [1]-[5].

Certain mAbs can specifically recognize and bind to these tumor-associated antigens. These agents are effective for treating cancer by binding to specific antigens of cancer cells and inducing an immune response against targeted cancer cells [6]-[8].

However, the effectiveness of treatment is often limited by the level of antibodies that cause cell death. While mAbs are highly discriminatory towards their targets, they can also be ineffective when used alone [9]-[14].

The lack of efficacy of most naked mAbs in cancer treatment can be overcome by adding radioactive isotopes or cytotoxic drugs to immunoglobulins, thus generating highly specific ADCs [15]-[20].

The manufacturing of therapeutic ADCs can be challenging due to the difficulty of demonstrating product consistency after changes in the process such as cell lines, manufacturing scale, conjugation reaction, production site, formulation, and purification process [1], [21]-[25].

ADC exhibits significant heterogeneity due to various modifications in the protein structure of the antibody itself, such as deamidation, amino acid substitution/deletion, differential glycosylation, glycation, etc. Additionally, the conjugation process by binding multiple drug molecules with antibodies increases ADC heterogeneity.

Such modifications can lead to the presence of various species in crude ADC preparations and final, purified products. Therefore, relevant methods should be used to characterize ADC.

Table I presents common analytical techniques for characterizing molecular heterogeneity or product-related impurities in mAbs [1].

As we can see in Table I, one of the molecular characteristics of ADC is charge heterogeneity. Several analytical methods can be used to characterize the charge heterogeneity of ADC including ion exchange chromatography (IEC), isoelectric focusing (IEF), and capillary electrophoresis (CE).

This study presents the different analytical techniques used to determine pI and the charge distribution profile of ADCs.

Table I: Analytical Techniques for Characterizing Molecular Heterogeneity or Product-Related Impurities in mAb or ADC Products

Molecular Characteristics	Analytical Technique
Purity and concentration determination	Size exclusion chromatography (SEC) SDS-PAGE (reduced and nonreduced) or CE-SDS, UV
Primary structure	Amino acid analysis, Mass spectrometry/peptide mapping N- and C-terminal sequencing

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Secondary structure	Circular dichroism (CD) Infrared spectroscopy (IR)
Tertiary and higher-order structure	Size exclusion chromatography (SEC) Analytical ultracentrifugation (AUC) Field-flow fractionation (FFF) Direct binding and biological assays
Charge variants	Ion exchange chromatography (IEC) Isoelectric focusing (IEF-gel) Chromatofocusing
Glycosylation	Mass spectrometry NP/RP-HPLC
Chemical modification (oxidation, photon cross-linking, glycation, etc)	Mass spectrometry/peptide mapping SDS-PAGE (reduced and nonreduced) Ion exchange chromatography (IEC)

II. ANTIBODY MOLECULAR STRUCTURE

Antibodies, also known as immunoglobulins (Ig), are glycoproteins secreted by specialized B lymphocytes called plasma cells. They consist of four polypeptides: two identical copies of the heavy and the light chain linked together by disulfide and noncovalent bonds. The resulting molecule is often represented by a schematic Y-shaped molecule diagram (Figure 1).

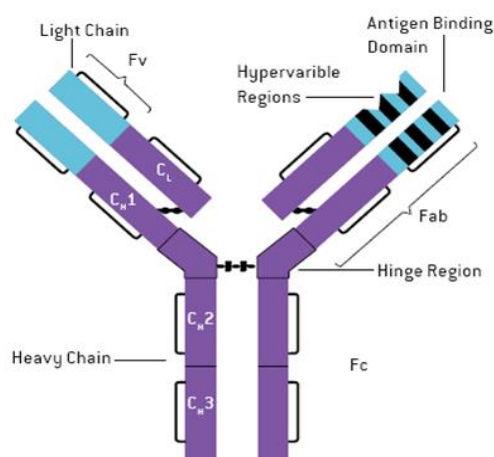


Figure 1: Structure of Monoclonal Antibody

Light chain (LC) consists of a variable region and a constant region of equivalent length. Similarly, the heavy chain (HC) is divided into variable and constant regions. However, the heavy chain has one variable and at least three constant zones.

The region of the antibody called the Fab (fragment antigen binding) consists of one constant and one variable domain for each heavy and light chain. The variable domain is the most important region for antigen binding. The hypervariable regions of the light chains and heavy chains are known as complementarity-determining regions (CDRs). They are responsible for binding to the antigen. The two arms (Fab) of the antibody molecule and the tail (Fc) or crystallizable part are connected by a region rich in proline, threonine, and serine, called the hinge [1].

Antibodies perform two essential roles:

Antibodies bind to an epitope on the antigen using Y arms. Each arm or monovalent antibody fragment (Fab) domain contains a binding site, making each antibody molecule at least bivalent.

The Fc domain of the Y imparts the antibody with

biological effector functions such as natural killer cell activation, activation of the classical complement pathway, and phagocytosis.

mAbs are antibodies produced by a single clone of B cells. Unlike polyclonal antibodies, mAbs are monospecific and homogeneous, making them powerful tools for treatment development.

III. THERAPEUTIC MONOCLONAL ANTIBODY

Since the early 1980s, mAbs have moved from discovery to clinical practice. Many of these mAbs, alone or attached to payloads (such as chemical drugs, toxins, radionuclides, enzymes, or cytokines), are used to treat cancer [1]-[10].

The first mAb approved by the US Food and Drug Administration (FDA) for human use was the murine anti-CD3 mAb, muromonab (OKT3), used to treat organ transplant rejection. OKT3 provided the first lesson for the therapeutic mAbs, i.e. murine mAbs have a short half-life, strong immunogenicity, and suboptimal effector functions when used in humans. These problems have been solved by converting mouse mAbs into human protein formats by genetic engineering [11]-[25].

From 1984 to 1988, the chimerization and humanization of mAbs were carried out. A chimeric mAb is designed to contain the variable regions of the mouse antibody and the constant regions of the human antibody, whereas in the humanized mAb, only the complementary determining regions (CDRs) are of murine origin (Figure 2).

Fully human mAbs were created by phage display or by selecting variable regions of human origin. In addition, human immunoglobulin (Ig) transgenic mice are currently being used to produce fully human antibodies.

The first mAb approved to treat cancer, rituximab, a chimeric anti-human CD20 mAb, was approved in 1997. A decade later, eight more mAbs were approved for cancer treatment and hundreds of mAbs are undergoing preclinical and clinical evaluation.

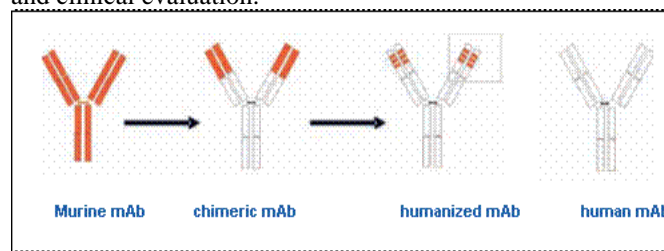


Figure 2: Structure of Murine, Chimeric, and Humanized mAb

IV. ANTIBODY-DRUG CONJUGATES (ADCS)

Naked mAbs have been used for the treatment of cancer. Indeed, since most naked mAbs are not effective enough in cancer treatment, different methods have been explored to improve their anticancer activity, including linking the antibodies to radioisotopes, chemotherapeutic drugs, or toxins (Figure 3).



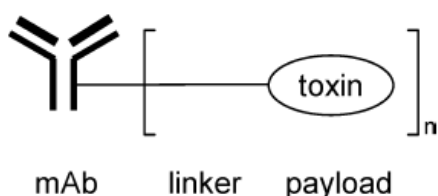


Figure 3: Schematic Representation of an Antibody-Drug Conjugate

The most developed of these is the radio-immunotherapy in which a radioisotope is conjugated to a mAb. Another treatment is based on a cytotoxic agent chemically linked to a monoclonal antibody that recognizes a tumor-associated antigen. mAbs preferentially deliver cytotoxic agents to tumor cells expressing the target antigen, thereby limiting systemic toxicity [20]-[25].

V. ANALYTICAL TECHNIQUES OF CHARGE CHARACTERIZATION

A. Chromatofocusing

Chromatofocusing allows the separation of proteins based on differences in their isoelectric point (pI), by creating a pH gradient through ion exchange stationary phases (cation exchangers CEX or anion exchangers AEX) [26]-[35].

To separate proteins according to their different pIs, a chromatofocusing medium is equilibrated with a starting buffer at a pH slightly higher than the highest pH required. The elution buffer (adjusted to the lowest pH required) passes through the column and begins the titration of the amines on the medium and the proteins. As the buffer flows through the column, the pH is lowered and a moving, decreasing pH gradient is generated (Figure 4) [27]-[28].

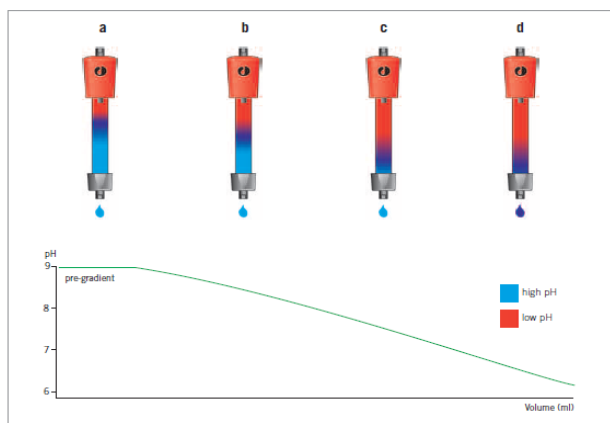


Figure 4: Development of a pH gradient in a Chromatofocusing Column. The column is Pre-Equilibrated With Start Buffer At High Ph (A) And Elution with Buffer At Low ph (b, c, d,) Generates A Descending Linear Ph Gradient

After a pre-gradient volume of elution buffer has passed, the sample (in the start buffer) is introduced into the positively charged column. The proteins in the sample are titrated (pH adjusted) immediately after being introduced into the column. Proteins in the sample become negatively charged at a pH above their pI. Thus, they are retained near the top of the column (bound to positively charged amino groups). Proteins, at a pH lower than their pI, will migrate

down the column with the buffer flow. They will not bind until they reach a region with a pH higher than their pI (Figure 5) [29].

As the pH continues to decrease near the top of the column, any protein that falls below its pI becomes positively charged, is repelled by the positively charged amine groups, and begins to migrate down the column with the elution buffer, moving faster than the pH gradient is moving down the column. However, as the protein moves down the column, the pH of the medium increases. When the protein reaches a region with pH above its pI, it becomes negatively charged and re-associated with the column again. The protein remains bound until the developing pH gradient lowers the local pH. Once again, the protein falls below its pI, becomes positively charged, and migrates down the column, catching up to the gradient. This process continues until the protein is eluted from the column at a pH close to its pI (when it has almost no net charge). Proteins with different pIs move at different speeds through the column as the pH gradient develops, continually associating and dissociating. During the chromatofocusing, they are concentrated into narrow bands and finally eluted. The protein with the highest pI elutes first and the protein with the lowest pI is eluted last [29].

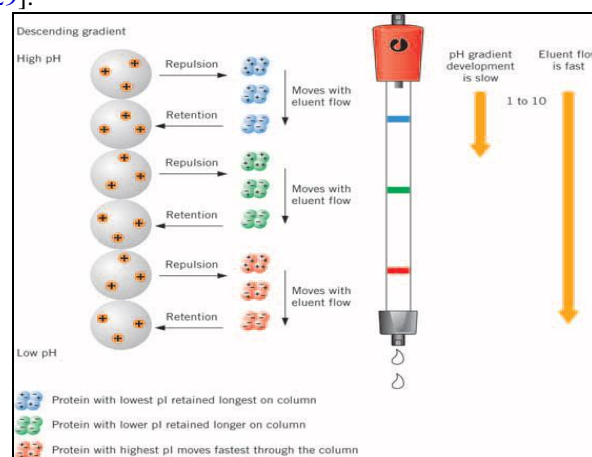


Figure 8: Proteins with Different pIs Separate as they Pass into the Column. Molecules with the Same Isoelectric Point are Focused in Narrow Bands During the Separation

A study was performed to characterize 10 model mAbs using the cation exchange pH gradient method [36]. The results demonstrated that retention and resolution can be modeled in cation exchange pH gradient mode.

A study was performed to evaluate the effects of some anion exchange chromatofocusing conditions on the characterization of the charge profile of a naked mAb and its drug conjugate [30]. Figure 9 shows chromatofocusing chromatograms of the naked mAb and its drug conjugates under the optimal chromatofocusing conditions. The naked mAb was less heterogeneous and acidic than the corresponding conjugate.



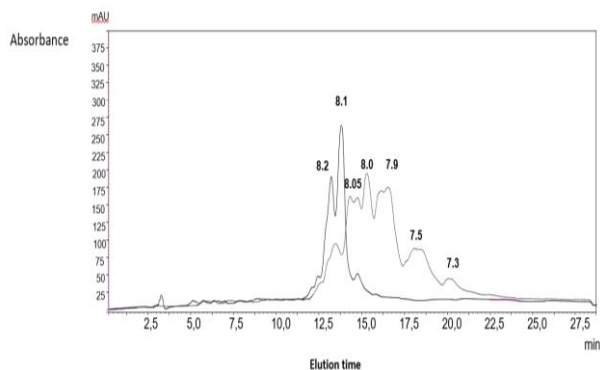


Figure 9: Chromatofocusing Profile of Naked mAb-1 and Drug- mAb-1 Conjugate

Research was performed to determine pI and relative charge variants of 23 therapeutic mAbs [37]. The results demonstrated that CEX conditions can be used to evaluate the relative amounts of mAb charge variant. Figure 10 shows the chromatograms of elotuzumab with generic and optimized gradient conditions.

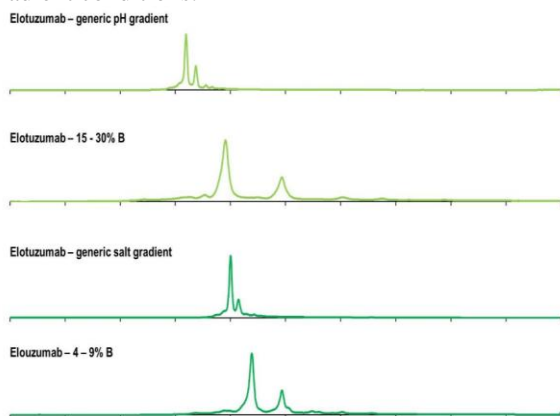


Figure 10: Comparison of Generic and Optimized Gradients in CEX Using Both pH And Salt Gradient Elution Modes of Charge Variants of Elotuzumab

B. Imaged Capillary Ief

Isoelectric focusing (IEF) is a high-resolution technique for separating proteins by their pI. It is commonly used for protein pI determination, identification, characterization, and stability monitoring. Compared to conventional gel IEF, cIEF offers higher resolution, speed, and quantitative analysis [38]-[58][59][60].

In capillary isoelectric focusing (cIEF), the capillary is filled with a solution of carrier ampholytes and sample. The anode end of the capillary is dipped into an acidic solution and the cathode end into a basic solution. When an electric field is applied, the presence of the ampholytes causes the creation of a pH gradient along the capillary. The charged components of the sample, such as proteins, then move into the capillary until they reach a pH region equal to their pI, where they become neutral. As a result, they stop migrating, leading to a series of narrowly focused zones. Conventional capillary isoelectric focusing (cIEF) is characterized by two steps: the focalization of analytes and the movement of the focused sample zone to the detection point (mobilization). The mobilization step can be achieved by applying a hydraulic force (pressure, vacuum, gravity). This step is also performed by adding ions. Indeed, the mobilization step

greatly affects the focusing ability, separation efficiency, and method reproducibility. Additionally, because the single-point detection cannot trace the analyte after injection into the column or monitor the progress of the separation process, detailed insights about the separation mechanism, separation dynamics, sample adsorption, and band broadening inside the column are unknown. As a result, single-point detection is not an ideal detection method. Whole-column detection (WCD), for which there is no mobilization step, allows for simultaneous detection along the entire length of a column and is a better option [38]-[58].

Several reviews have discussed the state of CE-based methods for characterizing mAbs and ADCs. There are only a few published studies on the different factors affecting the separation of charge isoforms of mAbs and their ADCs. For example, one study aimed to develop an imaged cIEF method to characterize the charge heterogeneity of ADCs [42]. The studied factors included focusing time, sample composition, pH range, carrier ampholyte percentage, conjugated antibody concentration, and urea concentration. Other work aimed to evaluate the charge variant profile of antibody-tobramycin conjugates using an icIEF. Figure 11 shows the good separation of charge isoforms charge of the cleavable conjugates of two antibodies with tomaymycin [43].

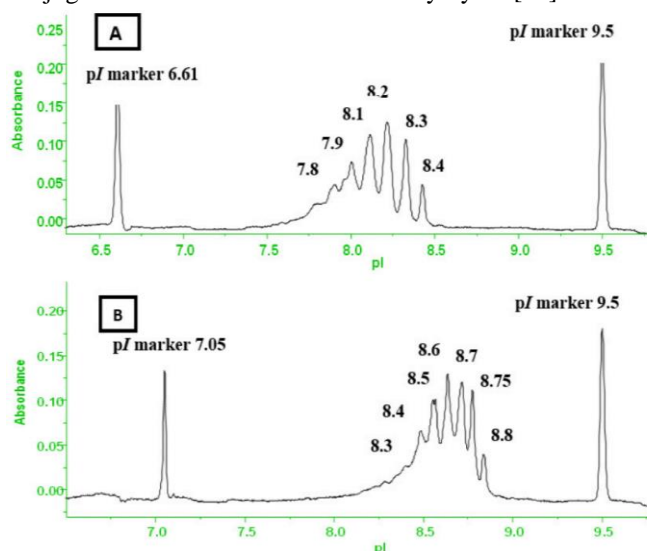


Figure 11. Analysis using icIEF of (a) Cleavable mAb-1 To Maymycin Conjugate, (b) Cleavable Mab-2 Tomaymycin Conjugate

Evaluation of charge variant profiles is one of the tools used to ensure the quality of mAbs and their ADCs. Several studies have compared the properties of icIEF with those of chromatofocusing in the separation of charge isoforms of mAbs and ADCs. For example, the charge variant profiles obtained by weak anion exchange chromatofocusing and icIEF methods for two unconjugated antibodies (mAb-1 and mAb-2) and their maytansine conjugates were compared. Significant differences were observed between the chromatofocusing and icIEF profiles for the mAbs and ADCs studied [36].



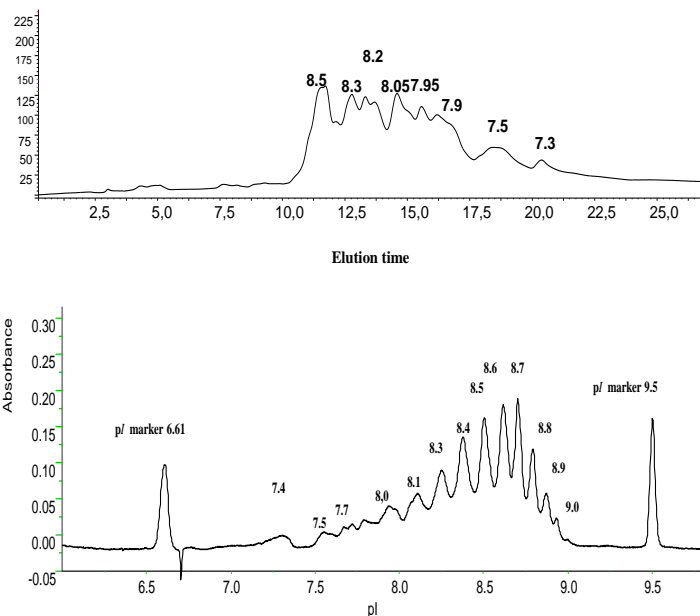


Figure 12: Chromatofocusing Profile of Conjugated mAb-2 (A): Ie IEF profile of Conjugated mAb-2 (B)

VI. CONCLUSION

Cancer is the second most common cause of death worldwide. One promising targeted therapy is antibody-drug conjugates. Antibody-drug conjugates have several isoforms distinguished by mass, charge, and pI. The quality of monoclonal antibodies and their drug conjugates are assessed using various analytical techniques. The charge heterogeneity profile ensures the quality of monoclonal antibodies and their drug conjugates. Chromatofocusing and imaged capillary isoelectric focusing methods are employed to achieve this goal. This review is dedicated to giving insights into the chromatofocusing and imaged capillary isoelectric focusing methods used to assess the charge heterogeneity profile of these compounds.

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Availability of Data and Material	Not relevant.
Authors Contributions	I am only the sole author of the article.

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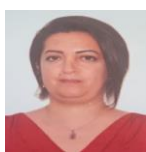


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