

# Detection of infectious agents in the airways by ion mobility spectrometry of exhaled breath

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**Abstract** Diseases of the lung, e. g. chronic obstructive pulmonary disease (COPD), interstitial lung diseases, bronchiectasis or cystic fibrosis, often lead to recurrent severe respiratory infections that cause exacerbations of the underlying disease. These acute or chronic inflammatory processes can result in a progressive destruction of the lung and in an ongoing decline in lung function. Therefore longer inpatient stays for intravenous antibiotic treatment are necessary and the quality of life in these patients is severely limited. A rapid detection of infectious agents in human lungs is often crucial, because the choice of the appropriate therapeutic regime depends at first on the identification of the infecting species. Standard methods for detection and identification are either time consuming, of low sensitivity or expensive. It is known that bacteria, and also mitosporic fungi, produce volatile organic compounds (VOCs)

that can be detected in exhaled breath by ion mobility spectrometry (IMS), were a distinct detection of a specific VOC is related to a “peak”. We investigated, whether the detection and characterisation of VOCs by Multi-capillary column coupled to IMS in exhaled breath of patients whose airways are either infected or colonized by *Pseudomonas aeruginosa* compared to healthy non-smoker controls is capable of identifying those infectious agents. To realize a non invasive identification of pathogens, the exhaled breath of 53 persons (24 patients suffering chronic or infectious on *Pseudomonas* and 29 healthy controls) was investigated using an ion mobility spectrometer type BioScout. In total 224 different signals were found. Actually, 21 different signals are able to differentiate the two groups, Control and *Pseudomonas*, with rank sum values less than 0.2. For all 224 signals Box-and-Wisker plots were realized. The peaks with the lowest rank sum values F (0,107) and PS0 (0,112) show rather good separation of both groups. Our preliminary results demonstrate that distinct patterns of a small number of IMS-peaks are sufficient for the identification of these infectious agents. Therefore MCC-IMS seems to be a promising method for the non-invasive identification of patients which are colonized or infected with bacteria such as *Pseudomonas aeruginosa*.

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MCC/IMS

## Introduction

Actually, there are several analytical detection approaches available for human breath investigations, including gas chromatography–mass spectrometry (GC-MS) [1–7], proton

**Table 1** Characteristics of ion mobility spectrometer (BioScout 2010)

Parameter	<sup>63</sup> Ni-IMS
Ionisation source	<sup>63</sup> Ni (555 MBq)
Electric field strength	320 V/cm
Length of drift region	12 cm
Diameter of drift region	15 mm
Length of ionisation chamber	15 mm
Shutter opening time	300 μs
Shutter impulse time	100 ms
Drift gas	synthetic air (20.5% O <sub>2</sub> (4.5), 79.5% N <sub>2</sub> (5.0))
Drift gas flow	100 ... 300 mL/min
Temperature	room temperature
Pressure	101 kPa (ambient pressure)
MCC	OV-5, polar
Column temperature	40 °C

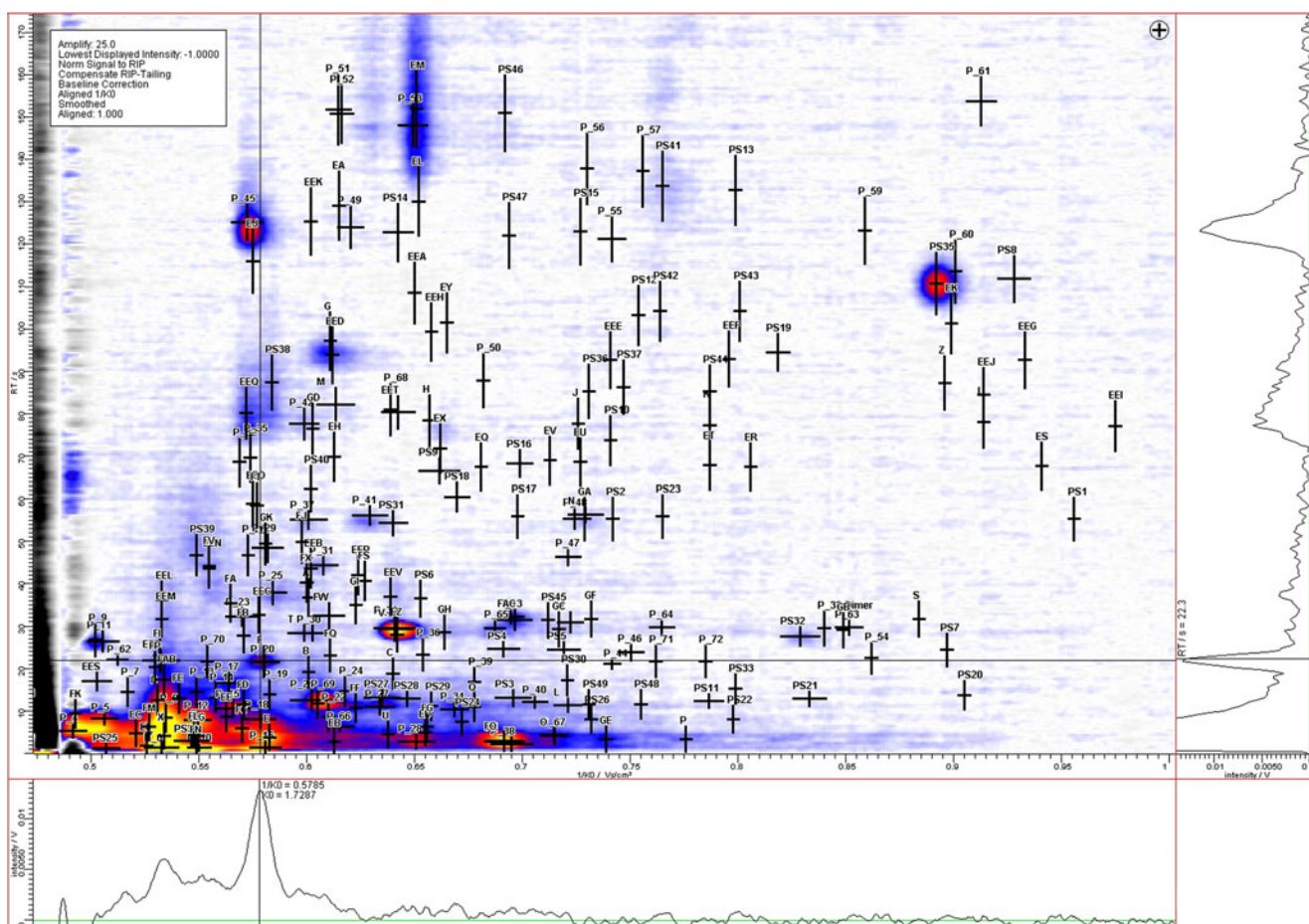
transfer reaction-mass spectrometry (PTR-MS) [8–11], selected ion flow tube-mass spectrometry (SIFT-MS) [12–18] and ion mobility spectrometry (IMS) [2, 19–28] and electronic

noses [29–33] and different types of sensors [34–40]. The sampling techniques include direct sampling, partly using sample loops [41–44], Tedlar bags [45–48], SPME [4, 5, 49–51] and different adsorbents [20, 26, 52]. In all cases mentioned a non-invasive and easy method for early diagnosis or therapy monitoring should be developed by identifying disease-specific biomarkers in the breath of patients.

On the other hand, first scientific evidence for microbial VOCs has been presented early in the last century [53, 54]. More recently, the detection of different VOCs and their relations to medical questions was reported, including ion mobility spectrometry [22, 55–71]. Some of the VOCs were related to bacteria taken from headspace of cultures [58, 72, 73].

The analytical technique used in the present paper is the same basic technique used to detect explosives or chemical warfare agents and was developed in a close cooperation of ISAS (Institute for Analytical Sciences, Dortmund) and the Lung Hospital Hemer, to examine hospital patients with lung cancer and airway infections [3, 21–23, 25, 74–78].

The technique, based on ion mobility spectrometry, is able to detect effectively metabolites in human breath down to the



**Fig. 1** Position of the peaks within the IMS-Chromatogram

**Table 2** Position of peaks and rank sum values of the peaks with rank sum <0.2

Control vs. <i>Pseudomonas</i>				
Pos	Area	Norm U	1/K <sub>0</sub> /Vs/cm <sup>2</sup>	RT/s
1	F	0,107	0,580	21,7
2	P_20	0,109	0,581	21,6
3	PS0	0,112	0,977	557,5
4	EL	0,164	0,652	130,1
5	PS46	0,170	0,692	151,0
6	PS13	0,171	0,799	132,8
7	PS47	0,172	0,694	122,1
8	P_57	0,180	0,756	137,3
9	PS41	0,182	0,765	133,8
10	P_51	0,184	0,615	151,8
11	P_52	0,186	0,616	150,8
12	PS17	0,187	0,698	55,9
13	PS4	0,188	0,691	24,6
14	P_46	0,188	0,750	23,9
15	P_55	0,189	0,742	121,4
16	GA	0,190	0,729	55,4
17	PS14	0,190	0,643	122,9
18	P_48	0,193	0,724	55,5
19	PS2	0,195	0,742	55,4
20	P_47	0,197	0,721	46,3
21	PS31	0,199	0,640	54,5

ppt, or pg/L-range. For investigations of human breath at a comparatively high level of humidity, a Multi-Capillary Column (MCC) for partly pre-separating of the analytes is used in combination with a conventional ion mobility spectrometer (IMS). An IMS coupled to a MCC allows the identification and quantification of volatile metabolites present in human breath, down to the ng/L- and pg/L-range of analytes within less than 500 s and without any pre-concentration. The IMS investigations are based on different drift times of swarms of ions from metabolites formed directly in air at ambient pressure. About 10 mL of breath is necessary to carry out a full analysis.

## Patients

All patients were recruited from the Department of Pulmonology, Ruhrlandklinik, University Hospital of Essen, Germany. The diagnosis of *Pseudomonas* was established according to the actual guidelines. Subjects with any other respiratory disease or any concomitant malignant, heart, renal, liver or collagen disease were excluded. All patients were clinically stable (no evidence of acute exacerbation for at least 4 weeks prior to enrolment). Healthy non-smokers, all employees of

the hospital, served as control group. The study was approved by the ethic committee of the University of Essen and all subjects provided an informed consent.

## Method

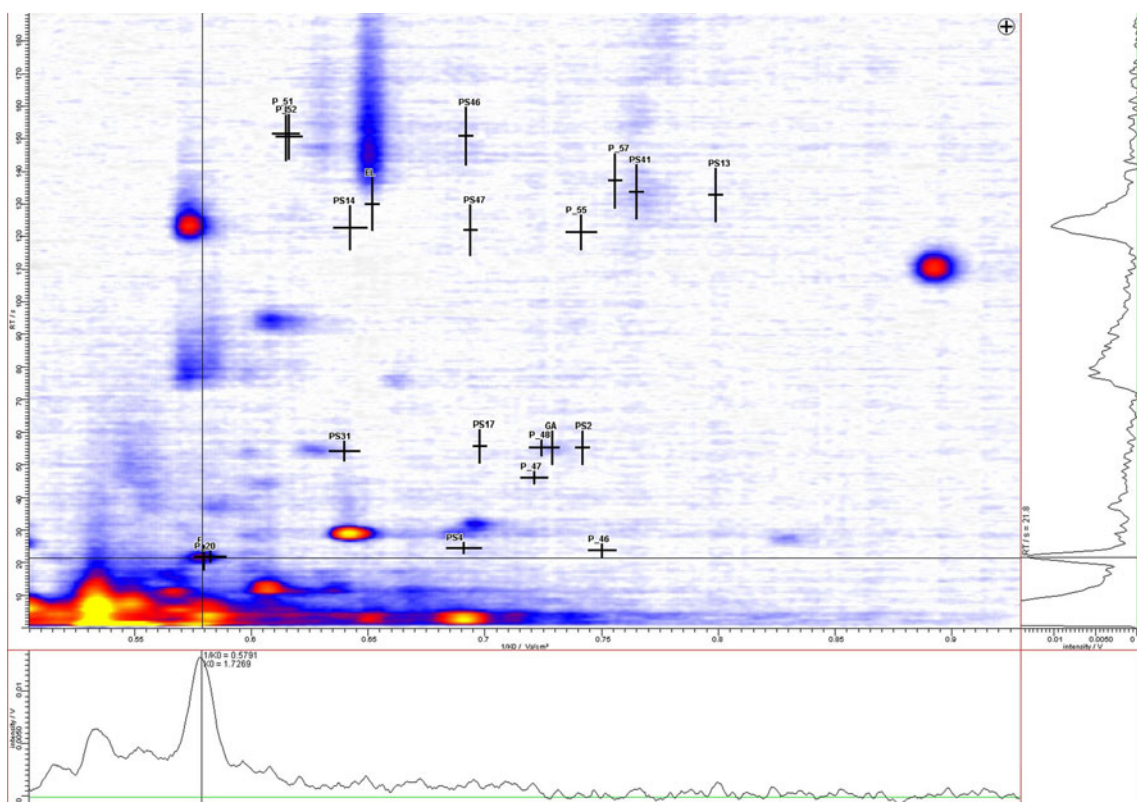
The IMS coupled to a multi-capillary column (MCC/IMS) used was a BioScout (B&S Analytik, Dortmund, Germany), consisting of the MCC/IMS and a SpiroScout (Ganhorn Medizin Electronic, Niederlauer, Germany) as sample inlet unit. The major parameters are summarized elsewhere [2, 3, 21–24, 74, 76, 79, 80]. In this spectrometer a 550 MBq [<sup>63</sup>Ni β-radiation source was applied for the ionization of the carrier gas (air). It is connected to a polar multi-capillary column (MCC, type OV-5, Multichrom Ltd, Novosibirsk, Russia) used as the pre-separation unit. In this MCC, the analytes of exhaled breath were sent through 1.000 parallel capillaries, each with an inner diameter of 40 μm and a film thickness of 200 nm. The total diameter of the separation column was 3 mm. The relevant MCC parameters are listed in Table 1.

All subjects were requested to exhale through a mouth piece connected to a Teflon tube. In each case, end-tidal breath controlled by a flow sensor, was collected in a sample loop of 10 mL in volume. The sample air was collected and transferred to the multi-capillary column for a first chromatographic separation after reaching three times 10 mL above the dead volume. Using the software VOCan 1.7 (B&S Analytik, Dortmund Germany), the dead volume was adjusted and fixed in the present case to 500 mL. The expiration was controlled by a CO<sub>2</sub>-sensor element integrated in the SpiroScout and recorded for each subject.

A preliminary relation between the peak position and the identity of the analyte was obtained using the database BSIMSDB 1.4 (B&S Analytik, Dortmund, Germany), but parallel measurements using e.g. GC/MSD should be realized with respect of further confirmation.

## Statistical evaluation

The peaks were characterized using the software Visual Now 2.5 (B&S Analytik, Dortmund Germany), which is described elsewhere [74, 81–84]. All peaks found were characterized by their position with drift time (corresponding 1/K<sub>0</sub>-value) and retention time and their concentration represented as the peak height. For all the peaks in both of the groups, Box-and-Wisker plots were realized. The rank sum as provided by Visual Now 2.5 was used to rank the peaks with the maximum difference between both groups. The value of the rank sum is related to the Mann–Whitney–Wilcoxon U value directly (rank sum = norm U = U/n<sub>1</sub>n<sub>2</sub>), were n<sub>1</sub> and n<sub>2</sub> are the numbers of cases in each group.



**Fig. 2** Position of the peaks with the maximum potential with respect to discrimination between the group of Pseudomonas and the healthy controls within the IMS-Chromatogram. The cross line related to the

single spectrum (*below*) and the chromatogram (*right*) shows the position of the peak with the lowest rank sum

**Results**

To realize a non invasive identification of pathogens the exhaled breath of 53 persons (24 patients suffering chronic or infectious on Pseudomonas and 29 healthy controls) was investigated using the ion mobility spectrometer type Bio-Scout. In total 224 signals were found as shown in Fig. 1.

For each of the peak the rank sum was calculated using Visual Now 2.2 to be able to find the signals with the maximum potential to discriminate between both of the groups, see Table 2.

In total, 21 signals seem to be able to differentiate the two groups control and pseudomonas with a rank sum values less than 0.2.

**Table 3** Sensitivity, specificity and predictive values related to the peaks F and PS0 by visual discrimination

Signal	F	PS0
Sensitivity	89%	100%
Specificity	77%	74%
Positive predictive value	83%	82%
Negative predictive value	86%	100%

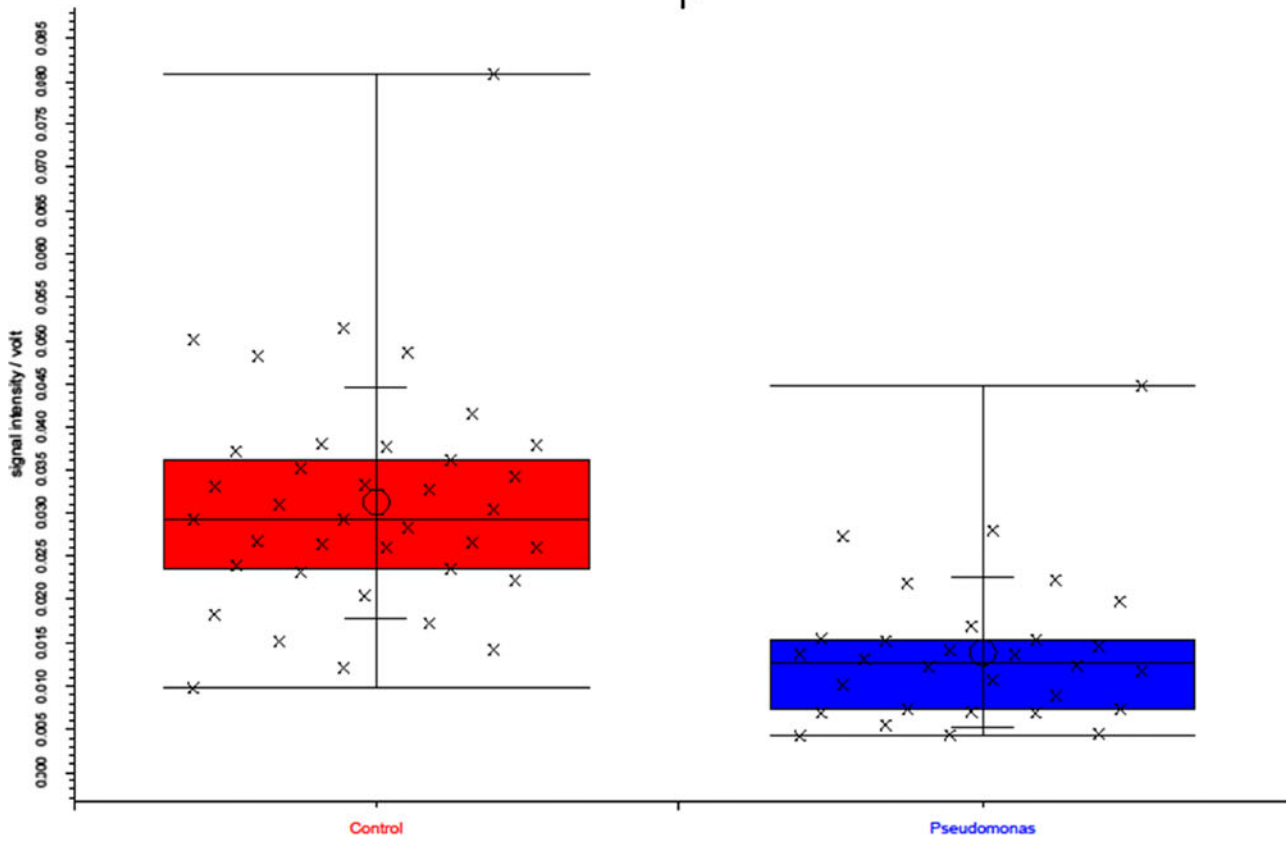
The position of the peaks with the rank sum less than 0.2 is shown in Fig. 2.

Furthermore, for all 224 signals Box-and-Wisker plots were realized. The peaks with the lowest rank sum values F (0,107) and PS0 (0,112) show rather good separation of both groups. A further discrimination between the first two peaks F and P\_20, which were rather close to each other, located by  $1/K_0$  and retention time, was not realized in the present study (see Table 2). Therefore, the first and the third peak should be considered more in detail. Surprisingly, in all cases the concentration of the analytes was significantly higher in the control group than in the Pseudomonas group.

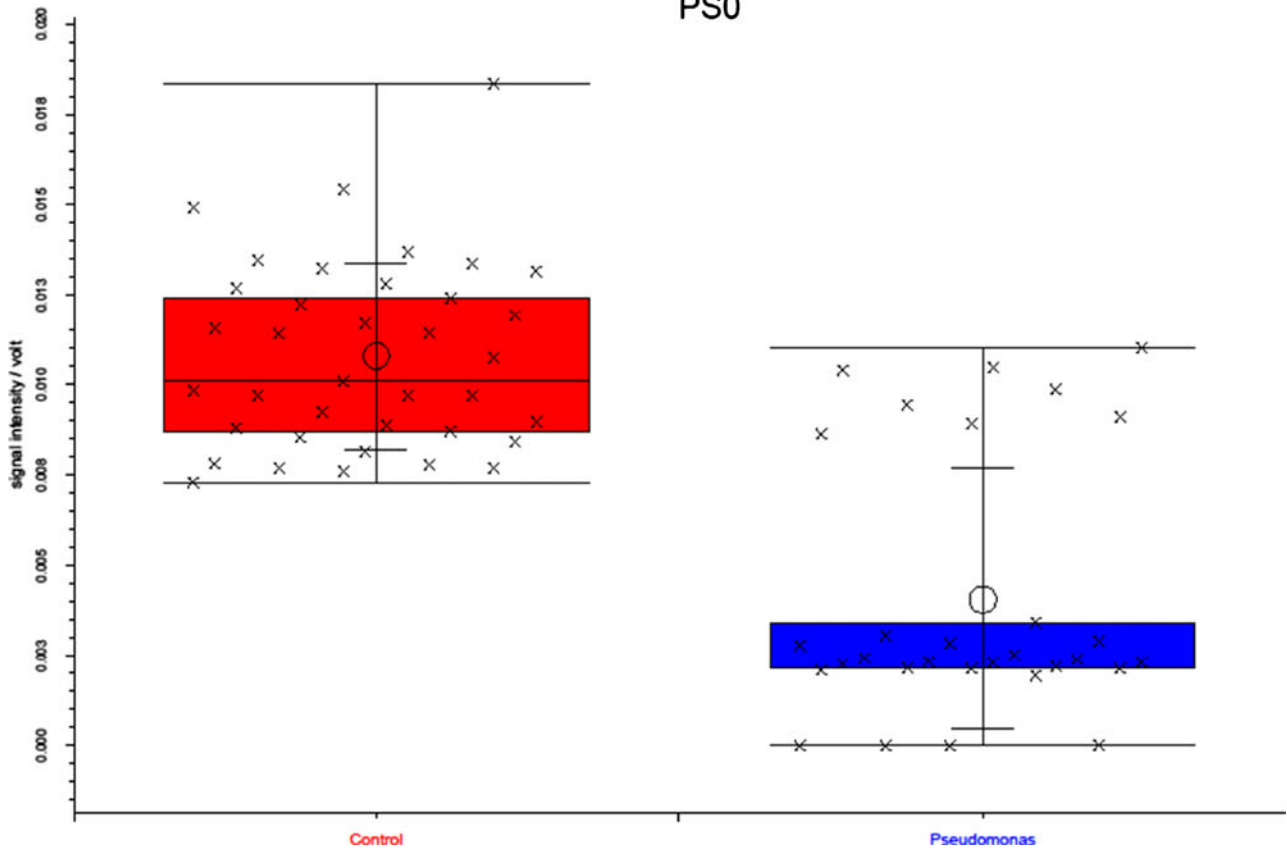
The values of sensitivity and specificity, and the positive and negative predictive value were summarized in Table 3 as obtained from visual discrimination. The peak PS0 shows a sensitivity and a negative predictive value of 100%. The sensitivity was higher than the specificity in both cases. But, the peak PS0 was really low and near to the noise and in some cases the measurements were not

**Fig. 3** Box-and-Wisker plot of the signals of peak F (*above*) and PS0 (*below*) in both the groups (Control vs. Pseudomonas) with a rank sum value of 0.107 and 0.112, respectively

F



PS0



**Table 4** Calculation of the best threshold to discriminate the two groups of healthy controls and Pseudomonas

	EL	F	PS0	PS13	PS46	PS47	P_20
Best threshold	0,010	0,017	0,007	0,006	0,007	0,005	0,023
Sens	0,757	0,892	1,000	1,000	0,973	1,000	0,784
Spez	0,833	0,800	0,733	0,600	0,633	0,600	0,900
Npv	0,528	0,579	0,627	0,673	0,655	0,673	0,518
Ppv	0,735	0,857	1,000	1,000	0,950	1,000	0,771
$a = \text{sen} - (1 - \text{spez})$	0,590	0,692	0,733	0,600	0,606	0,600	0,684
Accuracy	0,791	0,851	0,881	0,821	0,821	0,821	0,836

carried out until 600 s. This becomes visible from null values for four cases as shown in Fig. 3.

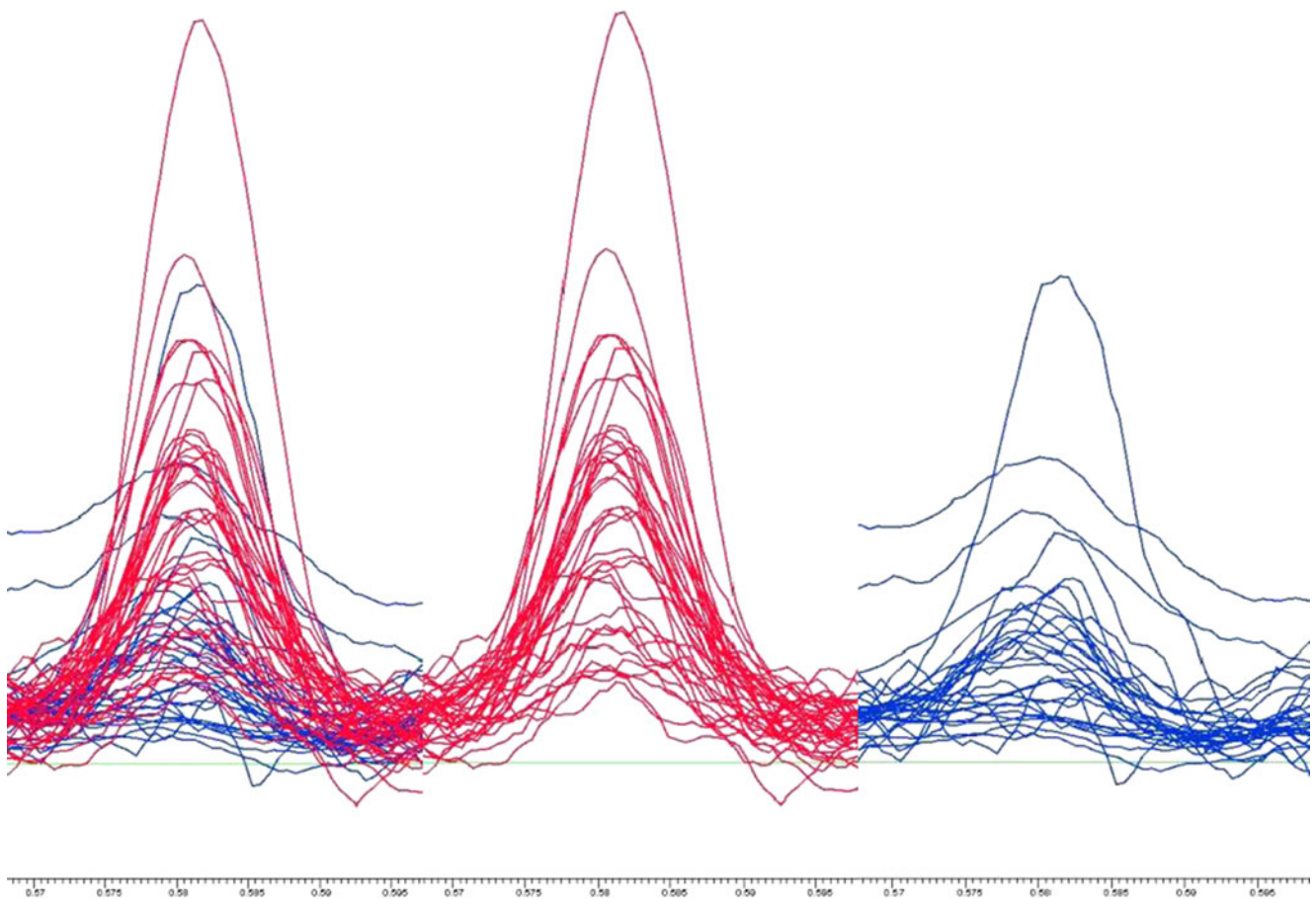
In addition, a calculation of the best position of a threshold with respect to differentiation of the two groups was realized for all 224 peaks. The Table 4 compares the results for the positions 1–7 of the rank sum from Table 2.

Surprisingly, the peak with rank sum position 3 delivers the best accuracy (0,88). For Peak PS0 the sensitivity found was 100, the specificity 74, the positive predictive value 82%, the negative predictive value 100%.

Therefore, the signal F should be considered for separation between control and pseudomonas group with the highest accuracy. Generally, the finding needs further confirmation and a higher number of subjects included within the study (Fig. 4).

### Summary

To realize a non invasive identification of pathogens, the exhaled breath of 53 persons (24 patients suffering chronic



**Fig. 4** Comparison of single spectra of Peak F (red control group—blue Pseudomonas group, *left*: both groups together, *center*: control group, *right*: Pseudomonas group)

or infectious on *Pseudomonas* and 29 healthy controls) was investigated using an ion mobility spectrometer type BioScout. In total 224 different signals were found in the exhaled breath. Actually, 21 different signals are able to differentiate the two groups Control and *Pseudomonas* with rank sum values less than 0.2. The best separation was found by peak F with rank sum 0,107. In this case, the sensitivity found was 89%, the specificity 77%, the positive and negative predictive values were 83% and 86%, respectively. Generally, the finding needs further confirmation and a higher number of subjects included within the study.

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