

## Rapid And Trace Level Determination Of Potential Genotoxic Impurity 2-Aminopyridine In Piroxicam Api Using Lc-MS/MS Technique

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### ABSTRACT

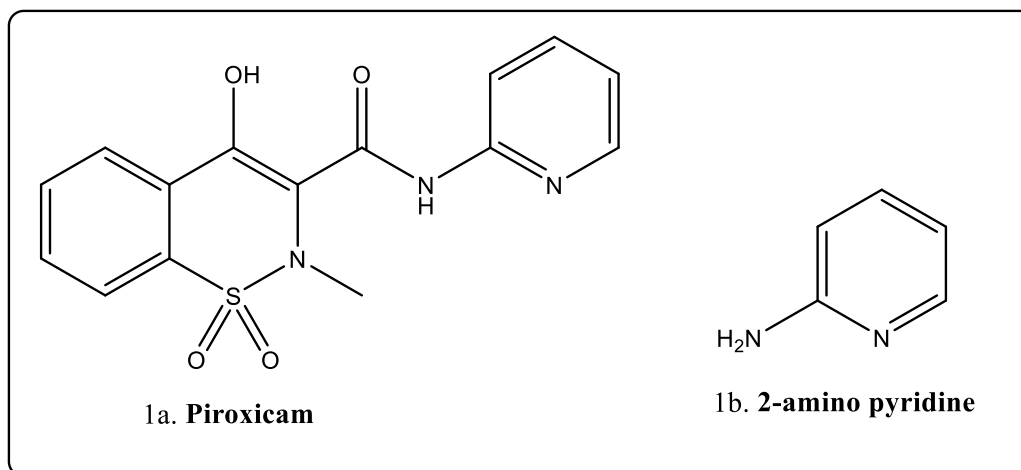
A highly sensitive method for the determination of genotoxic impurity 2-aminopyridine in Piroxicam employing hyphenated techniques have been presented. 2-aminopyridine was determined by LC-MS/MS method in selected ion monitoring mode (SIM) using LiChrospher RP-18 (100×4.6mm) 5.0 µm column. Gradient technique was applied for the elution of analytes using acetonitrile (mobile phase A) and 0.01M ammonium acetate buffer (mobile phase B) in different ratios. The gradient program (T/%B) was set as 0/5, 2.50/15, 5.00/30, 10.00/50, 15.00/95, 20.00/95. Developed method was validated as per International Conference on Harmonization guidelines. The LOD and LOQ values found for 2-aminopyridine were 5.25 ppm and 75 ppm. Method has accuracy within 97 -103.4% for the analyte. This method is a good quality control tool for quantitation of 2-aminopyridine impurity at very low levels in Piroxicam.

**Keywords:** Piroxicam, 2-aminopyridine, Genotoxic impurities, Selected Ion Monitoring (SIM), ICH guidelines.

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### INTRODUCTION

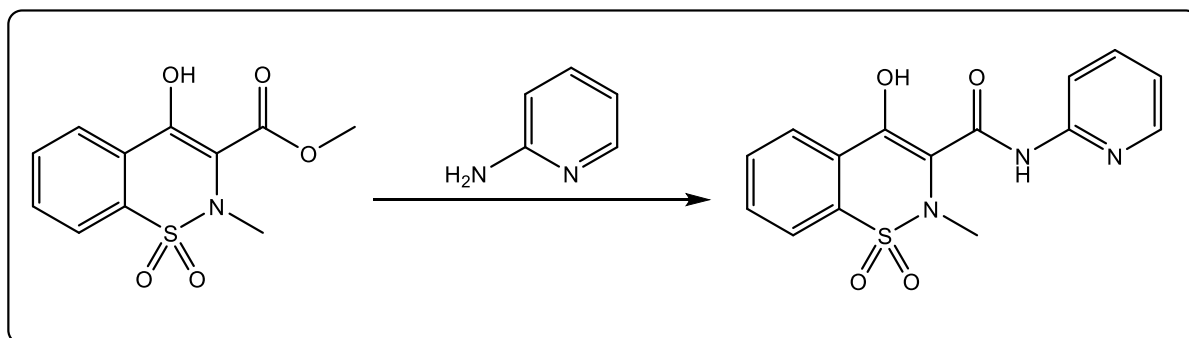
Piroxicam (Figure 1a) is a non-steroidal anti-inflammatory drug (NSAID) widely used against pain and inflammation. Piroxicam (4-hydroxy-2-methyl-3-(pyrid-2-yl-carbamoyl)-2H-1,2-benzothiazine 1,1-dioxide) belongs to the oxamic class of NSAIDs [1–5].



**Figure 1.** a) Piroxicam b) 2-aminopyridine

Impurities, especially genotoxic impurities, have been at the centre of increasing regulatory and industry attention in the past decade. Active pharmaceutical Ingredients prone to contain different impurities that may arise from starting materials, reagents employed for the synthesis and by products in the synthetic process [6]. During the chemical synthesis reactants are carefully selected owing to their appropriate reactivity in order to achieve the end product with sufficient yield. However, this same reactivity of the reactants could result in genotoxicity if any unreacted material left with the final product as an impurity, which makes these impurities to consider critically to eliminate them from the final drug product [7]. Often different synthetic process related modifications are employed to remove these impurities, yet it became impossible to completely eliminate the impurities from the final drug substances. According to the guidance of drug regulatory authorities it is crucial to regulate the level of genotoxic impurities in the drug substances based on the daily dose [8].

Hetero aromatic amines especially aminopyridines are generally employed in the synthetic process as building blocks and are categorized as potentially genotoxic impurities (PGIs) in pharmaceuticals [9]. Inherently aromatic amines genotoxicity is not owing to their reactivity but due to the generation of nitrenium ion ( $Ar-N^+H$ ) by the oxidative metabolic reactions, which is considered to be the active genotoxin that binds to DNA [10]. PGIs are known to induce genetic mutations or chromosomal aberrations and are reported as known carcinogens in rats and mice. Heteroaryl amines possess the regulatory limit of intake at  $1.5\mu\text{g}/\text{day}$  [11]. A few synthetic processes have been reported for the piroxicam which utilize the genotoxic substances as starting materials as well as intermediates. The condensation of 2-aminopyridine which is genotoxic in nature, with methyl 4-hydroxy-2-methyl-2H-benzo[e][1,2]thiazine-3-carboxylate 1,1-dioxide, finally produces the piroxicam [12,13].



**Figure 2:** Final step in the synthesis of Piroxicam with condensation of 2-aminopyridine

The potential presence of these genotoxins has attracted the attention of regulatory authorities. European Medicines Agency's (EMA) Committee for Medicinal products for Human use (CHMP) has published guidelines regarding limits of genotoxic impurities<sup>13</sup>. In 2008, regarding the genotoxic and carcinogenic impurities in drug substances, a draft of guidelines also outlined by US FDA. It consists of the different various routes to mitigate the potential lifetime cancer risk in patients with exposure to genotoxic and carcinogenic impurities. Based on the current regulatory guidance for genotoxic impurities, analytical methods should be developed to meet the required limit of 1.5µg/day daily intake of individual impurity [14].

In accordance with the amplifying concerns of regulatory authorities regarding the control of genotoxic impurities in pharmaceuticals, an attempt was made to develop the sensitive LC-MS/MS method to determine the 2-aminopyridine in very low levels in Piroxicam.

## EXPERIMENTAL

### Materials

2-aminopyridine was procured from Sigma Aldrich, Bangalore, India. Analytical grade ammonium acetate and acetonitrile were purchased from Merck, India. Piroxicam sample was procured from Shreeji Pharma, India.

### Chromatographic conditions

The chromatographic system used was Shimadzu LCMS 8040. The analytical column was LiChrospher RP-18 (100×4.6mm) 5.0 µm. Isocratic elution mode was applied for the operation and the mobile phase composed 50% acetonitrile and 0.01M ammonium acetate buffer (pH-4.0). The flow rate of the mobile phase was kept at 1.0mL/min. Column oven temperature and auto sampler temperature were set as 30°C and 25°C, respectively and injection volume was 10 µL. Instrument operation, data collection and processing were done by LCMS Lab Solutions.

### Mass spectrometer conditions

Following typical mass spectrometer conditions were applied: source temperature, 120 °C; desolvation temperature 300°C; sample cone, 30V; capillary voltage, 3.0KV; cone desolvation gas (N<sub>2</sub>) flow rate 1000 L/Hr, gas flow rate 50 L/Hr; Argon as CID gas for MS/MS experiments. The selective ion monitoring (SIM) was selected for quantification of analyte. Venting was done using valco valve (Valco Instruments Co. Inc., VICI AG International). Venting was given from 6 mins to 11 mins.

### **Validation study**

ICH guidelines were followed for the validation of the developed LC-MS/MS method for the determination of 2-aminopyridine in Piroxicam. By analysing the six concentrations of analyte from 0.3 ppm - 7.5 ppm, linearity of the method was established. Slope, intercept and regression coefficient were determined from the least square linear regression analysis. Six repetitive injections of standard solution were employed to establish the system precision of the mass spectrometric response. LOQ and LOD were determined via exhibiting precision, by running six replicate injections of analyte in lower concentrations. The LOQ and LOD were calculated on the basis of the lowest concentration of compound that gives %RSD < 10 (for LOQ) and %RSD < 15 (for LOD). The method precision was evaluated by spiking each analyte and determining the %RSD. Accuracy was determined by spiking the known amount of EMS with known amount of sample in six different volumetric flasks and it was calculated after making corrections for the amount pre-existed in the sample. Stability of analytes in sample solution was done by analysing spiked sample solution at different time intervals at room temperature.

### **Standard solution preparation**

Stock solution having concentration of 7.5 mg/mL of 2-aminopyridine was prepared by dissolving it in acetonitrile. From the stock solution, diluted stock solution of 0.075 mg/mL concentration was prepared by the dilution of 1 mL of the 7.5 mg/mL solution to 100 mL with acetonitrile. From this diluted stock solution, working standard solution of 37.5 ppm strength with respect to the sample concentration of 2 mg/mL of Piroxicam was prepared by the serial dilution in acetonitrile before injection into the chromatographic system. At all times the working standard solutions were prepared prior to the injection into chromatographic instrument.

### **Sample preparation**

Piroxicam sample solution of 10 mg/mL concentration was prepared before injection into system by dissolving about 10 mg of the drug substance with solvent in a HPLC vial.

## **RESULTS AND DISCUSSION**

### **Optimization of sample preparation**

In trace level analysis of GTI in a drug substance, sample preparation affects the analytical sensitivity, stability, recovery, and matrix effect. In order to achieve efficient extraction and analyte response different diluents such as methanol and acetonitrile were studied. Both the solvents produced satisfactory solubilization capacity for the analyte and drug substances. But acetonitrile was chosen finally as it provides better analyte response, proper peak shapes and good recovery levels.

### **Column selection and separation**

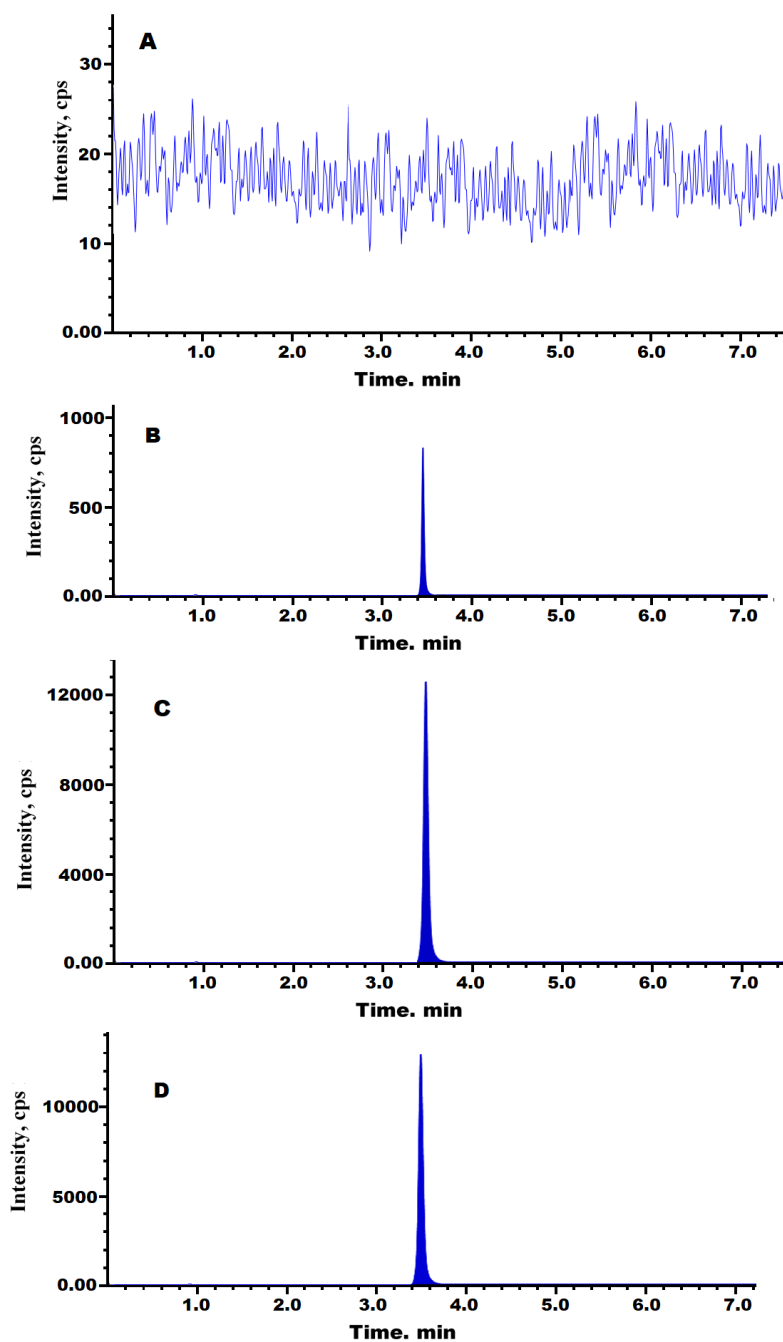
Selection of appropriate column has a huge impact on the resolution of analyte and drug substance peak. To achieve the proper resolution in trace level analysis of the GTI, it is very crucial to select the appropriate column as the concentration of drug substance was high leading to broad peak. Various columns like Phenomenex Luna C18, Kromasil C18 and LiChrospher 100 RP-18 of different dimensions were evaluated. Luna C18 and Kromasil C18 columns were found to be not suitable, since the observance of low resolution and improper analyte response. Satisfactory response for the

analyte 2-aminopyridine and good resolution between analyte and Piroxicam were achieved on the LiChrospher 100 RP-18 column of dimensions 100mm×4.6mm internal diameter, 5.0µm. Diverse composition of mobile phase using 0.1% formic acid 0.1% acetic acid, ammonium formate, and ammonium acetate with acetonitrile and methanol were studied. Decent response and separation were noticed with the combination of ammonium acetate buffer and acetonitrile in gradient elution modes. To avoid any shift in retention time the column was thermostated at 30°C and 1.0mL/min of mobile phase flow rate was maintained. The flow rate was reduced to 0.2 mL/min by utilizing a splitter prior to the electrospray ionization. Retention time of 2-aminopyridine was observed to be about 3.5 mins.

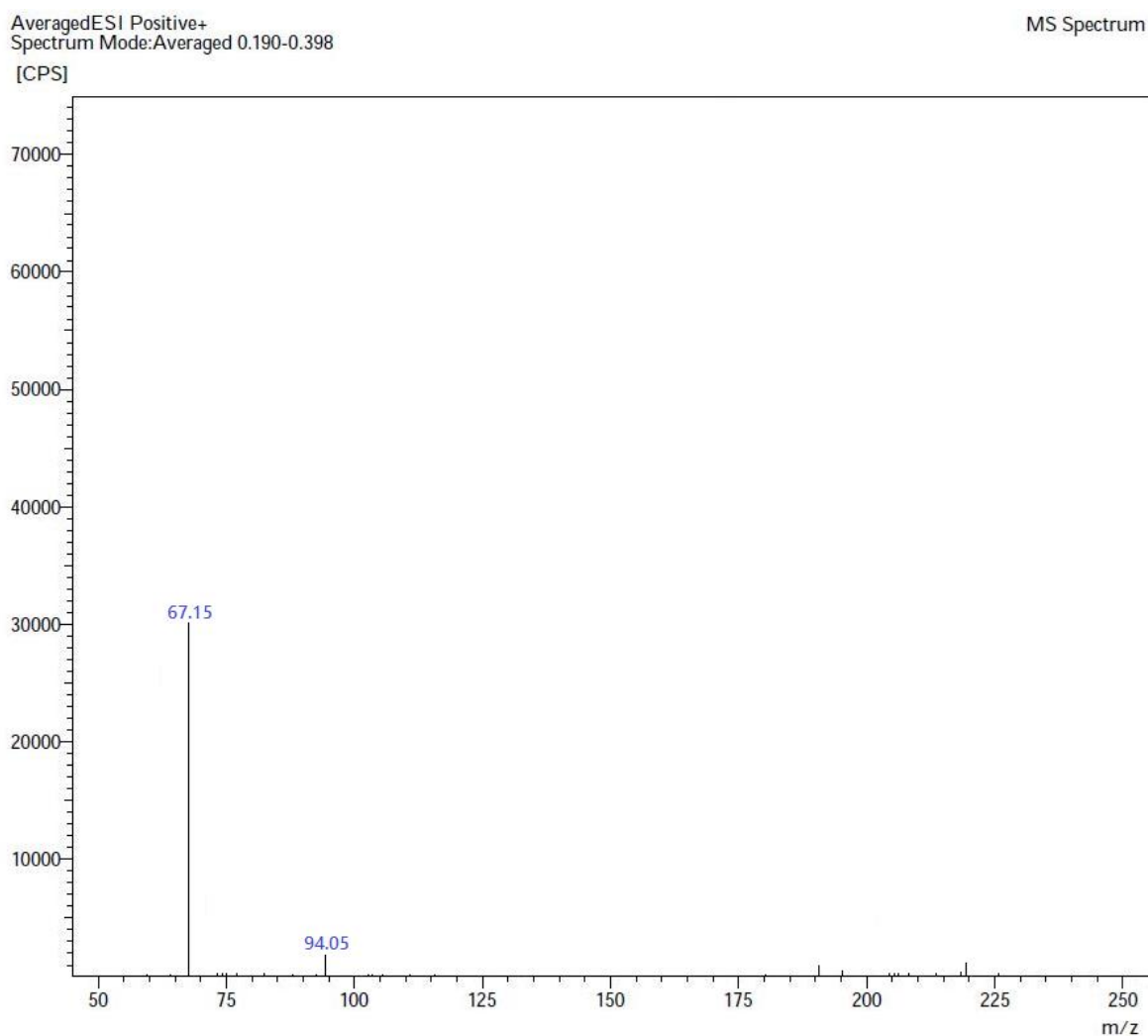
Piroxicam peak eluted at around 8 mins. Only the analyte, 2-aminopyridine peak was permitted enter the mass detector with the help of a switching valco valve, that executed the venting of drug substance peak. This technique enables the method development process to analyse the peak of interest and also avoids the matrix effect due to high concentration of drug substance.

#### **Optimization of mass spectrometric parameters**

In Chromatographic analysis, choice of detection method is pivotal fundamental for successful method development. Comparatively, LC-MS/MS method was chosen over HPLC – UV due to the greater sensitivity and specificity offered by the mass spectrometric detection for the trace analysis of 2-aminopyridine and the analysis was executed in multiple reaction monitoring mode (MRM) which further increased the specificity of the determination. 2-aminopyridine ion mass transactions corresponding to 94 > 67 were recorded for the quantification. The LC-MS/MS chromatograms are shown in Figure 2 & 3.



**Figure 2:** Chromatograms of 2-aminopyridine using SIM scan. (A) Chromatogram of blank, (B) Chromatogram of 2-aminopyridine in Piroxicam sample, (C) Chromatogram of standard containing 37.5ppm of 2-aminopyridine, (D) Chromatogram of Piroxicam sample spiked with 2-aminopyridine at 37.5ppm.



**Figure 3:** MRM Chromatogram of 2-aminopyridine

### Validation of Method

The newly developed LC-MS/MS method's validation was performed according to the ICH guidelines in relation to the analytical parameters such as [14] specificity, accuracy, linearity, limit of detection (LOD), limit of quantitation (LOQ), precision, and robustness in order to demonstrate the feasibility of the method.

### Specificity

Specificity of the developed LC-MS/MS method for the analyte response at specification level was indicated by the retention of the 2-aminopyridine at the time around 3.5 and the analyte response for 2-aminopyridine in MRM is about 67.15 on mass spectrum. The specificity of the developed LC-MS/MS methods was indicated by showing the m/z peak in peak as 67.15 for 2-aminopyridine.

### Linearity

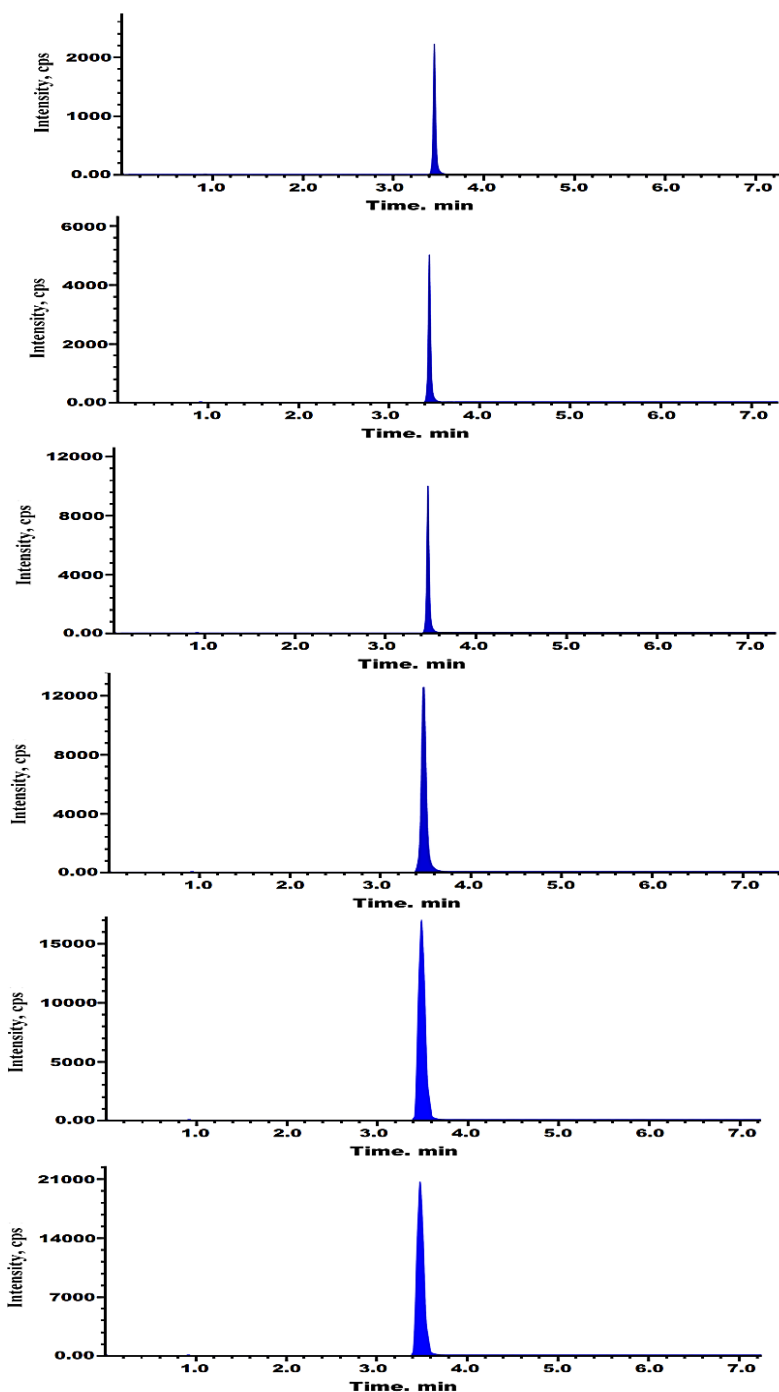
The linearity of method in terms of mass spectrometric response with respect to concentration of analyte was demonstrated by a six-point calibration graph between 5.25ppm and 75ppm corresponding to the concentration of 20 mg/mL of Piroxicam. Correlation coefficients for all

analytes were >0.998. Linearity results enumerated in Table 1 and Figure 4 & 5 depict the linearity graph and Chromatogram respectively.

**Table 1:** Linearity of 2-aminopyridine

S. No	2-aminopyridine	
	Concentration (ppm)	Area
1	5.25ppm	1492
2	15ppm	4227
3	18.75ppm	5281
4	37.5ppm	10589
5	56.25ppm	15399
6	75ppm	21083
Slope	139.22x	
Intercept	37.766	
Correlation Coefficient	0.9995	





**Figure 4:** Linearity Chromatograms

**Accuracy**

The accuracy was demonstrated by the percent recovery of 2-aminopyridine from the drug substance. Results displayed in Table 2 and chromatograms showing accuracy depicted in Figure 6. Satisfactory recoveries of 97.9-103.8% for 5.25, 37.5 and 56.25 ppm (six determinations, %RSDs 1.2 – 2.25) were obtained which are satisfactory at such low levels.

**Table 2:** Accuracy of method for 2-aminopyridine

	LOQ level			100% level			150% level		
<b>Amount Added (ng)</b>	10.5	10.5	10.5	75	75	75	112.5	112.5	112.5
<b>Amount found (ng)</b>	10.42	10.89	10.66	73.4	75.1	73.8	109.6	110.4	114.5
<b>% Recovery</b>	99.3	103.8	101.6	97.9	100.2	98.4	97.5	98.2	101.8
<b>AVG</b>	101.5666667			98.83333333			99.16666667		
<b>SD</b>	2.250185178			1.209683154			2.307234997		
<b>RSD</b>	2.215476053			1.223962719			2.326623527		

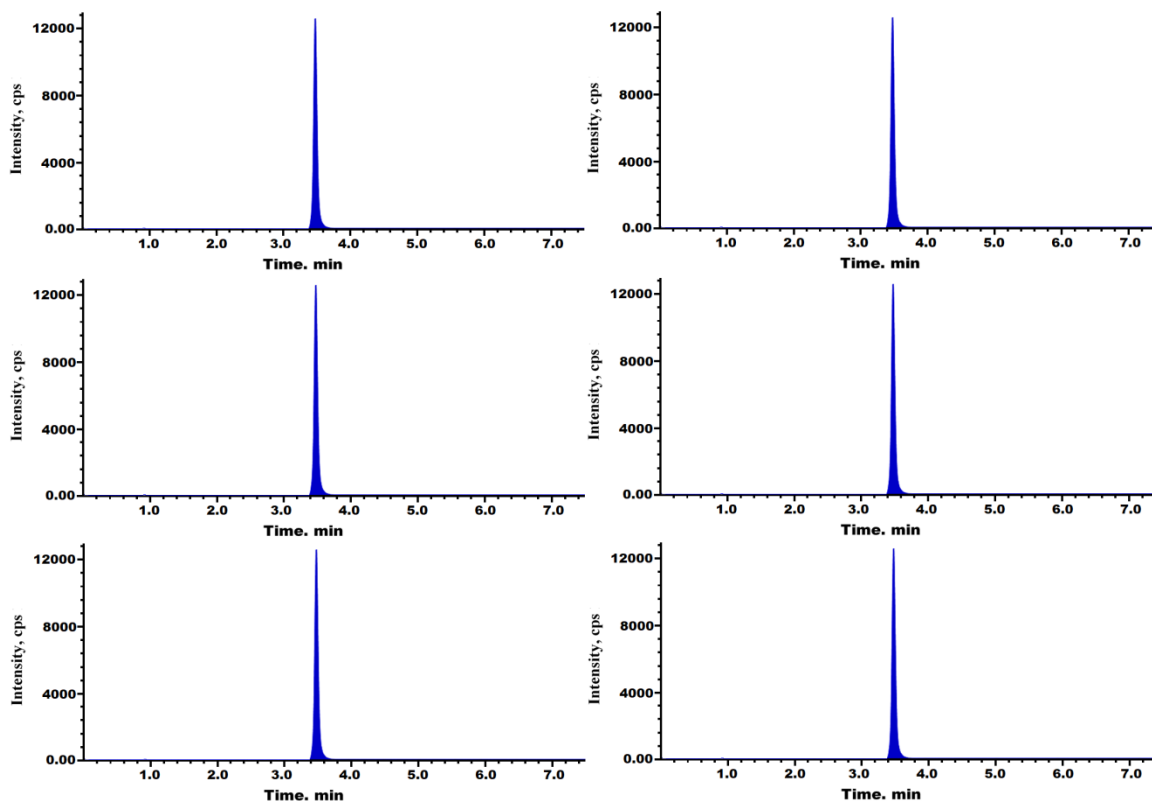


Figure 6: Accuracy at 100% level

**Limit of quantification (LOD) and detection (LOQ)**

The LOD and LOQ were calculated from S/N ratio data generated from six injections of 2-aminopyridine with respect to sample concentration of 10 mg/mL. Results disclosed in Table 3 and chromatograms displayed in Figure 7 & 8. The LOD and LOQ values observed for 2-aminopyridine were 0.003 µg/mL and 0.0105 µg/mL.

Table 3: LOD, LOQ Precision

Injection ID	2-aminopyridine	
	LOD (0.003 µg/mL) area	LOQ (0.0105 µg/mL) area

1	451	827
2	460	890
3	409	810
4	431	874
5	439	880
6	416	886
Mean	434.3333333	861.1666667
SD	18.01542549	30.96458551
% RSD	4.147833958	3.595655371

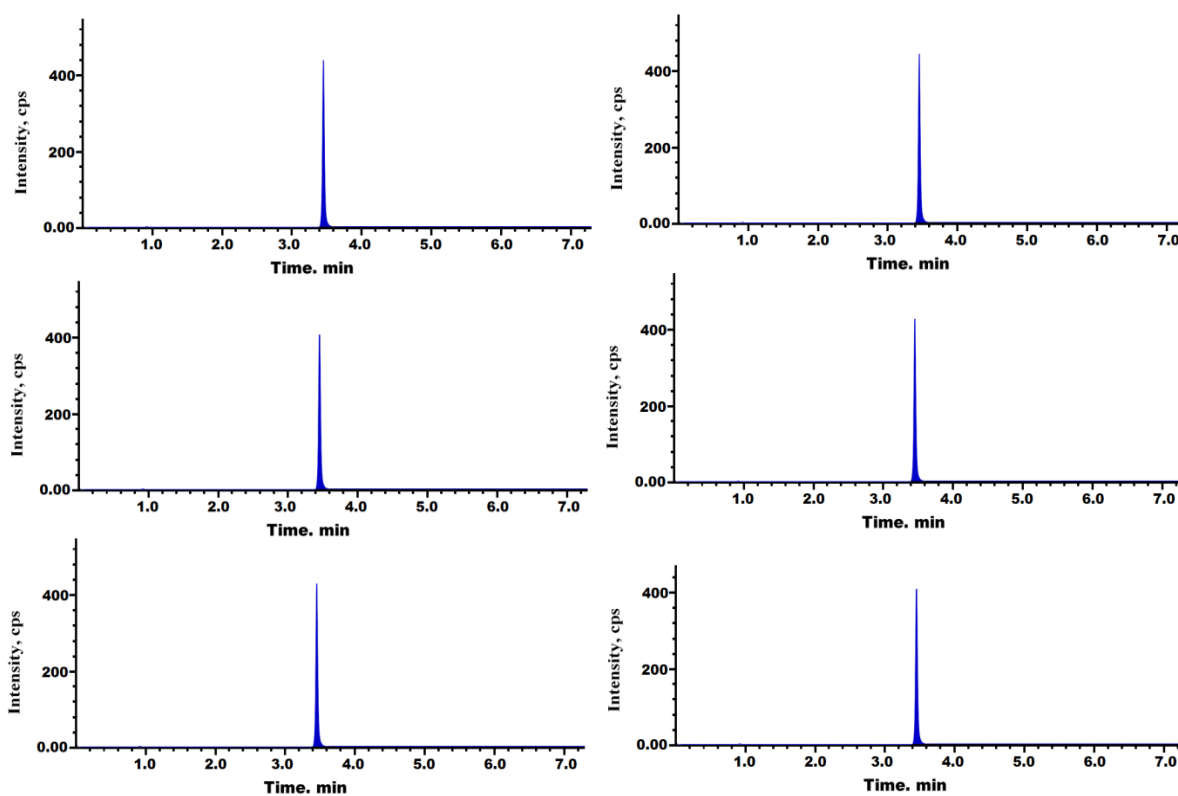
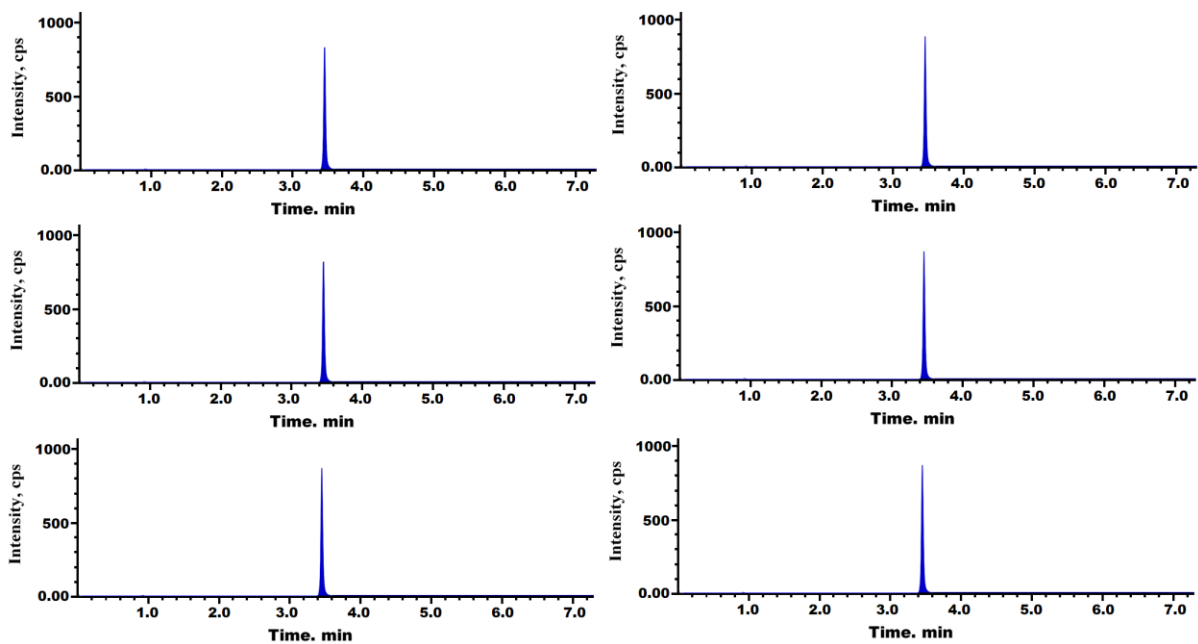


Figure 7: LOD Precision



**Figure 8:** LOQ Precision

**Precision**

The precision of the methods was checked by injecting 0.075 µg/mL solution for six times. The values of RSDs for areas of each 2-aminopyridine were calculated. The % relative standard deviation (%RSD) was found to be below 4% for both the analytes in system precision and the data were enumerated in Table 4.

**Table 4.** System precision

Injection ID	2-aminopyridine (0.075 µg/mL)
1	12849
2	12598
3	12745
4	11986
5	11890
6	12082
Mean	12358.33
SD	383.413
% RSD	3.102466
95 % Confidence interval	±102.5

### Robustness

The robustness of the method was ensured by getting the resolution between analyte and drug substance to be greater than 2.0, when mobile phase flow rate ( $\pm 0.2$  mL/min), organic solvent ratio in both mobile phases A and B ( $\pm 2\%$ ) and column temperature ( $\pm 5^\circ\text{C}$ ) were deliberately varied.

### CONCLUSION

In conclusion the developed method is a direct tandem mass spectrometric method for screening and quantification of 2,6 dichloroaniline in the Piroxicam drug substances. Selected ion monitoring (SIM) mode relatively provided better selectivity and sensitivity for the screening and quantitation of the analyte. The described analytical method is cost-effective, direct, accurate and convenient quality control tool for determination of 2-aminopyridine in Piroxicam. The method is advantageous owing to its improved sensitivity and simpler sample preparation technique to those formerly reported methods. Selected ion monitoring (SIM) mode consents radically discounts or eliminates the matrix effects that restricts the accuracy and LOD and LOQ levels. This method can be further studied for its application to other drug substances.

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