Method Development and Validation For Determining Stability of Omadacycline In Biological Matrices By Liquid Chromatography–Mass Spectrometry

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ABSTRACT

The validated protein precipitation method was applied for the estimation of Omadacycline (OM) in human plasma with Omadacycline-D9 (OMD9) as an internal standard (ISTD) by using HPLC-ESI-MS/MS. Zorbax Eclipse Plus C18, 2.1 x 50 mm, 3.5 μ m, was selected as the analytical column. The column temperature was set at 45°C. Mobile phase composition was 0.1% formic acid: methanol (80:20 v/v). Source flow rate of 300 μ L/min without a split. An injection volume of 10 μ L. Omadacycline and Omadacycline-D9 mesylate were eluted at 1.2 ± 0.2 min, with a total run time of 3.0 min for each sample. The mass transitions of Omadacycline and Omadacycline-D9 obtained were m/z 557.6 ® 456.6 and 566.7 ® 456.6, respectively. The standard curve shows a correlation coefficient (r²) greater than 0.9983 with a range of 5.00 to 12000.00 pg/ ml using the linear regression model.

Keywords: Bioanalysis, HPLC-ESI-MS/MS, Human plasma, Omadacycline.

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INTRODUCTION

Omadacycline is the first aminomethylcycline antibiotic in late-stage clinical development. Aminomethylcyclines are semisynthetic antibiotics related to tetracyclines.¹⁻⁹ Similar to their tetracycline counterparts, aminomethylcyclines inhibit bacterial protein synthesis. Importantly, however, the two main mechanisms of tetracycline resistance, namely, efflux pumps and ribosomal protection, are overcome by modifications present at the C-7 and C-9 positions in the chemical structure of omadacycline.⁸⁻¹⁵ Omadacycline has been shown to be active against a variety of bacterial pathogens: Gram-positive aerobes, including methicillin-resistant Staphylococcus aureus (MRSA), penicillin-resistant and multidrug-resistant Streptococcus pneumoniae, and vancomycin-resistant enterococcus (VRE); Gram negative aerobes; some anaerobes; and atypical bacteria, such as Legionella spp. and Chlamydia spp.¹⁰⁻²⁴

The chemical name of Omadacycline is ((4S, 4aS, 5aR, 12aR)-4,7- bis (dimethyl amino) -9-[(2, 2- dimethyl propylamino) methyl]-1, 10, 11, 12 a-tetrahydroxy-3, 12 – dioxo-4a, 5, 5a, 6-tetrahydro-4H – tetracene – 2-carboxamide. The molecular formula is C₂₉H₄₀N₄O₇ and the molecular

weight is 557.66.²⁵ The chemical structure of Omadacycline and Omadacycline 9 are given in Figure 1.

The literature survey reveals that one method was reported on the quantification of omadacycline by using LC-MS/MS.²⁶⁻²⁷ There is no method reported for estimation of omadacycline using deuterated internal standard in biological samples.

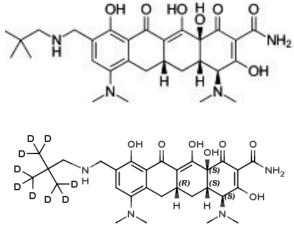


Figure 1: Chemical structures of A) Omadacycline B) Omadacycline-D9

The main goal of the present study is to develop and validate the novel simple, sensitive, selective, rapid, rugged and reproducible analytical method for the quantitative determination of omadacycline in human plasma by HPLC-ESI-MS/MS.

MATERIALS AND METHODS

Chemical Resources

Omadacycline and Omadacycline-D9 were obtained by TLC Pharma chem, Canada. LC grade methanol, Methyl t-butyl ether, and Dichloromethane were purchased from J.T. Baker Inc. (Phillipsburg, NJ, USA). Analytical Reagent grade formic acid and sodium carbonate were procured from Merck (Mumbai, India). Human plasma (K2EDTA) was obtained from Doctors pathological Lab, Hyderabad. Ultrapure water from the Milli-Q system (Millipore, Bedford, MA, USA) was used throughout the study. All other chemicals in this study were of analytical grade.

Instrument Resources

An API 4000 HPLC-ESI-MS/MS system (Applied Biosystems), 1200 Series HPLC system (Agilent Technologies, Waldbronn, Germany), data acquisition and processing were accomplished using Analyst® Software 1.4.1.

Chromatographic conditions

Zorbax Eclipse Plus C18, 2.1 x 50 mm, 3.5 μ m, was selected as the analytical column. The column temperature was set at 45°C. Mobile phase composition was 0.1% formic acid: methanol (80:20 v/v). Source flow rate at 300 mL/min without a split. An injection volume of 10 μ L. OM and OMD9 were eluted at 1.2 ± 0.2 min, with a total run time of 3.0 min for each sample.

Detection

The pure drug solutions of OM and OMD9 were prepared in methanol (10.00 ng/mL) and injected with a flow rate of 5 μ L/min into positive ion mode mass spectrometer for optimization of mass parameters like source temperature, IS, heater gas, nebulizer gas, curtain gas, CAD gas (all gas channels were purged with ultra-high pure nitrogen gas), EP, DP, CE, FP, and CXP were optimized. The analysis was performed using MRM positive ion mode with mass transitions of m/z (amu) 557.6 \circledast 456.6 and 566.7 \circledast 456.6 for OM and OMD9, respectively. The mass fragmentation pattern of parent and product ions mass spectra were depicted in Figure 2.

Standard calibration and quality control samples preparation

Stock solutions of OM (1000.00 μ g/mL) and OMD9 (1000.00 μ g/ml) were prepared in methanol. The internal standard (OMD9) spiking solution (500.00 ng/mL) was prepared in 75% methanol from OMD9 stock solution. Stock solutions of OM, OMD9 and intermediate spiking solutions were stored in refrigerated conditions (2–8°C) until analysis.

Calibration standards 5.00 to 12000.00 pg/mL, quality control samples of lower limit QC, low QC, mid-QC, high QC

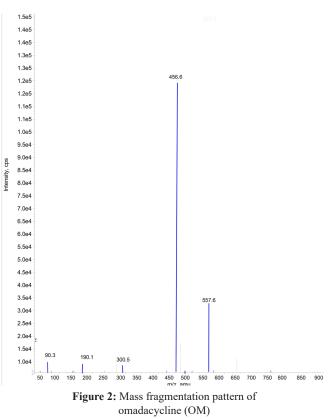
(5.00, 15.00, 4500.00, 9000.00 pg/mL) were used by spiking the appropriate amount of standard solution in the drug-free plasma and stored at -30° C till analysis.

Sample extraction

The liquid-liquid extraction procedure was used for the isolation of OM from the plasma samples. For this purpose, 50µL of OMD9 (IS) concentration of 10nglmL) 100µL plasma (respective concentration of plasma sample) was added into ria vials then vortexed approximately. Followed by 200µL of 1M Na₂C0₃ solution, 3mL of Extraction solvent (MTBE: DCM (3:1,v/v) was added to each tube and vortexed for 10 minutes. After that, the samples were centrifuged at 4000 rpm for approximately 10 minutes at 20°C temperature and transferred the supernatant into respective ria vials. These samples were allowed to dry under a nitrogen stream at 25°C. Finally, the residue was reconstituted with 200µL of reconstitution solution (MeOH: 0.1% formic acid (1:4). Further samples were centrifuged at 4000 rpm for approximately 2 minutes, and at 20°C and supernatant were transferred into autosampler vials with caps, and 10 μ L of sample was injected onto the LC-MS/MS system.

Method validation

The developed method was validated over a linear concentration range of 5.00 to 12000.00 pg/mL. The validation parameters include selectivity and specificity, LoQ, linearity, precision and accuracy, matrix effect, recovery, stability (freeze-thaw, autosampler, benchtop, long term) was evaluated under validation section.²⁸⁻³⁰



Selectivity and Specificity

Ten lots of blank plasma samples were analyzed, out of which six lots free from interference were selected for assessing the selectivity and specificity. The endogenous/potential interfering peak areas for blank samples must be less than 20% of the LLoQ peak area of OM retention time and less than 5% for OMD9 retention time.

Limit of Quantification (LoQ)

Six LLOQ standards were prepared in screened plasma lot along with IS (500 pg/mL), and signal to noise ratio (S/N) was calculated using analyst software.

Linearity

Calibration standards were prepared to obtain linearity range of 5, 10, 100, 600, 1200, 2400, 4800, 7200, 9600 & 12000 pg/ ml and assayed in five replicates on five different days.

Precision and Accuracy

One set of calibration standards and one set contains four different concentrations of quality control standards of lower limit QC (5.00 pg/mL), low QC (15.00 pg/mL), mid QC (4500.00 pg/mL) and high QC (9000.00 pg/mL) concentrations were prepared in screened plasma and analyzed each quality control (QC) standards in six replicates on the same day (Intra-day) and five different days (Inter-day).

Matrix Effect

Six extracted blank plasma samples in three replicates were spiked with the un-extracted concentration of mid-QC (4500.00 pg/mL) and compared with un-extracted standards of the same concentration.

Recovery

The recovery of samples was performed by protein precipitation method. The extraction recovery was determined in six replicate by comparing the extracted QC standards with un-extracted QC standards at three different concentrations of low (15.00 pg/mL), medium (4500.00 pg/mL), high (9000.00 pg/mL).

Stability studies

• *Benchtop Stability (Room Temperature Stability, 24hours)* Six replicates of spiked low and high concentrations (Benchtop stability samples) were set aside at ambient temperature up to 24-hour. Samples were processed and compared with newly prepared low and high concentrations (comparison samples).

• *Freeze and thaw stability (after 3^{rd} cycle at -30^{\circ}C)*

Six replicates of low and high concentrations (FT stability samples) were frozen at -30°C and subjected to three freezethaw cycles of 24, 36, and 48-hour (-30°C to room temperature) and compared with newly prepared low and high concentrations (comparison samples).

• Autosampler stability (2–8°C, 65-hour)

Six replicates of low and high concentrations (AS stability samples) were stored in auto-sampler up to 65 h at 2-8°C.

Stability samples were compared with newly prepared low and high concentrations (comparison samples).

• Long-term Stability (-30°C, 64 Days)

After completion of the stability period stored at -30 $^{\circ}$ C (64 days) six replicates of low and high concentrations (LT stability samples) were compared with newly prepared low and high concentrations (comparison samples).

RESULTS AND DISCUSSION

Method development

Initially, a mobile phase consisting of ammonium acetate and acetonitrile in varying combinations were tried, but a low response was observed. The mobile phase containing acetic acid: acetonitrile (20:80 v/v) and acetic acid: methanol (20:80 v/v) gives a better response, but poor peak shape was observed. A mobile phase of 0.1% formic acid in water in combination with methanol and acetonitrile with varying combinations were tried using a mobile phase containing 0.1% formic acid in water in combination with methanol (20:80 v/v), the best signal along with a marked improvement in the peak shape was observed for OM and OMD9. Short length columns, such as symmetry shield RP18 (50mm x 2.1 mm, 3.5 m), Inertsil ODS-2V (50mm x 4.6 mm, 5 m), Hypurity C18 (50mm x 4.6 mm, 5 m) and Rypurity Advance (50 mm x 4.0 mm, 5 m), YMC basic (50 mm x2 mm, 5 m), Zorbax Eclipse Plus C18, (2.1mm x 50 mm, 3.5μ m) were tried during the method development. The best signal and good peak shape was obtained using the Zorbax Eclipse Plus C18, 2.1 x 50 mm, 3.5 mm, column. It gave satisfactory peak shapes for both OM and OMD9. A flow rate of 0.3mL/min without splitter as used and reduced the run time to 3.0 min. Both Analyte and IS were eluted with a shorter time at 2.0 min. For an LC-MS/MS analysis, utilization of stable isotope-labeledd or suitable analog drugs as an internal standard proves helpful when a significant matrix effect is possible. In our case, OMD9 was found to be best for the present purpose. The column oven temperature was maintained at a constant temperature of about 45°C.

An injection volume of a 10µL sample is adjusted for better ionization and chromatography. Prior to load the sample for LC injection, the co-extracted proteins should be removed from the prepared solution. For this purpose, initially, we tested with different extraction procedures like PPT (Protein Precipitation), LLE (liquid extraction), and SPE (Solid Phase extraction). We found ion suppression effect in protein precipitation method for drug and internal standard. Further, we tried with SPE and LLE. Out of all, we observed LLE is suitable for the extraction of drugs and IS. We tried with several organic solvents (ethyl acetate, chloroform, n-hexane, dichloromethane, and methyl tertiary butyl ether) individually as well with combinations in LLE to extract analyte from the plasma sample. In our case methyl tertiary butyl ether: dichloromethane (75:25) combination served as suitable extraction solvent. Autosampler wash is optimized as 80% methanol. Several compounds were investigated to find a suitable IS, and finally, OMD9 found the most appropriate internal standard for the present purpose. There was no significant effect of IS on analyte recovery, sensitivity, or ion suppression. Righ recovery and selectivity were observed in the Liquid-Liquid extraction method. These optimized detection parameters, chromatographic conditions, and extraction procedure resulted in reduced analysis time with accurate and precise detection of omadacycline in human plasma. The parent and production mass spectrums of OM and OMD9 were shown in Figure 3.

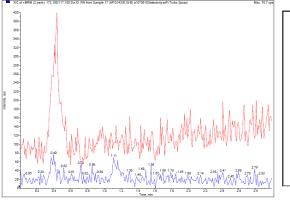
Method validation

Selectivity and Specificity, Limit of Quantification (LoQ)

No significant response was observed at retention times of OM and OMD9 in blank plasma as compared to LLoQ and blank with IS samples. The limit of quantification for this method was proven as the lowest concentration of the calibration curve, which was proven as 5.0 ng/mL. Representative chromatograms were shown in Figure 4.

Linearity

Linearity was plotted as a peak area ratio (OM peak area/ OMD9 peak area) on the y-axis against OM concentration (pg/mL) on the x-axis. Calibration curves were found to be consistently accurate and precise for OM over a linearity range of 5.00 to 10000.00 pg/mL.



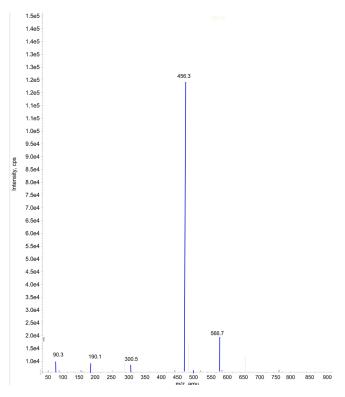


Figure 3: Mass fragmentation pattern of Omadacycline D9 (OMD9)

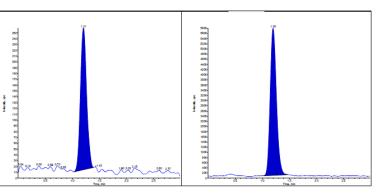


Figure 4: Representative chromatograms of Omadacycline in plasma a) Blank plasma chromatogram for interference-free OM and OMD9 b) Chromatogram of LLOQ sample (OM with OMD9).

The correlation coefficient was greater than 0.9980 for OM. The %CV was less than 15%, and mean %accuracy was ranged between 95.58-100.53%. The results were presented in Table 1.

Precision and Accuracy

was ranged Intra and inter batch % accuracy for OM was ranged between ted in Table 1. 95.83 to 101.44 and 89.10 to 101.59. % CV is 1.46 to 4.51 and **Table 1:** Calibration curve details

Spiked plasma Concentration	Concentration measured $(measured + S D)$	0/CV(r-5)	0/ 1
(pg/mL)	(pg/ml) (Mean \pm S.D)	% $CV(n = 5)$	% Accuracy
5	4.96 ± 0.09	1.80	99.20
10	8.81 ± 0.35	3.95	88.10
100	95.58 ± 3.33	3.48	95.58
600	599.88 ± 1.97	0.33	99.98
1200	1184.00 ± 16.70	1.41	98.67
2400	2408.00 ± 63.00	2.62	100.33
4800	4676.00 ± 152.72	3.27	97.42
7200	6904.00 ± 254.76	3.69	95.89
9600	9032.00 ± 210.85	2.33	94.08
12000	11893.40 ± 139.27	1.17	99.11

	Table 2: Precision and accuracy (Analysis with spiked samples at three different concentrations)							
Spiked Plasma	Within-run (Intra-day) Concentration measured			Between-run (Inter-Day) Concentration measured				
Concentration								
(pg/ml)	$(n = 6; pg/mL; mean \pm S.D)$	%CV	% Accuracy	$(n = 6; pg/mL; mean \pm S.D)$	%CV	%Accuracy		
15.00	14.92 ± 0.23	1.54	99.44	14.58 ± 0.26	1.77	97.21		
4500.00	4497.45 ± 65.87	1.46	99.94	4529.36 ± 73.48	1.62	100.65		
9000.00	9129.42 ± 411.56	4.51	101.44	9143.43 ± 161.07	1.76	101.59		

Table 3: Stability studies of omadacycline in plasma

	Room temperature Stability		Processed sample Stability		Long term stability		Freeze and thaw stability	
	24h		65h		64 days		Cycle (48-hour)	
Spiked Plasma concentration (pg/mL)	Concentration measured (n = 6; pg/mL; mean $\pm S.D)$	% CV (n = 6)	Concentration measured (n = 6; pg/mL; mean $\pm S.D)$	% <i>CV</i> (<i>n</i> = 6)	Concentration measured (n = 6; pg/mL; mean $\pm S.D)$	% <i>CV</i> (<i>n</i> = 6)	Concentration measured (n = 6; pg/mL; mean $\pm S.D)$	% <i>CV</i> (<i>n</i> = 6)
15.00	14.99 ± 0.77	4.12	14.79 ± 0.30	2.01	15.45 ± 0.42	2.69	16.20 ± 2.92	5.8
9000.00	9571.86 ± 394.82	5.12	8552.23 ± 266.65	3.12	8579.36 ± 249.51	2.91	9486.43 ± 520.63	5.49

1.62-7.09. Results are presented in Table 2.

Recovery

The mean % recovery for LQC, MQC, HQC samples of OM were 94.12%, 97.76%, and 96.06%, respectively. The overall mean % recovery and % CV of OM across QC levels is 94.12% and 5.12%. For the OMD9 (internal standard), the mean % recovery and % CV is 91.68% and 7.09%, respectively.

Matrix Effect

No significant matrix effect found in different sources of rat plasma tested for OM, OMD6. The % CV was found to be 3.71.

Stability (freeze-thaw, autosampler, benchtop, long term)

Quantification of the OM in plasma subjected to three freezethaw cycles (-30°C to room temperature), autosampler (processed), room temperature (Benchtop), long-term stability details was shown in Table 3.

CONCLUSION

The method described in this manuscript has been developed and validated over the concentration range of 5.00 –12000.00 pg/ml in human plasma. The intra and inter-batch precision (% CV) was less than 15.0%, and % accuracy ranged from 95.83%–101.59%. The overall % recovery for OM, OMD9, was greater than 90%. The selectivity, sensitivity, precision, and accuracy obtained with this method make it suitable for the present study. In conclusion, the method used in the present study is easy and fast to perform; it is also characterized by adequate accuracy, precision, selectivity, and stability. The simplicity of the method, and using rapid protein precipitation extraction with less run time of 3.0 min per sample, make it an attractive procedure in high-throughput bioanalysis of Omadacycline.

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