

DATA REPORT

Sequencing Report of a Monoclonal Vasoinhibin Antibody

Jakob Triebel, Thomas Bertsch

Institute for Clinical Chemistry, Laboratory Medicine and Transfusion Medicine, General Hospital Nuremberg & Paracelsus Medical University, Nuremberg, Germany

Abstract

Background: Vasoinhibin is an antiangiogenic fragment of the pituitary hormone prolactin which is of interest in diseases of the eye, the heart, and pregnancy complications. This is the first report of the sequence of a monoclonal antibody against vasoinhibin.

Methods: Whole transcriptome shotgun sequencing of a hybridoma cell culture producing a monoclonal anti-vasoinhibin antibody was performed and the protein sequences of the complementarity determining regions were determined by Kabat, IMGT and Chotia definitions.

Results: A mouse IgM-kappa antibody was identified, and the complete protein sequences were determined. The complementarity determining regions were identified according to Kabat, IMGT, and Chotia definitions.

Conclusions: The sequences of the antibody can be used for its recombinant production and antibody engineering.

Keywords

16 K PRL, 16-kDa PRL, prolactin, vasoinhibin, monoclonal antibody

Abbreviations

vi-mab, monoclonal anti-vasoinhibin antibody; CDRs, complementarity determining regions; HC, heavy chain; LC, light chain; VH, variable heavy; VL, variable light

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Correspondence

Jakob Triebel, Editor-in-Chief
E-mail: eic_cpr@protonmail.com

Introduction

Vasoinhibin, an antiangiogenic fragment of the pituitary hormone prolactin (PRL), is of interest in the context of proliferative retinopathies (1, 2), retinopathy of prematurity (3), peripartum cardiomyopathy (4, 5) and preeclampsia (6, 7). Vasoinhibin has also been referred to as 16 K PRL or 16-kDa PRL (8). Monoclonal antibodies against vasoinhibin without cross-reactivity to PRL have been generated recently and have been shown to be useful for immunoneutralization and employment in a sandwich ELISA (7, 9). The present study reports the full protein sequence of a monoclonal anti-vasoinhibin antibody which can be used for the recombinant production of the antibody (subject to licensing) and antibody engineering procedures. The vi-mab (monoclonal anti-vasoinhibin antibody), produced by the hybridoma technique, is commercially available at Davids Biotechnologie GmbH (Regensburg, Germany).

Materials and Methods

Sequencing of hybridoma cells expressing a vi-mab, generated as reported earlier (9), was performed by whole

transcriptome shotgun sequencing (RNA-Seq). This is a proprietary approach to antibody sequencing developed exclusively at Absolute Antibody (Oxford, UK). Total RNA was extracted from cells and a barcoded cDNA library generated through RT-PCR using a random hexamer. Next Generation Sequencing was performed on an Illumina HiSeq sequencer. Contigs were assembled using a proprietary approach and data were mined for antibody sequences identifying all viable antibody sequences (i.e. those not containing stop codons). Variable heavy and variable light domains were identified separately and relative abundance of each identified gene was reported in transcripts per million (TPM). The species and isotype of the identified antibody genes were confirmed. Sequences were compared with known aberrant (i.e. non-functional) antibody genes that are present in many hybridomas and these genes were removed from analysis. For each chain the variable domain is reported along with the constant domain. The heavy chain and light chain type was identified based on the sequence of the constant domain. For each heavy and light chain two measurements of abundance are reported. TPM (transcripts per million) is an abundance measurement from next generation sequencing which scores the relative abundance of each gene in the whole transcriptome pool. The percent column

converts the TPM into a percentage antibody gene abundance. This enables simple identification of high and low abundance antibody genes. The data is automatically filtered to only report antibody genes with an abundance of greater than 1%. The complementarity determining regions (CDRs) have been automatically identified on a 'CDR identification' worksheet using Excel formulas working to the Kabat, IMGT and Chotia definition for CDRs. CDR identification was only performed for the primary VH and VL sequences.

Results

The complete sequencing of the primary heavy and light chain demonstrated the protein sequence of a HC and LC of a mouse IgM-kappa antibody (Table 1). The CDRs

were determined according to Kabat, IMGT and Chotia and constitute the sequences presented in Table 2.

Discussion

The vi-mab, the sequence of which is shown here, is the first vasoinhibin-specific monoclonal antibody reported. The antibody originates from a mouse, which was injected with an immunizing peptide comprising amino acids 40–58 of mature human PRL (FDKRYTHGRGFITKAINSC) and subsequent monoclonal antibody production by the hybridoma technique. The sequences of the antibody can be used for its recombinant production and antibody engineering, such as species switch, isotype switch, subtype switch, reformatting to scFv, Fab, engineered Fc, or bispecificity.

Table 1 Protein sequences of HC and LC variable and constant regions.

| Protein sequence | TPM ¹ | % ² |
|---|------------------|----------------|
| Primary HC sequence, Mouse IgM, variable: EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYMSWVVRQPPGKALEWLGFI RNKANGY TTEYSASVKGRFTISRDNQSILYLQMNLT LRAEDSATYYCARDRGYYDYWGQGTTLTVSS | 16294.85 | 6.42 |
| Primary HC sequence, Mouse IgM, constant: ESQSFPNVFPLVSCESPLSDKNLVAMGCLARDFLPSTISFTWNYQNNTEVIQGIR TFPTLRTGGKYLATSQVLLSPKSILEGSDEYLVCKIHYGGKNRDLHVPIPAVAE MNPVNVVFPVPRDGFSGPAPRKS KLICEATNFTP KPITVSWLKDGLVSGFTT DPVTIENKGSTPQTYKVISTLTISEIDWLN LNVYTCRVDHRGLTFLKNVSSTCAA SPSTDILTFTIPPSFADIFLSKSANLTCLVSNLATYETLNISWASQSGEPLTKIKIM ESHPNGTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPS PQKFI SKPNEVHKH PPAVYLLPPAREQLNLR ESATV TCLVKGFS PADISVQWLQR GQLLPQEKYVTSAPMPEPGAPGFYFTHSILTV TEEEWNSGETYTCVVGHEALPHLV TERTVDKSTGKPTLYNVSLIMSDTGGTCY | | |
| Primary LC sequence, Mouse kappa, variable: DVVMTQTPLSLPVSLGDAQISCRSSQSLVH SNGNTYLHWYLQKPGQSPKLLIYK VSNRFSGVPDRFSGSGSGTDFTLTKISRVEAEDLG VYFCSQSTHVPWTFGGGTKLEIK | 237588.64 | 93.58 |
| Primary LC sequence, Mouse kappa, constant: RADAAPTVSIFPPSSEQLTSGGASVVCFLN NFYPKDINVKWKIDGSERQNGVLN SWTDQDSKDYSTYSMSSTLT LTKDEYERHNSYTCEATHKSTSPIVKSFNRNEC | | |

¹transcripts per million; ²percentage antibody gene abundance.

Table 2 CDRs of the vi-mab according to Kabat, IMGT and Chotia.

| | Kabat | IMGT | Chotia |
|--------|---------------------|--------------|-------------------|
| CDR-H1 | DYYMS | GFTFTDYY | GFTFTDY |
| CDR-H2 | FIRNKANGYTTEYSASVKG | IRNKANGYTT | RNKANGYT |
| CDR-H3 | DRGYYDY | ARDRGYYDY | DRGYYDY |
| CDR-L1 | RSSQSLVH SNGNTYLH | QSLVH SNGNTY | RSSQSLVH SNGNTYLH |
| CDR-L2 | KVSNRFS | KVS | KVSNRFS |
| CDR-L3 | SQSTHVPWT | SQSTHVPWT | SQSTHVPWT |

The antibody has been tested in a sandwich ELISA to determine vasoinhibin concentrations in aqueous solutions and human serum (7, 10). A recommended concentration for coating a microplate is 4 µg/ml. The antibody is suitable for neutralizing the antiangiogenic activity of vasoinhibin (7); this feature is expected as the immunizing peptide includes the HGR-motif, which is the antiangiogenic determinant of vasoinhibin (11).

Review Board Statement

The animal studies have been registered, reviewed and approved in 2019 by the government of Lower Franconia in Würzburg, Germany.

Conflict of Interest Statement

The vi-mab and the sequence information are subjects of an international patent application filed by J.T. (international application no.: PCT/EP2024/073698) at the European Patent Office. The commercial production and distribution of the antibody has been licensed to Davids Biotechnologie GmbH, Regensburg, Germany (website: <https://davids-science.de/>).

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