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During related substance analysis of montelukast bulk drug, a potential unknown impurity was detected in routine reverse phase impurity profiles by high performance liquid chromatography (HPLC). This impurity was identified by LC-MS and characterized by (¹H NMR, ¹³C NMR, gDQCOSY, gHSQC, LC/MS/MS, elemental analysis and FTIR) after isolation from montelukast drug substance exposed to sunlight. Based on sperctral data, the impurity was unambiguously named as (E)-2-(3-(3-(2-(7-chloroquinolin-2-yl) vinyl)phenyl)-3-((2-methylenebutyl)thio) propyl)phenyl)propan-2-ol. To the best of our knowledge, this impurity has not been reported elsewhere. Structural elucidation of the impurity by spectral data is discussed in detail.

1. Introduction

Montelukast is a leukotriene receptor antagonist $(LTRA)^1$ used for the maintenance treatment of asthma and to relieve symptoms of seasonal allergies. Montelukast is a CysLT1 antagonist;² it blocks the action of leukotriene D4 (and secondary ligands LTC4 and LTE4) on the cysteinyl leukotriene receptor CysLT1 in the lungs and bronchial tubes by binding to it. This reduces the bronchoconstriction otherwise caused by the leukotriene and results in less inflammation. Chemically montelukast sodium is (sodium (R,E)-2-(1-(((1-(3-(2-(7chloroguinolin-2-yl)vinyl)phenyl)-3-(2-(2-hydroxypropan-2-

yl)phenyl)propyl)thio)methyl)cyclopropyl)acetate.³ The empirical formula of montelukast is $C_{35}H_{35}CINNaO_3S$ and molecular weight is 607.19. It belongs to quinoline series developed by Merck & Co. The molecular structure of montelukast is shown in Fig.1



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Fig. 1 Structure of Montelukast Sodium

During the related substance analysis of montelukast base, one non-polar impurity at RRT~1.53 was observed in the range of 0.10-0.30% level along with the main product peak in the HPLC analysis. As per International conference on Harmonization (ICH) guideline (ICH Q3A, R2) for a new drug substance having maximum daily dose ≤ 2 g/day, the reporting and identification thresholds for a unknown related compound (impurity) are 0.05% and 0.10%, respectively.⁴ In order to meet the stringent regulatory requirements, a comprehensive study was undertaken to identify, synthesize and characterize potential unknown impurity of montelukast. The present manuscript deals with the identification, isolation and characterization of potential unknown impurity of montelukast by preparative HPLC followed by structure elucidation by LC/MS/MS, 1H, 13C and 2D NMR spectroscopy. This impurity was observed during the analysis of montelukast base [4] in process development⁵ of montelukast sodium (Fig. 2).

Montelukast sodium is a light sensitive drug substance subjected to photolytic degradation. Chromatographic methods were reported using RP-HPLC⁷ and UPLC methods for quantitative determination of montelukast and related substances. In some references Fluorescence⁸ detector and mass spectrometry¹¹ has used for quantitation of montelukast in urine and plasma. Impurity profiling and metabolic study of montelukast was reported using mass spectrometric techniques.¹² Montelukast Sodium is a US pharmacopeia listed drug substance where six impurities are reported.¹³ The impurity identified in present work is different from reported impurity.

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Fig. 2 Synthetic scheme for montelukast Sodium

2. Experimental

2.1. Materials and reagents

The investigated samples of montelukast and crude samples were in house synthesized [Dr. Reddy's Laboratories]. Analytical reagent acetonitrile and methanol were obtained from SD Fine Chemicals Limited, Mumbai, India. LC-MS grade acetonitrile and trifluroacetic acid used for LC-MS analysis was obtained from Biosolve BV, Valkenswaard, Netherland. Deuterated Chloroform-d and dimethylsulfoxide (DMSO-d6) were purchased from Aldrich Chemicals Co., USA. IR spectroscopy grade potassium bromide was procured from Merck (India) limited. Water used for the preparation of mobile phase was purified using Millipore Milli-Q plus (Milford, MA. USA).

2.2 High-performance liquid chromatography

A Waters Alliance 2690 separation module equipped with 2998-photodiode-array (PDA) detector and Empower pro data handling system [Waters Corporation, Miliford, MA, USA] was used. The analysis was carried out on a stainless steel column 150 mm long, 4.6 mm internal diameter filled with phenyl groups chemically bonded to porous silica partials of 3.5 μ m diameter [Zorbax SB Phenyl column (make: Agilent technologies)] maintained at 30°C. Mobile phase A was aqueous solution of 0.015% trifluroacetic acid, prepared by dissolving 1.5 ml of trifluroacetic acid in 1000 ml water. Mobile phase B was 0.015% trifluroacetic acid in mixture of acetonitrile and water (95:5). Diluent was prepared by mixing

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900 ml methanol with 100 ml water. The flow rate was kept as 1.5 ml min-1, injection volume was 20 μ l, chromatographic data acquisition time was 35 min and UV detection was carried out at 230 nm. The pump was in gradient mode and time program was as follows: Time (min)/%B (v/v) 0.01/40, 3/40, 15/51, 20/60, 25/70, 30/70, 32/40, 35/40.

2.3 Preparative Liquid chromatography

Agilent 1200 series preparative liquid chromatograph equipped with G1315D PDA detector, Rheodyne 2260A series injector with 1.8 ml loop and G3146B Fraction collector [Agilent technologies, Santa Clara, CA, 95051 USA] was used. Phenomenex Luna C_{18} (2) 250 mm long, 21.2 mm i.d., Preparative HPLC column packed with 10 μ m particle size was employed for isolation of impurity. Mobile phase consists of 0.01% trifluroacetic acid solution in mixture of acetonitrile and water (80:20). Flow rate was set as 15 ml min⁻¹ and UV detection was carried out at 230 nm.

2.4 LC/MS/MS

LC/MS/MS analysis was carried out using AB SCIEX Triple TOF 4600 (Time of Flight) mass spectrometer (AB SCIEX, USA) coupled with Agilent 1290 series RRLC system. Analyst [®] TF 1.6 software was used for data acquisition and data processing. Ion spray voltage for DuoSpray[™] ion source in ESI mode was maintained at 4500V and temperature was set at 450°C. The auxiliary gas and curtain gas used was high purity nitrogen. Zero air was used as nebulizer gas. The resolution of AB Sciex 4600 Time of Flight mass spectrometer for ALILTLVS, a synthetic peptide [m/z 829.5398] was more than 25000. The High resolution mass spectra [HRMS] were acquired from m/z 50-1000 in accumulation time of 1000 ms. All chromatographic conditions used for HRMS analysis were same as mentioned under High-performance liquid chromatography.

2.5. NMR spectroscopy

¹H NMR, ¹³C NMR and 2D NMR experiments were performed on Varian Mercury plus 400 MHz FT-NMR spectrometer [Agilent technologies, Palo Alto, California, USA] using DMSOd₆ as solvent and tetramethylsilane (TMS) as internal standard. **2.6. FT-IR spectroscopy**

The FT- IR spectra were recorded as KBr pellet on a Perkin-Elmer instrument model-spectrum one.

3. Results and Discussion

3.1. Detection and identification of impurity

Montelukast sample was accurately weighed and diluted to the required concentration (0.5 mg ml⁻¹) and injected into HPLC using chromatographic conditions mentioned above. One unknown peak was identified in the chromatogram at a relative retention time of about 1.53 with respect to the montelukast peak along with pharmacopoeial impurities. The same sample was subjected to LC-MS analysis to identify mass of the impurity. A typical representative HPLC chromatogram of montelukast is shown in Fig. 3. Unknown impurity at RRT-1.53 elutes at about 22.817.



Fig. 3 HPLC chromatogram of montelukast Laboratory Batch

3.2. Synthesis and isolation of impurity by preparative HPLC

Unknown impurity in montelukast base was enriched by exposing about 1.0 g of montelukast base to sun light for about 6 h at ambient temperature in dry conditions. The content of unknown impurity in photolytic degraded sample of montelukast base was found 6.0% when analysed as per related substance chromatographic conditions.



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About 1.0 g of photolytic degraded sample of montelukast base was taken in 50 ml volumetric flask and diluted up to the mark with diluent. This solution was loaded into the preparative column using the conditions mentioned in the preparative liquid chromatography section. Fraction of impurity ≥95% were pooled together and concentrated on a rotavapour to remove organic solvent. The aqueous solution was lyophilized using freeze dryer (Virtis Advantage 2XL). The impurity obtained was an yellow powder in description and chromatographic purity was 90.11% determined by the HPLC method.

3.3 Structure elucidation of Montelukast

ESI mass spectrum of the montelukast in positive ion mode exhibited molecule ion peak at m/z 586.2179 [(MH)⁺] indicating the mass of this compound to be 585.2. The high resolution mass spectrometry for m/z 586.2179 proposed elemental composition $C_{35}H_{36}CINO_3S$ complies with the structure of montelukast. LC/MS/MS spectrum for mass m/z 586.2179 displayed daughter ion peaks at m/z 568.2, 524.2, 440.2, 422.1, 292.1 and 278.1. Probable fragmentation pattern is displayed in Fig. 5.



Fig. 5: Probable fragmentation pattern of Montelukast

In ¹H NMR spectrum, multiplet signal (δ 0.39) corresponding to cyclopropyl ring and signal at (δ 11.2) corresponding to acid OH were observed. In FT-IR spectrum, a broad band at 3428.98 cm⁻¹ corresponding to acid OH, a band at 1633 cm⁻¹ corresponding to acid C=O bond and a band at 1131.04 cm^{-1} corresponding to aromatic C-Cl were observed. Based on the above spectral data structure of montelukast was confirmed as (R,E)-2-(1-((1-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-(2-(2hydroxypropan-2-yl)phenyl)propylthio)methyl)cyclopropyl) acetic acid (Fig. 6). The spectral data of montelukast are given in Table 1.



Fig. 6: Structure of Montelukast

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3.4 Structure elucidation of Impurity

ESI mass spectrum of the impurity in positive ion mode exhibited molecule ion peak at m/z 542.2280 [(MH)⁺], which is 44 amu less than that of the montelukast protonated molecular ion. The probable elemental composition proposed

by high resolution mass spectrometry for mass m/z 542.2280 is $C_{34}H_{36}CINOS$. LC/MS/MS spectrum for mass m/z 542.22280 displayed daughter ions peaks at m/z 524.2, 440.2, 422.1, 292.1 and 278.1 which are same as that of montelukast. Probable fragmentation pattern displayed in Fig. 7.



Fig. 7: Probable fragmentation pattern of the impurity

In ¹H NMR and ¹³C NMR spectra of the impurity, chemical shift (δ) values were similar to montelukast except at cyclopropylacetic acid moiety. Moreover, when close inspection of structure of montelukast and impurity (Figs. 6 and 8) with ¹H NMR and ¹³C NMR data (see Table 1) multiplet signal at (δ 0.39) in ¹H NMR corresponds to cyclopropyl and signal at (δ 11.2) corresponding to acidic OH of montelukast disappeared in ¹H NMR spectrum of the impurity. This observation suggested the cleavage of cyclopropane ring and loss of terminal carboxylic acid. Triplet at (δ 0.93) and quartet at (δ 2.07) in ¹H NMR spectrum of impurity indicate cyclopropyl ring opening. Singlet signal at (δ 4.82) in ¹H NMR spectrum of impurity corresponds to alkenes further supported by the presence of additional signals at δ 111.561 and δ 146.3 in ¹³C NMR spectrum. In FT-IR spectrum C–O band at 1129.40 cm⁻¹ was absent and a strong alkenes broader band was observed at 1691.52 cm⁻¹. Based on the above spectral

data the molecular formula of impurity is confirmed as $C_{35}H_{34}CINO_2S$ and its chemical name is proposed as (E)-2-(2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-((2-methylenebutyl)thio)propyl)phenyl)propan-2-ol (Fig. 8).

Fig. 8 Structure of the unknown impurity

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Table 1 Comparative 1H, 13C NMR assignments for montelukast and Impurity and gDQCOSY, gHSQC data interpretation

Position	Montelukast		Impurity			
	1H δ (ppm), multiplicity, $J_{1\mathchar`2}$	13C δ (ppm)	1H δ (ppm), multiplicity, $J_{1\text{-}2}$	gDQCOSY	13C δ (ppm)	gHSQC
1		125.6			125.8	
2	7.59 (dd, 1H, 8.4 & 2.0)	126.6	7.59 (dd, 1H, 8.4 & 2.0)	3H, 8.02	126.5	2H, 7.40
3	7.98 (d, 1H, 8.4)	129.7	8.02(d, 1H, 8.4)	2H, 7.59	130.1	3H, 8.02
4	8.04(d, 1H, 2.0)	127.2	8.05 (d, 1H, 2.0)		127.3	4H, 8.05
5		148.0			146.9	
6		134.3			135.3	
7	8.38 (d, 1H, 8.40)	136.5	8.49(d, 1H, 8.40)	8H, 8.0.	138.2	7H, 8.49
8	7.93(d, 1H, 8.40)	120.3	8.01(d, 1H, 8.40)	7H, 8.49	120.4	8H, 8.01
9		156.8			156.4	
10	7.89 (d, 1H, 18.0)	135.0	7.94(d, 1H, 16.4)	10H, 7.51	136.0	10H, 7.94
11	7.50 (d, 1H, 16.4)	128.4	7.51(d, 1H 16.4)	11H, 7.94	129.1	11H, 7.51
12		136.1			137.0	
13	7.64 (d, 1H, 7.20)	125.9	7.62(d, 1H, 7.20)	14H, 7.43	127.0	13H, 7.62
14	7.44 (m, 1H)	125.3	7.43 (m, 1H)	13H, 7.61 15H,	125.5	14H, 7.43
15	7.40 (m, 1H)	128.4	7.34 (m, 1H)	14H, 7.43	127.4	15H, 7.34
16		143.7			143.6	
17	7.76 (s, 1H)	126.8	7.71 (s, 1H)		126.9	17H, 7.71
18	4.06 (t, 1H, 6.8)	49.4	3.85(t, 1H 6.8)	19H, 2.20	48.8	18H, 3.85
19	2.20 (m, 2H)	38.5	2.20 (m, 2H)	18H, 3.84, 20,2H	29.2	19H, 2.20
20	3.09 & 2.81 (m, Ha & Hb)	31.9	3.05, 2.74 (m, Ha/Hb)	19H, 2.20	32.1	20H,
21		139.8			139.9	
22	7.15 (m, 1H)	131.0	7.10 (m, 1H)	23H, 7.10	131.2	22H, 7.10
23	7.14 (m, 1H)	126.4	7.10 (m, 1H)	24H, 7.09, 22H,	126.3	23H, 7.10
24	7.09 (m, 1H)	125.2	7.04 (m, 1H)	25H, 7.35, 23H,	125.4	24H, 7.04
25	7.42 (m, 1H)	128.9	7.35 (m, 1H)	24H, 7.09	129.2	25H, 7.35
26		146.7			146.7	
27		71.6			71.8	
28	1.47 (s, 3H)	31.7	1.42 (s, 3H)		31.7	28H, 1.42
29	1.47 (s, 3H)	31.8	1.42 (s, 3H)		31.8	29H, 1.42
30	2.36 (s, 2H)	40.1	2.04 (s, 2H)		40.4	30H,2.04
31		16.7			146.5	
32	2.57 & 2.53 (d, Ha & Hb, 12.8)	38.9	4.82 (s, 2H)		111.5	32H, 4.82
33	0.37 (m, 2H)	11.9	2.07 (q, 2H, 6.8)	34H, 0.93	28.6	33H, 2.07
34	0.45 (m, 2H)	12.1	0.93 (t, 3H, 7.2)	33H, 2.07	12.1	34H,0.93
35		173.1				
36	5.24 (s, OH)		5.70 (s, OH)			
37	12.09 (s. OH)					

s, singlet; d, doublet; t, triplet, q, quartet; m, multiplet; dd, doublet of doublet; J, coupling constant, Refer the structural formulae given in Figs. 6 and 8 for numbering

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Table 2 FT-IR spectral data for montelukast and Impurity

IR (KBr) absorption bands (Vmax/cm-1)								
Monteluka	ast	Impurity						
3428(b)	OH Stretching	3431(b)	OH Stretching					
2971(s)	aromatic C-H	2969(s)	aromatic C-H					
2926(s)	aliphatic C-H	2928(s)	aliphatic C-H					
1634(s)	C=O stretching							
1610(s)	C=C stretching	1691(b)	C=C stretching					
1596(b)	C=N stretching	1594(s)	C=N stretching					
1497(s)	aliphatic C-H bending	1497(s)	aliphatic C-H bending					
1132(s)	C-O stretching	1129(s)	C-O stretching					
1053(s)	C-Cl stretching	1053(s)	C-Cl stretching					
837(s)	aromatic C-H bending	824(s)	aromatic C-H bending					
697(s)	C-S stretching	719(s)	C-S stretching					

4. Conclusion

A new unknown impurity observed in montelukast drug substance resulting from photolytic degradation of montelukast base was identified by HPLC and LC-MS. The impurity was isolated, characterized by various spectroscopic techniques like NMR (¹H, ¹³C, gDQCOSY and gHSQC), LC/MS/MS and FT-IR and the probable structure of impurity is proposed.

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