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Ali Kadar, Ludovic Peyre, Henri Wortham, Pierre Doumenq. A simple GC–MS method for the determination of diphenylamine, tolylfluanid propargite and phosalone in liver fractions. Journal of Chromatography B Biomedical Sciences and Applications, 2019, 1113, pp.69-76. 10.1016/j.jchromb.2019.03.005 . hal-02469623

HAL Id: hal-02469623 https://hal.science/hal-02469623v1

Submitted on 6 Feb 2020

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1 A simple GC-MS method for the determination of diphenylamine,

2 tolylfluanid propargite and phosalone in liver fractions

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- 8
- 9 ABSTRACT
- 10 In this study, an accurate and robust gas chromatography/mass spectrometry method was developed for
- 11 quantitative analysis of diphenylamine, tolylfluanid, propargite and phosalone in liver fractions.
- 12 Different injector parameters were optimized by an experimental design of experiment technique
- 13 (central composite design). An optimal combination of injector temperature (°C), splitless time (min)
- 14 and overpressure (KPa) values enabled to maximize the chromatographic responses. Sample preparation
- was based on protein precipitation using trichloroacetic acid followed by liquid-liquid extraction (LLE)
- 16 of the pesticides with hexane. All compounds were quantified without interference in selected ion
- 17 monitoring mode using endrin as internal standard. The calibration curves for diphenylamine,
- 18 tolylfluanid, propargite and phosalone compounds were linear over the concentration range of
- 19 0.1 to 25 μM (i.e.0.1, 0.5, 2.0, 5.0, 15.0 and 25.0 $\mu M)$) with determination coefficients (R²) higher than
- 20 0.999. A lower limit of quantification of 0.1 μM was obtained for all analytes, i.e. 422.5, 868.0, 876.2
- 21 and 919.5 µg/kg of liver fraction (hepatocytes) for diphenylamine, tolylfluanid, propargite and
 - phosalone, respectively. All compounds showed extraction recoveries higher than 93%, with a
 - maximum RSD of 3.4%. Intra- and inter-day accuracies varied from 88.4 to 102.9% and, imprecision
- varied from 1.1 to 6.7%. Stability tests demonstrated that all pesticides were stable in liver extracts
- during instrumental analysis (20°C in the autosampler tray for 72 h) following three successive freeze-
- 26 thaw cycles and, at -20°C for up to 12 months. This simple and efficient analytical procedure is thus
- 27 suitable for assessing mammals liver contamination or metabolism studies.
- 28 Keywords: Bioanalytical method, Pesticides mixture, Experimental design, GC-MS, Liver fractions,
- 29 Protein precipitation.

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1. Introduction

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For more than half a century, agricultural practices have involved the use of a large amounts of pesticides. These pesticides provide better agricultural yields and allow extending the shelf life of perishable fruits and vegetables to fulfill the need of the growing worldwide population [1]. Unfortunately, these helpful active compounds may at the same time constitute a significant risk to animal and human health [2]. Indeed, pesticide residues are widespread in the whole environment and are likely to be present in water resources and agricultural products [3-5]. Water and food crop consumption is the predominant pathway of exposure for the general population [6-12]. On this population scale, several authors evaluated the dietary exposure to pesticides residues and pointed out that the consumers may be simultaneously exposed to different residues [13-22]. In their work [23], Crepet et al. concluded that depending on the foodstuff consumed the French general population was mainly and most heavily exposed to 7 different pesticide mixtures composed of 2 to 6 compounds. Diphenylamine, tolylfluanid, propargite and phosalone belong to a mixture that was significantly correlated to common fruits such as apples and pears. Once these potentially contaminated fruits have been consumed and the compounds have passed into the body, these latter are transported by the blood flow to the liver for metabolization [24]. Therefore, in the scope of metabolism [24] or biomonitoring [25-27] studies, a sensitive and reliable analytical method is needed to assess the pesticides level in liver fractions. Until now, as far as we know, bibliographic research shows that no work has been published on the simultaneous determination of diphenylamine, phosalone, propargite and tolylfluanid in human biological samples. However, Oliveira et al. and Kaczynski et al. have recently published multiresidues analytical protocols including the determination of propargite and phosalone [24] or the quantification of propargite and tolylfluanid [25] in fish liver. These methods were based on the use of liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS). The study reported by Russo et al. [26] is, to the best of our knowledge, the only one dealing with real human liver samples. Authors carried out the development of a gas chromatography coupled to a negative chemical ionization mass spectrometry (GC-NCI-MS) method for the analysis of several organophosphorus pesticides including phosalone. Valente et al. [27] 58 quantified this latter in human blood along with other organophosphates thanks to a GC-MS method. In 59 the same matrix, Sharma et al. [28] successfully quantitated phosalone using gas chromatography 60 coupled to a flame thermionic detector (GC-FTD). For sample purification, works published by Valente et al. [27] and Sharma et al. [28] depicted a one-61 step phosalone extraction/clean-up from blood liquid samples using either silica based C 18 reversed-62 63 phase [27] or florisil [28]. Robles-Molina et al. [x] extracted diphenylamine and phosalone from water 64 with Oasis HLB sorbent. Lehotay et al. [y] validated automated mini-SPE with MgSO4/primary secondary amine (PSA)/C18/CarbonX sorbent for the analysis of diphenylamine and propargite in food 65 66 samples. On the other hand, solvent extractions proved to be suitable for the analysis of phosalone, propargite 67 and tolyfluanid in liver samples [24-26]. 68 An analytical protocol using solvent extraction followed by a GC separation and MS detection seemed 69 70 convenient for assessing liver contamination by the present pesticide mixture. 71 Thus, this work aimed at developing and validating a simple, accurate and robust analytical method for 72 the analysis of diphenylamine, tolylfluanid, propargite and phosalone in human liver fractions 73 (hepatocytes). 74 2. Experimental 75 2.1. Chemicals, materials and biological samples 76 Certified standards of diphenylamine, tolylfluanid, propargite, phosalone and endrin with purities higher 77 than 99.5 %; ammonium sulfate salts and trichloroacetic acid (TCA) of research grade purity were 78 purchased from Sigma-Aldrich (St Quentin Fallavier, France). n-Hexane, ethyl acetate and acetonitrile 79 of ultra-trace analysis grade were purchased from Carlo Erba (Val de Reuil, France). Standard stock solutions were prepared from pure compounds and appropriately diluted in acetonitrile. 80 81 A high-throughput tissue grinder (MM 300) produced by Retsch (Haan, Germany) was used as a 82 powerful transversal shaker for the LLE experiments. Phase separation was achieved using a Thermo IEC Micromax RF benchtop centrifuge from Thermo Fisher Scientific (Illkirch, France). 83

All experiments on human tissues were carried out according to the ethical standards of the responsible committee on human experimentation and the Helsinki Declaration. Cellular (hepatocytes) fractions were obtained after mechanical decomposition of liver tissues. Here we decided to carry out the experiments with thermally (100°C for 3 min) inactivated hepatocytes previously isolated following Berry and Friend procedure [29]. 2.2 Sample treatment A 400 µL volume of thermally inactivated liver cells (16 mg) in 100 mM phosphate potassium buffer (pH 7.4) was added to 1.8 mL Eppendorf® tubes. Prior to a brief vortex mix of the samples, the required amounts of diphenylamine, tolylfluanid, propargite, phosalone and endrin were added as internal standard (IS). Then, $100 \,\mu\text{L}$ of ice-cold trichloroacetic acid (20%) and $400 \,\mu\text{L}$ of Hexane were added to the tubes. The samples were vigorously shaken for 3 minutes and centrifuged at 16000g and 4°C for 4 min, enabling the precipitation of the denatured proteins and full separation of the liquid phases. The supernatant was then transferred into a 200 µL GC vial insert for GC analysis. 2.3. GC-MS Analysis Separation and quantification of the pesticides mixture were performed using a TRACETM ultra gas chromatograph coupled to a DSQ II single quadrupole mass spectrometer (Thermo Fisher Scientific, Courtaboeuf, France). The gas chromatograph was equipped with a programmable split/splitless injector, a capillary column and a programmable oven. A sample volume of 2 μL was injected at 271°C, in splitless mode, in a baffle Siltek-deactivated liner (2 mm \times 2.75 mm \times 120 mm) provided by Thermo Fisher Scientific . A surge pressure of 490 kpa was applied for a 1.25 min period right after injection. The separation of the four compounds was achieved on a TRACE TR5-MS (Thermo Fisher Scientific) capillary column (30 m \times 0.25 mm, i.d., 0.25 μ m film thickness). The electron impact ion source and transfer line temperatures were set at 250 and 280°C, respectively. The elution was carried out using a 1.0 ml/min constant flow rate of helium carrier gas and a temperature gradient. After optimization of the standards mixture separation, the oven temperature was programmed as follows: the initial temperature set at 50 °C for 2.0 min followed by a first ramp of 35 °C .min⁻¹ up to 210 °C and held for 4.0 min; then a second ramp of 35 °C min⁻¹ up to 280 °C was set and maintained for 4.1 min. The total

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optimized run time was 17 min. The criteria for positivity used to identify the compounds were both retention times and characteristic m/z signals. Quantification was accomplished in the selected ion monitoring (SIM) mode and the monitored ions are displayed in **Table 1**.

Table 1. Ions monitored under the SIM mode by GC-MS^a and their relative intensities (%).

1111011011100 (70)	•		
Compound	Molecular ion (m/z)	Base peak ion ^b (<i>m/z</i>)	Fragment ion 1 (m/z)
Diphenylamine	169	169(100)	168(50)
Endrin (IS)	380	263(100)	281(65)
Phosalone	367	182(100)	184(33)
Propargite	350	135(100)	173(15)
Tolylfluanid	346	137(100)	238(48)

^a The compounds were quantified with the sum of both base peak and fragment peak signals.

2.4. Optimization of splitless injection parameters

To achieve the lowest instrumental detection limits, in addition to preliminary optimization of chromatographic and ionization source settings, the splitless injection was optimized. For that purpose, a central composite design (CCD) with three independent variables (X_1 , Temperature; X_2 , Surge pressure; X_3 , Splitless Time) was performed. Preliminary experiments with one factor at a time allowed to determine the appropriated ranges of these independent variables: X_1 : 133–318 °C; X_2 : 0–490 kPa; X_3 : 0–2.50 min. As shown in **Table 2A**, five levels were used for optimization of the three factors. Design and analysis of the central composite experiment were carried out using Statistica 8.0 software (Statsoft, Maison Alfort, France). A total of 48 assays described in **Table 2B** were carried out by automated injections of 2μ L of a $10\,\mu$ M multi-compounds standard solution containing diphenylamine, tolylfluanid, propargite and phosalone.

^b Ionized in the positive mode with an electron energy of 70 eV.

Table 2. Values of the factors at the five levels examined (A) and experiments undertaken for the central composite design (B).

(A)	Ter	nperature (°C)	Time (ı	nin)	Surge pressure (kPa)	
Lowest	133		0.00	0		
Low	170		0.50	10	00	
Center	225		1.25	24	45	Factor levels
High	280		2.00	39	90	
Highest	318		2.50	49	90	
(B)	No.	\mathbf{X}_{1}	X_2	3	\mathbf{X}_3	
1		225	1.25	0		
2		170	2	100		
3		225	1.25	245		
4		225	2.51	245		
5		170	2	390		
6		318	1.25	245		
7		225	0	245		
8		225	1.25	490		
9		280	2	100		
10		280	0.5	390		
11		280	0.5	100		
12		170	0.5	390		
13		225	1.25	245	Experiments	
14		170	0.5	100	Experiments	
15		133	1.25	245		
16		280	2	390		
17		225	1.25	0		
18		170	2	100		
19		225	1.25	245		
20		225	2.51	245		
21		170	2	390		
22		318	1.25	245		
23		225	0	245		
24		225	1.25	490		
25		280	2	100		
26		280	0.5	390		

(B)	No.	$\mathbf{X}_{\scriptscriptstyle 1}$	X_2	X_3
	27	280	0.5	100
	28	170	0.5	390
	29	225	1.25	245
	30	170	0.5	100
	31	133	1.25	245
	32	280	2	390
	33	225	1.25	0
	34	170	2	100
	35	225	1.25	245
	36	225	2.51	245
	37	170	2	390
	38	318	1.25	245
	39	225	0	245
	36	225	1.25	490
	37	280	2	100
	38	280	0.5	390
	39	280	0.5	100
	40	170	0.5	390
	41	225	1.25	245
	42	170	0.5	100
	43	133	1.25	245
	44	280	2	390
	45	225	1.25	0
	46	170	2	100
	47	225	1.25	245
	48	225	2.51	245

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2.5. Method validation

Validation was achieved according to the Food and Drug Administration (FDA) guidance for

bioanalytical methods [30].

The LLOQ, established as the lowest concentration that can be measured with acceptable imprecision

141 (<20%) and accuracy (±20%), was assessed with four serial dilutions of spiked sample extract

Commenté [ZZ1]: Si plusieurs échantillons spikés mettre sample au pluriel

containing 0.400 mM of each compound (six replicates). To validate a specific LLOQ, the chromatographic peak area of the corresponding analyte should be at least five times higher than the noise background of blank samples (i.e. peak to peak signal-to-noise ratio, S/N=5). The LLOQ were established as 422.5, 868.0, 876.2 and 919.5 µg/kg of liver for diphenylamine, tolylfluanid, propargite and phosalone, respectively. Selectivity was evaluated on ten different blank human cells extracts by checking that chromatographic peaks of pesticides and endrin (IS) did not co-elute with any endogenous compound. The evaluation consisted in verifying that specific retention times and SIM responses of pesticides were well discriminated from potential interfering signals. In addition, the matrix effect criterion was studied: extracting ten different blank matrices were extracted and spiked with the pesticides mixture at the predetermined LLOQ concentrations and quantified. Figure 2. presents both a typical chromatogram at the LLOQ and a chromatogram of a blank sample extract. The results were compared with those obtained for fortified aqueous extract of the same concentration levels. In the absence of acceptable limits defined in the FDA guidance and, as previously reported by Kadar et al. [31], to be acceptable, the deviation between the calculated and the nominal values should be less than $\pm 5\%$. To study the linearity for diphenylamine, tolylfluanid, propargite and phosalone, 6 replicates of calibration standard samples from the validated LLOQ (0.1 μ M) to 25 μ M were prepared in hexane and analyzed by GC-MS. Recovery rates of analytes were evaluated at low (0.1 μM), medium (5.0 μM) and high (50.0 μM) concentration levels. Despite the detector linearity being validated up to 25 µM only, a validation of the last concentration allowed expanding the concentration range of applicability of the method. Three replicates were prepared by fortifying thermally inactivated human hepatocytes samples before extraction and analysis. The ratio between mean peak areas from these samples and the one from postextracted spiked samples allowed determining each pesticide percentage recovery. The imprecision (intra- and inter-day) and accuracy of the method were studied at four different concentration levels: low (0.1 μM), medium (5.0 μM) and high (50.0 μM). For intra-day imprecision

and accuracy, five replicate samples per concentration level were prepared and analyzed on the same

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day. For inter-day imprecision, six different days on a 15 days period were chosen to repeat the preparation and analysis of sample duplicates at the same spiking levels. Intra- and inter-day imprecision were considered acceptable if the relative standard deviations (RSD%) were below 15% [31]. On the other hand, accuracy, expressed as the mean percentage deviation (Intra-day: Ar% and Inter-day: Br%) from the spiked value, was in accordance with the guidance when the yields ranged between 85 and 115% of the nominal concentrations.

To check the stability of the compounds, degradation tests were carried out in triplicate using processed samples previously spiked at 5 μ M with the pesticides mixture. Various storage conditions were experimented: 96 h in the autosampler tray at +25°C, after three freeze – thawing cycles from -20°C to room temperature during 15h or, long term storage for either 1 month, 3 months or 9 months at -20°C. For this criterion, the FDA did not set acceptable limits. Then, after samples' analysis using freshly prepared calibration curves, imprecision and accuracy were respectively considered acceptable if below 15% and if between 85% and 115% of their nominal values as depicted by Gonzalez et al. [3]. In addition, after consecutive analysis of 8 samples, a blank sample and a standard at 0.1 μ M were analyzed to check for any pollution or significant drift (> 10%) of the instrument signal.

3. Results and discussions

- 186 3.1. Method development
- 187 3.1.1. Sample treatment

On the basis of previously published works [32-35], hexane and ethyl acetate seemed to be good solvents candidates for liquid/liquid extraction of the studied pesticides mixture from a 400 μ L sample of thermally inactivated human liver cells. As presented in **Table 3**, the assay was optimized through a sequence of experiments aiming at establishing the best sample treatment prior to GC-MS analysis. First, the extraction efficiencies of the two hydrophobic solvents were compared on 400 μ L spiked phosphate potassium buffer samples. As displayed in **Table 3**, in the absence of matrix, hexane proved to be the best compromise for the whole pesticides mixture. Then, the experiment was repeated on a sample spiked liver cells sample. However, due to the formation of a very compact emulsion, no clear layers appeared, thus preventing GC-MS analysis. Partial solubilization of proteins, highly present, could

explain the outbreak of this emulsion. Thanks to their combined hydrophobic and hydrophilic properties, these proteins are attracted to both the non-polar solvent and the aqueous medium. Afterwards, comparison of simultaneous protein precipitation and LLE versus sequential protein precipitation and LLE was carried out. For this purpose, two efficient protein precipitators were compared: TCA and ammonium sulfate [36]. Globally, the results in **Table 3** show that regardless of the assay procedure (either simultaneous or sequential), recoveries obtained were higher with TCA compared to ammonium sulfate. In fact, contrarily to ammonium sulfate [37], TCA is known to help with the release of bound analytes into solution [38]. Indeed, at pH lower than the protein isoelectric point, TCA interacts with the positively charged amine group of proteins to form an insoluble salt [39]. In addition, as displayed in **Table 3**, simultaneous protein precipitation and LLE gave the best recoveries with TCA. This is probably because the vigorous shaking enabled a rapid solvent exchange between aqueous and organic solution while precipitation of protein was taking place simultaneously.

Table 3. Pesticides recoveries of a 10 μM concentration spiked samples regarding the chemical treatment applied.

Treatment	Recovery, RSD (%, n = 2)						
	Diphenylamine	Tolylfluanide	Propargite	Phosalone			
Buffer/hexane ^a	95, 1.6	100, 2.8	99, 5.0	99, 4.7			
Buffer/ethyl acetate ^a	98, 2.6	99, 3.3	96, 6.1	93, 4.3			
Medium/hexane ^a	n/a	n/a	n/a	n/a			
Medium + SO ₄ (NH ₄) ₂ /hexane ^b	84, 4.8	70, 13.9	71, 24.2	81, 6.4			
Medium + TCA/hexane ^b	87, 4.3	81, 3.9	96, 2.3	88, 4.6			
Medium/SO ₄ (NH ₄) ₂ + hexane [©]	87, 4.0	75, 2.4	91, 2.5	89, 3.6			
Medium/TCA + hexane [©]	90, 1.5	86, 0.9	96, 1.8	93, 0.6			

²¹² a LLE.

^b Proteins precipitation followed by LLE.

^c Simultaneous proteins precipitation and LLE.

Highest recoveries were obtained using simultaneous proteins precipitation and LLE after TCA and hexane were added. Recoveries varied from 86 % for tolylfluanide to 98 % for endrin, with a maximum RSD value of 1.8 %.

The final protocol was as follows: 100 µL of 20 % TCA and 400 µL of hexane were added to the human hepatic preparation before 3 minutes vigorous shaking. Then, the sample was centrifuged for 4 minutes at 16000 g and 4°C. Finally, the supernatant was transferred into a vial prior to GC-MS analysis.

3.1.3 Optimization of splitless time, temperature and surge pressure using response surface

222 methodology

The experimental results were analyzed by multiple linear regression to fit to the postulated model (1)

where Y is the instrumental response, X_1 , X_2 and X_3 are the three independent variables described above

and $\beta_i,\,\beta_{ii}$ and β_{ij} are the fitting coefficients.

$$226 \qquad Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_{12} X_1 X_2 + \beta_{13} X_1 X_3 + \beta_{23} X_2 X_3 + \beta_{11} {X_1}^2 + \beta_{22} {X_2}^2 + \beta_{33} {X_3}^2 \qquad (1)$$

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Table 4. Second polynomial equations obtained for the different pesticides.

Pesticides	Equations	\mathbb{R}^2	Adj. R²
Diphenylamine	$\begin{array}{l} Y{=}1.62E8{-}1.82E6X1{+}5.87E8X2{+}8.83E5X3{-}2.99E5X1X\\ 2{+}7.03E3X1X3{-}3.87E5X2X3{+}1.10E03X12{-}1.61E08X22\\ -2.37E03X32 \end{array}$	0.9180	0.8985
Tolylfluanid	Y=-9.11E8+9.66E6X1+5.25E8X2+2.89E5X3-3.87E5X1 X2+6.02EX1X3-2.00E05X2X3-2.64E4X12-1.06E8X22 -1.34E3X32	0.8531	0.8183
Propargite	$\begin{array}{l} Y{=}{-}1.72E9{+}1.26E7X1{+}6.93E8X2{+}1.29E6X3{-}3.23E5X1\\ X2{+}4.8E3X1X3{-}3.44E5X2X3{-}2.64E4X12{-}1.46E8X22{-}\\ 2.10E3X32 \end{array}$	0.8922	0.8667
Phosalone	Y=-1.65E9+1.17E7X1+6.16E8X2+1.45E6X3-2.19E5X1 X2+4.10E3X1X3-2.03E5X2X3-2.41E4X12-1.46E8X22 -2.58E3X32	0.9363	0.9212

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Calculated coefficients of the pesticides response model, corresponding determination coefficients (R^2) and adjusted determination coefficients (Adj. R^2) are reported in **Table 4**. ANOVA results presented in **Table 5** demonstrated that the model was highly significant for each compound. The values of R^2 and

Adj. R² (0.9180 and 0.8985 for diphenylamine; 0.8531 and 0.8183 for tolylfluanid; 0.8922 and 0.8667

Table 5. ANOVA of central composite design for <u>diphenylamine</u>, tolylfluanid, propargite and phosalone.

Parameter	SS	df	MS	F	р	
Diphenylamine						
X_1	7327E+16	1	7327E+16	19.029	0.000095	
X_2	5603E+17	1	5603E+17	145.522	0.000000	
X_3	5806E+17	1	5806E+17	150.802	0.000000	
X_{1^2}	3056E+14	1	3056E+14	0.079	0.779694	
X_1X_2	3663E+15	1	3663E+15	0.951	0.335552	
X_1X_3	7543E+16	1	7543E+16	19.590	0.000078	
X_{2^2}	2249E+17	1	2249E+17	58.423	0.000000	
X_2X_3	4241E+16	1	4241E+16	11.015	0.002001	
X_{3}^{2}	6971E+16	1	6971E+16	18.104	0.000132	
Error	1463E+17	38	3850E+15			
Total SS	1782E+18	47				
Tolylfluanid						
X_1	1853E+17	1	1853E+17	31.71080	0.000002	
X_2	3570E+17	1	3570E+17	61.10285	0.000000	
X_3	4680E+17	1	4680E+17	80.08768	0.000000	
X_{1^2}	1771E+17	1	1771E+17	30.31713	0.000003	

Parameter	SS	df	MS	F	р
X_1X_2	6119E+15	1	6119E+15	104,716	0.312633
X_1X_3	5527E+16	1	5527E+16	945,954	0.003881
X_{2^2}	9680E+16	1	9680E+16	16.56632	0.000229
X_2X_3	1136E+16	1	1136E+16	194,441	0.171290
X_{3^2}	2231E+16	1	2231E+16	381,869	0.058073
Error	2220E+17	38	5843E+15		
Total SS	1512E+18	47			
Propargite					
X1	2897E+17	1	2897E+17	45.7029	0.000000
X_2	6701E+17	1	6701E+17	105.7338	0.000000
X ₃	7132E+17	1	7132E+17	112.5357	0.000000
X_{1^2}	1770E+17	1	1770E+17	27.9339	0.000005
X_1X_2	4257E+15	1	4257E+15	0.6717	0.417570
X_1X_3	3514E+16	1	3514E+16	55,450	0.023801
X_{2^2}	1840E+17	1	1840E+17	29.0286	0.000004
X_2X_3	3368E+16	1	3368E+16	53,143	0.026706
X_{3}^{2}	5496E+16	1	5496E+16	86,716	0.005490
Error	2408E+17	38	6338E+15		
Total SS	2233E+18	47			

Phosalone

Parameter	SS	df	MS	F	р
X ₁	3225E+17	1	3225E+17	102.556	0.000000
X_2	5291E+17	1	5291E+17	168.278	0.000000
X_3	6332E+17	1	6332E+17	201.362	0.000000
X_{1^2}	1477E+17	1	1477E+17	46.986	0.000000
X_1X_2	1956E+15	1	1956E+15	0.622	0.435201
X_1X_3	2570E+16	1	2570E+16	8174	0.006863
X_{2^2}	1845E+17	1	1845E+17	58.665	0.000000
X_2X_3	1166E+16	1	1166E+16	3708	0.061661
X_3^2	8276E+16	1	8276E+16	26.321	0.000009
Error	1195E+17	38	3144E+15		
Total SS	1874E+18	47			

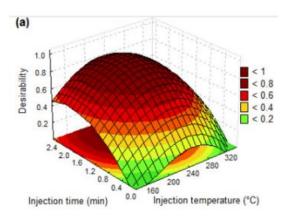
 $SS = sum \ of \ squares, \ ddl = degree \ of \ freedom, \ MS = mean \ square, \ F = ratio \ and \ p = probability \ level.$

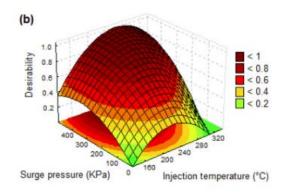
Even if it was possible to find the optimal injector settings for a single response using surface response design, here the study aimed at finding a compromise for the simultaneous optimization of responses from diphenylamine, tolylfluanid, propargite and phosalone. Consequently, the multicriteria methodology established by Derringer and Suich [40] was implemented for the ensuing work. This methodology first involves the construction of an individual desirability function (di) for each compound. Then, as depicted by Eq. (2), the overall desirability function (D) is defined as the weighted geometric average of the individual desirability (di).

$$D = \sqrt[4]{d_1 d_2 d_3 d_4} \tag{2}$$

A value of D close to 1 means that each individual pesticide's response is maximized and that the corresponding levels of factors are globally optimum. As can be observed in Fig. 1, the desirability

252 surfaces obtained by Eq. (2) show the effect of operating conditions on the overall pesticides 253 chromatographic responses in the range of the investigated variables. 254 Therefore, applying the numerical optimization function from the Statistica software to the Derringer's 255 desirability function allowed to find the following injection experimental conditions: X1 (271.7°C), X2 (1.25 min) and X3 (490 KPa); which simultaneously maximized the signals of all the compounds. 256 257 258 3.2 Performance of the analytical method 259 No instrumental carry-over or significant drift were noticed during all the validation process. The absence of interfering peaks on chromatograms from ten different blank human hepatocyte samples, 260 261 compared chromatograms acquired from reference standard in neat solvents led to the full validation of 262 the method selectivity. Indeed, chromatographic signals of pesticides were always satisfactorily discriminated on the basis of their specific retention times and SIM responses. In addition, no matrix 263 effects waere observed at the LLOQ level for all pesticides. 264 265 **Table 6** lists the key elements of the method validation. The determination coefficient values (R2) were always greater than 0.999 indicating that there was a 266 267 good correlation of linearity through the concentrations range used and a homoscedastic distribution of 268 replicates at all levels. On the basis of recovery results ranging from 96.5% to 100.0%, with a maximum 269 RSD of 3.4%, the implemented sample treatment was considered satisfactory. 270 In addition, intra- and inter-day imprecision and accuracy exhibited acceptable values, ranging from 271 1.1% to 6.7%. 272 Moreover, stability tests demonstrated that all the analytes did not degrade in the final extract while 273 stored at -20°C or manipulated at room temperature. Finally, all the data met the validation criteria set 274 by the FDA guidelines, rending this method suitable for future researches. 275 The evaluated LLOQ for diphenylamine (422.5 µg/kg), tolylfluanid (868.0 µg/kg), propargite (976.2 276 μg/kg) and phosalone (919.5 μg/kg) are higher than the values published by other authors in the context 277 of biomonitoring studies. Indeed, for diphenylamine and propargite, Marschner et al. [41] obtained an 278 LLOQ of 166.5 µg/kg on animal liver. Moreover, the phosalone LLOQ published by Russo et al. [26] 279 was 15 µg/kg of human liver.





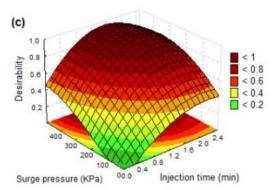


Fig. 1. Response surface and contour plots of (a) injection time and injection temperature, (b) surge pressure and injection temperature and (c) surge pressure and injection time on the

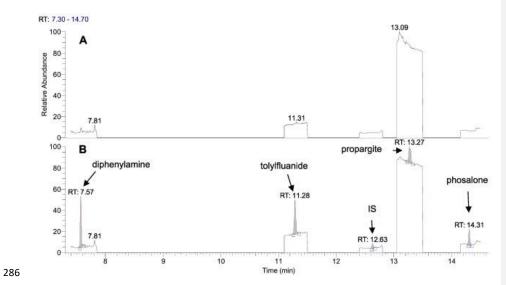


Fig. 2. Hepatocytes liver extract chromatograms, A: blank sample, B: sample at the LLOQ.

Table 6. Results of the analytical method validation: linearity (n = 6), recovery (n = 3), within-run accuracy (n = 5), between-run accuracy (n = 2, 6 days).

Parameter	Dipher	ylamine	Tolylf	luanid	Prop	argite	Phos	salone	Limits
Linearity									
Slope	62,715	±285	274,740	±790	62,186	±295	40,608	±258	
Intercept	-6447	±2672	-18,292	±7398	5862	±2767	-5546	±2420	
\mathbb{R}^2	0.999	±0.001	1.000	± 0.000	± 1.000	± 0.000	0.999	± 0.001	
Recovery	R%	RSD%							
Low	99.0	1.2	96.5	1.9	98.1	1.1	99.3	2.0	
Medium	95.0	1.1	97.8	2.0	97.2	1.2	97.2	1.5	n.a
High	99.1	1.0	99.6	1.1	98.4	1.2	97.8	1.5	
Accuracy									
Intra-day	Ar%	RSD%							
Low	98.2	3.9	93.7	3.5	84.4	2.1	99.7	3.2	±20%, ≤20%
Medium	93	1.5	99.1	2.8	96.3	1.8	95.7	2.2	±15%, ≤15%

Parameter	Diphe	nylamine	Toly	fluanid	Pro	pargite	Pho	salone	Limits
High	99.6	1.3	100.3	1.3	92.6	1.6	98.3	2.1	
Inter-day	Br%	RSD%							
Low	96	6.2	99.5	5.8	95.6	6.5	102.9	6.6	±20%, ≤20%
Medium	92.4	4.9	93.2	4.6	94.4	5.2	93.2	5.8	±15%, ≤15%
High	99.9	3.0	100.4	2.7	101.2	2.5	100.8	4.9	
Stability									
Cold-warm	SCt%								
-20/20 °C-15 h	100.2	1.1	99.8	1.2	100.0	1.3	99.8	1.0	±15%, ≤15%
Long term	SLt%								
1 month	100.3	1.4	100.1	1.3	99.7	1.5	100.5	1.2	±15%, ≤15%
6°months	99.8	1.2	99.6	1.1	99.8	1.3	100.1	1.4	
12 months	100.4	1.8	100.0	1.5	100.2	1.4	99.7	1.7	
Autosampler	SA%								
72 h	100.0	0.7	99.9	0.9	100.1	0.5	100.3	1.0	±15%, ≤15%

291 R%: percent recovery; RSD%: percent relative standard deviation.

Ar%: intra-day percent accuracy rate; Br%: inter-day percent accuracy rate.

SCt%: cold-war percent stability; SLt%: long term percent stability; SA%: autosampler percent stability.

4. Conclusion

In this paper, a simple and selective GC-MS method was developed to simultaneously determine the amounts of diphenylamine, tolylfluanid, propargite and phosalone in human liver samples. The instrumental settings were optimized to obtain the highest chromatographic responses for the above-mentioned compounds. The optimum splitless injection conditions obtained through RSM and global Derringer's desirability function were 271.7°C, 1.25 min and 490 KPa for injection temperature, splitless time and surge pressure, respectively.

Convenient optimization of simultaneous protein precipitation and LLE extraction conditions allowed to achieve very good recoveries and efficient sample purification using a user-friendly sample treatment. This one-step LLE and cleanup method followed by GC-MS analysis complied with current FDA requirements and showed satisfying selectivity, linearity, recovery, precision and accuracy. The limits

of quantification obtained in this work are satisfying, considering previously published works related to human and animal liver samples. This procedure is thus appropriate for the monitoring of the parent compound loss during $in\ vitro$ human 310 liver metabolism studies. Finally, upgrading it to a more sensitive technology (MS/MS) it may also be useful for conducting human or mammalian biomonitoring studies.

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313	Acknowledgements
314	This work was funded by the Agence Nationale de la Recherche (under reference ANR-2008-CESA-
315	016-01) by the Office National de l'Eau et des Milieux Aquatiques (ONEMA) and by the Agence
316	Nationale de SÉcurité Sanitaire de l'alimentation, de l'environnement et du travail (ANSES) in the
317	frame of the MEPIMEX Project.
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