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(Article begins on next page)

1 **A step forward in the equivalence between thermal and differential-flow**
2 **modulated comprehensive two-dimensional gas chromatography methods**

3

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19

20 **Abstract**

21 Comprehensive two-dimensional gas chromatography (GC×GC) based on flow-modulation (FM) is
22 gaining increasing attention as an alternative to thermal modulation (TM), the recognized GC×GC benchmark,
23 thanks to its lower operational cost and rugged performance. An accessible, rational procedure to perform
24 method translation between the two platforms would be highly valuable to facilitate compatibility and
25 consequently extend the flexibility and applicability of GC×GC. To enable an effective transfer, the
26 methodology needs to ensure preservation of the elution pattern, separation power, and sensitivity.

27 Here, a loop-type thermal modulation system with dual detection (TM-GC×GC-MSD/FID) used for the
28 targeted analysis of allergens in fragrances is selected as reference method. Initially, six different columns
29 configurations are systematically evaluated for the flow-modulated counterpart. The set up providing the
30 most consistent chromatographic separation (20 m x 0.18 mm d_c x 0.18 μm d_f + 1.8 m x 0.18 mm d_c x 0.18
31 μm d_f) is further evaluated to assess its overall performance in terms of sensitivity, linearity, accuracy, and
32 pattern reliability. The experimental results convincingly show that the method translation procedure is
33 effective and allows successful transfer of the target template metadata. Additionally, the FM-GC×GC-
34 MSD/FID system is suitable for challenging applications such as the quantitative profiling of complex
35 fragrance materials.

36

37

38 **Key-words:**

39 Two-dimensional comprehensive gas chromatography-mass spectrometry and flame ionization detection;
40 reverse-inject differential flow modulation; suspected fragrance allergens; method translation; method limit
41 of detection; repeatability and precision

42 1. Introduction

43 Comprehensive two-dimensional gas chromatography GC×GC coupled with mass spectrometry (MS)
44 is a powerful technique for detailed profiling and effective fingerprinting of medium-to-high complexity
45 samples. Thermal modulators implementing cryogenic cooling are widely used and, to date, considered the
46 “gold standard” for GC×GC. The effective in-space band-focusing induced by this modulator results in a peak
47 capacity gain (G_n) that is close to the achievable theoretical limit [1]. At the same time, the signal-to-noise
48 ratio greatly increases resulting in a sensitivity gain of one order of magnitude compared to a conventional
49 1D-GC analysis. Despite these advantages, thermal modulators have some drawbacks related to hardware
50 and operational costs limiting their widespread adoption in quality control and high-throughput screening.

51 Differential-flow modulators (FMs), such as those based on the Seeley *et al.* design [2,3], are an
52 interesting alternative to thermal modulators (TMs). Configurations can have an adjustable volume/length
53 accumulation loop, as those proposed by Tranchida *et al.* [4–6]. Large accumulation loop volumes limit the
54 overloading, extends the re-injection period and provides multi-stage dynamics with some benefits on
55 separation power and peak symmetry. The first commercial FM used fixed volume accumulation loop devices
56 obtained with Capillary Flow Technology (CFT) microfluidic plates. They implement both the forward fill/flush
57 (FFF) injection dynamics described by Seeley *et al.* [7] and the reverse fill/flush (RFF) dynamics connoted by
58 a more efficient band re-injection, improved 2D peak widths and symmetry, and effective handling of
59 collection-channel overloading [8–12]. Commercial RFF modulators are available from Agilent Technologies
60 [13] and by Sep-Solve with the FM named Insight™ [14]. More recently, Seeley *et al.* [15] proposed the multi-
61 mode modulator (MMM). This device, as it is engineered in the commercial platforms by LECO (Flux™),
62 enables the adoption of conventional column combinations and carrier gas operational flow in both
63 separation dimensions but is characterized by a low duty cycle.

64 The growing interest in robust and cryogen-free modulators certainly is driven by the possibility they
65 offer to describe in depth the chemical dimensionality of samples [16] with a relative ease of use and low
66 operational costs. FM gives access to peculiar features of GC×GC separations such as group-type
67 characterization, accurate profiling, and advanced fingerprinting based on 2D separation patterns [17–21].
68 However, FM dynamics are connoted by a limited flexibility in terms of operative flows in the two separation
69 dimensions which in turn require a careful selection of column dimensions/characteristics to fully exploit the
70 separation potential.

71 If the price to pay is mainly related to the actual separation power of the system, absolute method
72 sensitivity is another important issue to consider; to date this method characteristic lacks of dedicated
73 research especially in the perspective of application transfer between TM to FM platforms. This study fills
74 this gap by systematically examining six different column combinations, almost equivalent to a reference TM
75 system, for their chromatographic performances and method’s figures of merit. Method translation
76 principles [22–25] are here applied for a rational and effective translation of the reference methodology

77 developed for a loop-type TM system to the six FM tested column configurations, instead of a trial-and-error
78 approach to set chromatographic parameters. By this rational approach, the first-dimension (¹D) elution
79 order and resolution of the original TM method are preserved and resulting 2D peak patterns are coherent
80 between mutually translated methods. At the same time, in view of routine applications, analysis speed is
81 also evaluated.

82 The best performing configuration is then examined for method performance parameters in terms
83 of linearity over a 3 order of magnitude in analytes concentrations, sensitivity and quantitation accuracy. As
84 a challenging application, raw fragrance materials of medium complexity are considered and a selection of
85 targeted analytes referred to as “established contact allergens in humans” by the EU Scientific Committee
86 on Consumer Safety [26] are subjected to quantitative profiling. They included 60 analytes (single compounds
87 or mixtures of isomers) covering a wide range of polarity and volatility.

88

89 **2. Materials and methods**

90 **2.1 Raw materials, pure reference compounds and solvents**

91 Pure standards of *n*-alkanes (from *n*-C9 to *n*-C25) for Linear Retention Indices (*I'*) calibration were
92 from Merck (Milan, Italy). Pure standards (or isomers mixtures) of tested analytes listed in **Table 1** were
93 purchased from Merck (Milan, Italy) or kindly provided by Firmenich SA (Geneva, Switzerland). Solvents
94 (cyclohexane and dichloromethane) were all HPLC-grade from Merck (Milan, Italy). Pure standards of 1,4-
95 dibromobenzene and 4,4'-dibromobiphenyl used as Internal Standards (ISTDs) were from Merck (Milan,
96 Italy).

97 Commercial raw fragrance materials for accuracy assessment were kindly provided by Farotti srl
98 (Rimini, Italy). Test sample #1 (TS1) consisted of a *citrus-like* fragrance while test sample #2 was a *flowery-*
99 *like* fragrance (TS2).

100

101 **2.2 Reference solutions and calibration mixtures**

102 Standard Stock Solutions (SS) of reference analytes were prepared at a concentration of 10 mg/mL
103 in dichloromethane or cyclohexane and stored at -18°C. The Model Mixture (MMix) stock solution was
104 prepared by mixing suitable amounts of SS at a final concentration of 200 mg/L in cyclohexane. Fresh
105 calibration solutions were prepared every week by diluting suitable amounts of MMix in cyclohexane.
106 Calibration levels covered were: 0.1-0.2-0.5-1-5-10-20-50-100 mg/L. ISTDs were at a final concentration of
107 50 mg/L. Standard reference solutions for purity evaluation (by 1D-GC-FID) were prepared from SS at a
108 nominal concentration of 100 mg/L in cyclohexane.

109 Raw fragrances TS1 and TS2 were diluted 20% (w/v) immediately before analysis in cyclohexane. For
110 accuracy evaluation, spiked samples were prepared by adding suitable volumes of MMix up to +10 mg/L and
111 +1 mg/L concentration levels. ISTDs were added to all analyzed samples at 50 mg/L.

112 **2.3 GC×GC with reverse-inject differential flow modulation: instrument set-up**

113 GC×GC analyses with reverse-inject differential flow modulation were run with a GC-MS system
114 consisting of an Agilent 7890A GC unit provided with a 4513A auto injector sampler (Agilent, Little Falls, DE,
115 USA) and coupled to an Agilent 5977B HES (High Efficiency Source) fast quadrupole MS detector (Agilent,
116 Little Falls, DE, USA) operating in EI mode at 70 eV and a fast FID detector. The GC transfer line was set at
117 280°C. The MS was tuned using the *HES Tune* option. The scan range was set to m/z 40-240 with a scanning
118 rate of 12,500 amu/s to obtain a spectrum generation frequency of 28 Hz. The flame ionization detector (FID)
119 conditions were: base temperature 280°C, H₂ flow 40 mL/min, air flow 350 mL/min, make-up (N₂) 20 mL/min,
120 and sampling frequency 200 Hz.

121 The system was equipped with a reverse-inject FM (Supplementary Material **Figure SF1**) consisting
122 of a CFT plate connected to a three-way solenoid valve that receives a controlled supply of carrier gas
123 (helium) from an auxiliary electronic pressure control module (EPC). The CFT plate schematic and modulation
124 dynamics description are provided in the Supplementary Material (**SF1**).
125

126 **2.4 GC×GC with thermal modulation: instrument set-up**

127 The TM GC×GC system consisted of an Agilent 7890B GC unit with a 4513A auto injector sampler
128 (Agilent, Little Falls, DE, USA) coupled with a Bench TOF-Select™ time of flight mass spectrometer (Markes
129 International, Llantrisant, UK). Electron ionization was set at 70 eV. The ion source and transfer line were set
130 at 290°C. The MS optimization option was set to operate in Single Ionization with a mass range between 35
131 and 550 m/z; data acquisition frequency was 100 Hz; filament voltage was set at 1.60 V. For parallel
132 detection, the FID was set with a base temperature of 280°C, H₂ flow 40 mL/min, air flow 350 mL/min, make-
133 up (N₂) 20 mL/min, and sampling frequency 200 Hz.

134 The system was equipped with a two-stage KT 2004 loop thermal modulator (Zoex Corporation,
135 Houston, TX) cooled with liquid nitrogen controlled by Optimode™ V.2 (SRA Instruments, Cernusco sul
136 Naviglio, MI, Italy). The hot jet pulse time was set at 250 ms, modulation period was 5 s, and cold-jet total
137 flow was progressively reduced with a linear function from 35% of Mass Flow Controller (MFC) at initial
138 conditions to 5% at the end of the run.

139 Injections of the Calibration mixtures (CAL), as well as those for I^T_S determination, were carried out
140 with a 4513A auto injector under the following conditions: injection mode: split, split ratio: 1/20 for CAL and
141 1/50 for *n*-alkanes, injection volume 2 μL, temperature 270°C.
142

143 2.5 Column set, connections and auxiliary control modules

144 The reference method (i.e., TM-GC×GC) columns configuration and those tested with FM-GC×GC to
145 achieve comparable method performance are summarized in **Table 2**. Pressure settings (S/SL injector and
146 Auxiliary EPC), carrier gas (helium) volumetric flows in the two dimensions, linear velocities across capillaries,
147 and oven temperature programs also are reported. Calculations were by reference equations and/or by a
148 validated pneumatic model designed for the CFT plate [27].

149 Connections between the second-dimension (²D) column and deactivated silica capillaries toward MS
150 and FID for parallel detection were by a three-way un-purged splitter (G3181B, Agilent, Little Falls, DE, USA)
151 while columns connection in the TM-GC×GC was by deactivated ultimate unions (G3182-61580 Agilent, Little
152 Falls, DE, USA). ¹D columns DB-1, ²D columns OV17 and deactivated capillaries were from Agilent - J&W (Little
153 Falls, DE, USA).

154

155 2.6 Performance parameters: reference equations

156 To evaluate the performances of the tested FM configurations compared to the reference method,
157 several chromatographic performance parameters were considered. The reference parameters and
158 equations are described here.

159 Re-injection pulse width (² σ_i) directly affects the actual ² σ_t with an additive effect on ²D peak-
160 broadening due to the chromatographic process (² σ_c). Re-injection pulses were defined as peak standard
161 deviation (² σ_i) and estimated on un-retained solvent peaks from FID channel (200 Hz sampling frequency)
162 [28].

163 The net separation measure ($S_{GC\times GC}$) [29] describes system's separation ability under the experimental
164 conditions applied. $S_{GC\times GC}$ extends the concept of separation measure (S) to GC×GC separations [30] and
165 refers to the product of S in each chromatographic dimension:

$$166 S_{GC\times GC} = S_1 \times S_2 \quad \text{Eq. 1}$$

167 where S_1 and S_2 are calculated, for ¹D and ²D respectively, using the reference equation:

$$168 S = \Delta t / \sigma_{av} \quad \text{Eq. 2}$$

169 where Δt is the arbitrary time interval between two peaks a and b , $\Delta t = t_b - t_a$, and σ_{av} is the peak- standard
170 deviation (σ) of a and b :

$$171 \sigma_{av} = \frac{(\sigma_a + \sigma_b)}{2} \quad \text{Eq. 3}$$

172 In this study the time interval was that between the first (i.e., benzaldehyde) and the last (i.e., sclareol) eluting
173 peaks of the MMix for the ¹D and the P_M for the ²D.

174 Pattern coherence was evaluated by relative retention (RR) in the two chromatographic dimensions
175 [11] and taking as reference centroid methyl salicylate and sclareol as last eluting peak. In the ²D the relative
176 retention is normalized to P_M . Here follows reference equations:

177 ${}^1D RR = ({}^1D Rt_i - {}^1D Rt_{\text{methyl salicylate}}) / {}^1D Rt_{\text{sclareol}}$ **Eq. 4**

178 ${}^2D RR = ({}^2D Rt_i - {}^2D Rt_{\text{methyl salicylate}}) / P_M$ **Eq. 5**

179 Within method performance parameters, linearity in the calibration range (0.1 – 100 mg/L) was
 180 evaluated with the determination coefficient of the linear model (R^2) while limits of detection (x_{LOD}) for MS
 181 and FID channels were calculated according to EU guidelines [31] as:

182 $x_{LOD} = 3.9 \frac{s_{y,b}}{b}$ **Eq. 6**

183 where $s_{y,b}$ is the standard deviation of the blank signal and b is the slope of the calibration curve within the
 184 lower calibration levels (i.e., 0.1-1 mg/L).

185 Precision was estimated over a one-week validation protocol as repeatability [32] and expressed as
 186 percent relative standard deviation (% RSD). It was calculated on retention times in the two dimensions (1t_R
 187 and 2t_R) at all calibration points ($n=8$) and for all analytical replicates ($n= 2$). Repeatability on absolute and
 188 normalized 2D volumes were calculated for the analytical replicates in the middle of the calibration range at
 189 1 and 10 mg/L.

190 Accuracy was estimated initially at two spiking levels (i.e., 1 and 10 mg/L in the final sample) and for
 191 two commercial fragrances of medium complexity. Bias was expressed as *relative error* % according to the
 192 following equation:

193 $Relative\ error\ \% = \frac{(x_m - x_{exp})}{x_{exp}} \times 100$ **Eq. 7**

194 where x_m is the estimated amount and x_{exp} is the expected amount after spiking. Accuracy was established
 195 analysing TS1 and TS2 samples and spiked ones in triplicate. The *rel. err. %* reported in **Table 1** are those
 196 resulting from FID signals except for analytes affected by co-elutions and reported in the table with the
 197 symbol “\$”.

198 **2.7 Data acquisition and 2D data processing**

199 Data were acquired by TOF-DS software (Markes International, Llantrisant, UK) in the reference TM-
 200 GC×GC method and Enhanced MassHunter (Agilent Technologies, Little Falls, DE, USA) in the translated FM-
 201 GC×GC methods. 2D data were processed by GC Image® GC×GC Edition Software, Release 2.9 (GC Image, LLC
 202 Lincoln NE, USA).

203

204 **3. Results and Discussion**

205 **3.1 Background for the present study and reference method**

206 In previous studies, we successfully applied the principles of method translation from a reference
 207 method, implemented with a loop-type thermal modulator GC×GC-MS/FID platform, to a reverse-inject
 208 differential flow modulated GC×2GC-MS/FID platform [11,12]. The configuration tested in the FM-GC×GC
 209 consisted of a 1D with reduced internal diameter and length, compared to the reference set up, and two-
 210 parallel 2D columns each one directed to a different detector (MS and FID). The column combination included

211 a polyethylene glycol (PEG) stationary phase in the ¹D and 86% polydimethylsiloxane, 7% phenyl, 7%
212 cyanopropyl in the ²D. Based on the models developed by Blumberg and Klee [22,33], translatable
213 parameters were set to preserve ¹D peak elution order, ¹D peak capacity, and chromatographic resolution.
214 Temperature programming was therefore modified according to the estimated speed gain and corresponding
215 to the ratio between column void times (t_{Mref} and t_{Mtr}). The operation was supported by the method
216 translation software and available as free application on the web [34].

217 Results were satisfactory and included a reduction of a factor of 2 for the total analysis time (t_A) of
218 the translated method (32.67 min instead of 65.53 min of the original method) and the preservation of the
219 elution order and of the relative retention in the two chromatographic dimensions (i.e., pattern coherence).
220 Pattern coherence, between mutually translatable methods, enabled effective transfer of metadata from the
221 reference methodology by template matching algorithms [11,12,35].

222 More recently, Aloisi et al. [36] explored the possibility of defining an equivalent standard column set
223 between TM and FM GC×GC. Their strategy was driven by the choice of two equivalent column sets, in terms
224 of separation power, in consideration of the flow restrictions posed by the two systems. Their set up included
225 a TM platform with a ¹D 30 m x 0.25 mm d_c x 0.25 μ m d_f and a ²D of 1.5 m x 0.25 mm d_c x 0.25 μ m d_f with a
226 delay loop of 1.5 m x 0.18 mm d_c while the FM was with a ¹D 20 m x 0.18 d_c x 0.18 μ m d_f and a ²D of 5 m x
227 0.32 d_c x 0.25 μ m d_f . The two set-ups provided almost equivalent separation power (referred to the efficiency
228 expressed as number of theoretical plates N) and analytes relative retention in the two dimensions. However,
229 the FM method had lower sensitivity because of the compensation for the lower re-injection efficiency of the
230 FM system. The authors report that “... A sample amount 4 x higher was introduced onto the ¹D column in
231 the FM analysis, to compensate for the higher sensitivity of CM (i.e., cryo-modulator)” [36].

232 Although the sensitivity drop observed with the FM-GC×2GC-MS/FID set up in translated conditions
233 [12] was less drastic, the FM method did not match TM performances. In the mentioned study [12], cocoa
234 volatiles fingerprinting covered 75 of the 130 targeted peaks (58%) and 450 of the 595 (76%) reliable peak-
235 regions compared to the reference TM procedure.

236 In this study, to make a step forward in the direction of matching, at the same time, separation power
237 and sensitivity, the RFF FM modulator is tested in its full flexibility by combining three different ¹D columns
238 with two ²Ds for a total of 6 configurations. The application context is that of the routine quantification of
239 established volatile allergens in fragrances and the reference method that proposed by Belhassen *et al.* [37].
240 The system included a loop-type TM, with liquid nitrogen, and a parallel dual-secondary column/dual parallel
241 detection configuration (i.e., TM-GC×2GC-MS/FID). The linearity ranges examined were between 2-100
242 mg/kg for MS and 100-10,000 mg/kg for FID. Accuracy was good and quantitation bias was below 20% of
243 error for the majority of the analytes (85%) [37].

244 For this study, the reference TM method adopted for benchmarking FM configurations implied a
245 longer ¹D column, compared to that of Belhassen *et al.* [37], (e.g., 60 m x 0.25 mm d_c x 0.25 μ m d_f) and a

246 single ²D of wider diameter (e.g., 1.8 m × 0.18 mm d_c × 0.18 μm d_f). Parallel detection by time of flight mass
247 spectrometry (TOF MS) and FID was obtained by post-column splitting with a passive-tee junction and a flow
248 ratio of about 30:70 (MS/FID) in order to balance the relative sensitivity of the two channels. **Table 2** reports
249 in detail the reference method column configuration, helium carrier flows and linear velocities as they were
250 estimated by reference equations, oven programming and total analysis time (t_A), modulation parameters
251 and operative pressure at the inlet (p_i) at the midpoint between the two dimensions (p_{mid}) and at the tee-
252 union. The TM-GC×GC-TOF MS/FID method was tested for its linearity within 0.1 to 100 mg/L; calibration
253 levels below 1 mg/L were explored because of the industrial needs of a quantitation method able to monitor
254 regulated substances even below the conformity limits. The platform including TOF MS and FID (30:70)
255 enabled to cover this requirement for both channels. In addition, the larger ²D column d_c compensates for
256 the limited loadability of 0.1 mm d_c columns while helping in situations where highly abundant components
257 may overload it to the detriment of both ²D separations and TOF MS ionization efficiency.

258 Based on the reference method, the six different FM combinations are detailed in **Table 2** (Set-up
259 #1a and b; #2a and b; #3a and b). The rationale for their design was based on limitations due to the
260 modulation dynamics, which requires low carrier flow in the ¹D and high flows in the ²D. ¹D columns tested
261 were therefore 0.10 mm and 0.18 mm d_c with variable phase ratios to enable higher loadability (e.g., 10 m ×
262 0.10 mm × 0.1 or 0.4 μm d_f). ²D columns were set to afford adequate loadability and efficiency to match with
263 the benchmark peak-capacity. Chromatographic performance parameters were at first examined to evaluate
264 the best configuration. The next section reports experimental results on chromatographic performance in a
265 critical perspective.

266

267 **3.2 Chromatographic performances of FM-GC×GC-MS/FID in translated conditions**

268 The workflow to translate chromatographic parameters is visualized in the Supplementary Material
269 in **Figure SF2**. In practice, estimated operative pressures at the inlet (p_i) and outlet (p_{out} or p_{mid}) of the ¹D
270 column in the reference TM method are input in the calculator and used by the model to translate conditions
271 for the FM method. For the FM configuration, the p_i and p_{out} or p_{aux} are set based on the *a priori* fixed flow
272 conditions in both dimensions. The model calculates the oven temperature programming for the FM method
273 by normalizing it according to the system void time (t_m).

274 Each modulation period (P_M) was defined after a scouting run with each configuration and evaluating
275 the ¹D baseline peak-width (w_b) to obtain a comparable modulation ratio (M_R) for all methods [38].

276 Results are visualized as pseudocolored images in **Figure 1** for the MMix at 10 mg/L from the FID
277 signal. The accordance between relative retention in both chromatographic dimensions (i.e., pattern
278 coherence) was evaluated through peaks relative retention against a centroid (methyl salicylate) and the last
279 eluting peak (sclareol) for the ¹D and against the P_M for the ²D (**Eq. 4** and **Eq. 5**). Results are visualized in
280 **Supplementary Figure 3 (SF3)** for all configurations. The reference method, visualized in **Figure 1A**, was

281 characterized by an average re-injection pulse of 20 ms against an average value of 40 ms for the FM-GC×GC
282 (**Figure 2A**). The average $^1\sigma$ for reference peaks (first and last eluting) was 2.34 s with a resulting S_1 of 934
283 (**Figure 2C and 2D**). **Supplementary Table 1 (ST1)** reports $^1\sigma$ and $^2\sigma$ for all targeted peaks. On the other hand,
284 the best performing set for FM, considering only 1D separation efficiency by $^1\sigma$, was Set up #1a the one
285 combining 1D 10 m x 0.1 mm d_c x 0.1 μm d_f with a 2D of 0.18 mm d_c that showed an average $^1\sigma$ of 1.85 s.
286 However, the S_1 value of this combination was only 304 (**Figure 2D**) due to the lower capacity factors (k)
287 expressed by this set-up.

288 **Insert Figure 1 here**

289 Conversely, average $^2\sigma$ were almost comparable for all FM methods (average value of 0.11 s in **Figure**
290 **2E**) and, in turn, even better than those estimated for the reference method (i.e., $^2\sigma$ 0.17 s). For this reason,
291 all FM systems had comparable separation power in the 2D (**Figure 2F**) with S_2 values ranging between 23 for
292 the Set up #1a [10 m x 0.1 mm d_c x 0.1 μm d_f + 1.8 m x 0.18 mm d_c x 0.18 μm d_f] and 42 for the Set up #3b
293 [20 m x 0.18 mm d_c x 0.18 μm d_f + 2.5 m x 0.25 mm d_c x 0.25 μm d_f].

294 **Insert Figure 2 here**

295 The best performing approach in terms of separation power (i.e., $S_{GC\times GC}$) was Set up #3a, [20 m x 0.18
296 mm d_c x 0.18 μm d_f + 1.8 m x 0.18 mm d_c x 0.18 μm d_f], with a $S_{GC\times GC}$ value of 22809 against 27464 (~ 83%) of
297 the TM method and a shorter analysis time (~ 78%).

298 Based on these premises, the FM-GC×GC-MS/FID set up #3a, consisting of [DB1 of 20 m x 0.18 mm
299 d_c x 0.18 μm d_f + OV17 of 1.8 m x 0.18 mm d_c x 0.18 μm d_f], was selected to proceed with the evaluation of
300 performance parameters in a one-week validation protocol. The next section reports experimental results on
301 linearity, limit of detection (LOD), pattern reliability, and accuracy.

302

303 **3.3 Method performance parameters of the translated FM-GC×GC-MS/FID**

304 **3.3.1 Linearity**

305 The calibration ranges explored for reference and translated methods were designed to span 3 to 4
306 orders of magnitude of concentrations, as it is in general with natural and synthetic fragrance materials
307 [37,39]. Calibration at low levels, between 0.1 and 1 mg/L, was explored to cover trace amounts for analytes
308 of concern.

309 The reference method confirmed its good linearity at the MS channel (TIC signal) within both: (a) the
310 0.1-20 mg/L range with a median R^2 of 0.9983 – mean 0.9980 (min 0.9954 / max 0.9998); and (b) in the full
311 range 0.1-100 mg/L with median R^2 of 0.9942 – mean 0.9902 (min 0.9522 / max 0.9999). Benzaldehyde
312 exhibited the worst performance with R^2 0.9522. Linearity at the FID was satisfactory; the median value for
313 R^2 was 0.9963 – mean 0.9959 (min 0.9949 / max 0.9987) within 0.1-100 mg/L although better performances
314 were registered in the higher calibration range (10-100 mg/L) with R^2 median value of 0.9996 – mean 0.9995
315 (min 0.9984 / max 0.9999). The reference method mean (red cross mark) and median (red line) are reported

316 in red in the scatter plot of **Figure 3A** showing linearity results. R^2 values calculated on linear regression
317 models for the translated method are reported in **Table 1**.

318 **Insert Figure 3 here**

319 The translated candidate method exhibited very good linearity; it has to be considered that the FM-
320 GC×GC includes a single quadrupole MS with high efficiency source (HES) and actual sampling frequency was
321 lower (i.e., 28 Hz) compared to the TOF MS operating at 100 Hz. Despite these configuration differences, the
322 qMS data was highly satisfactory, with results visualized in the scatter diagrams of **Figure 3A**. Median R^2 value
323 for the MS TIC signal was 0.9967 – mean 0.9957 (median – green line / mean – green mark) with a min of
324 0.9850 for hexadecanolactone and a max of 0.9994 for eugenyl acetate in the range 0.1-20 mg/L. Conversely,
325 FID in the full range (0.1-100 mg/L), had median value for R^2 of 0.9972 – mean 0.9964 (median – green line /
326 mean – green mark) with a min of 0.9784 for damascenone delta and a max of 0.9995 for
327 dimethylbenzylcarbonyl acetate (DMBCA).

328 Results indicate that, in terms of linearity within the examined ranges, FM-GC×GC-MS/FID has
329 performances comparable to the reference method. The FID channel has indeed better linear models
330 although, as it will be discussed in the next section, absolute sensitivity for this channel is slightly lower.

331 3.3.2 Limit of detection

332 Absolute sensitivity was estimated according to the EU guidelines for food and feed [31], generally
333 more restrictive than those for other fields of application (**Eq. 6**). Results are reported as histograms in **Figure**
334 **4** for FID (**Figure 4A**) and MS (**Figure 4B**). On average, the MS detection channel had higher sensitivity: the
335 mean LOD value of the reference method was 7.25 $\mu\text{g/L}$, with a maximum value for sclareol (i.e., 29.5 $\mu\text{g/L}$)
336 and a minimum for limonene (i.e., 2.93 $\mu\text{g/L}$). The translated method followed exactly the same trend with
337 slightly higher LODs (+ 1.4%). To note: the two platforms were equipped with different MS systems,
338 consequently this data should be read in light of linearity performances. However, if one considers the FM-
339 GC×GC as a suitable system for routine controls, reliability in the established conditions are not affected by
340 the slower acquisition frequency of the qMS.

341 **Insert Figure 4 here**

342 In accordance to MS results, the FID channel sensitivity with the FM-GC×GC was perfectly comparable
343 to that of the TM-GC×GC, revealing an average LOD of 6.36 $\mu\text{g/L}$ vs. 6.25 $\mu\text{g/L}$ of the TM (+ 1%).

344 LODs also inform about the relative sensitivity of the two detectors (i.e., MS and FID) and, at the
345 same time, confirm that TIC MS exceeds FID of a factor of 2.3. Of course, by selecting diagnostic ion traces,
346 MS can be even more sensitive and, at the same time, more flexible enabling to overcome co-elution issues.

347 The next section examines pattern reliability, through retention times precision and responses
348 stability.

349 3.3.3 Repeatability: retention times and responses

350 Retention time stability is a fundamental characteristic for GC×GC separations, since a primary

351 criterion for analytes identification is their position in the 2D pattern. **Table 1** reports precision data,
352 expressed as RSD % on 1t_R and 2t_R calculated over 8 calibration points and 2 analytical replicates each (n=16
353 runs). Along the 1D , absolute retention times for the FM method were highly similar showing a RSD % of 0.12.
354 Slightly higher values were obtained for 2D retention, with a RSD% of 0.98. To note, retention of analytes
355 with 2D tailing and/or distortion effects is less precise; linalool resulted in a 1.55 RSD % while vanillin and α -
356 amylocinnamaldehyde had RSD% of 1.40 and 1.68 respectively.

357 Responses were indeed highly stable; for the FID channel, absolute 2D volumes registered an average
358 precision of 3.51 % (RSD) while normalized values (over respective ISTDs) were on average 2.71%. The TIC
359 MS signal was comparable with RSD% of 3.30 and 3.20 for absolute and normalized responses, respectively.

360 The next section briefly presents accuracy data on medium complexity fragrances spiked at 1 and 10
361 mg/L levels.

362 3.3.4 Accuracy: medium complexity fragrance mixtures

363 Accuracy was preliminarily assessed for targeted analytes spiked in commercial raw fragrances at 1
364 and 10 mg/L concentration levels. Bias was expressed as *relative error %* (**Eq. 7**) and calculated on the FID
365 signal. In case of co-elutions, the TIC-MS data were adopted and indicated in Table with the symbol “\$”.
366 Results are reported in **Table 1** and visualized as scatter plots in **Figure 3B**. Supplementary Figure **SF4** shows
367 pseudocolored chromatographic images of raw commercial fragrances spiked at 1 and 10 mg/L together
368 with targeted peaks template (coloured circles) and connection lines for ISTDs.

369 The *relative error* at the higher spiking level (i.e., + 10 mg/L) was lower for *flowery-like* TS2 sample
370 with a median of 6.16 %, calculated on absolute values, compared to the 8.82% at the lower level (i.e., + 1
371 mg/L). For the *citrus-like* TS1 sample, median values were 7.53% (+ 10 mg/L) and 5.8% (+ 1 mg/L). Minimum
372 and maximum error values were always below $\pm 30\%$. Results are in line with those validated for the same
373 analytes in the reference method [37], and indicate that the translated FM-GC \times GC-MS/FID method is a good
374 candidate for a routine quantification of targeted analytes in medium complexity fragrances.

375

376 **4. Conclusions**

377 This study evidences the flexibility of RFF FM-GC×GC while suggesting a rational approach to translate
378 chromatographic conditions by keeping coherent separation patterns and avoiding chromatographic
379 distortions (overloading of the accumulation loop, generation of asymmetrical 2D peaks etc.). Moreover, the
380 method translation enables the operator to obtain a separation power in line with a reference methodology
381 with TM-GC×GC and, thanks to a rational procedure, to exploit the flexibility by acting on column
382 characteristics that have direct impact on re-injection efficiency and analysis time.

383 The best FM configuration, when tested for performances of interest in the context of quantitative
384 profiling, demonstrated linearity, sensitivity, and accuracy comparable to the TM counterpart. However, the
385 need for higher flows to the ²D of a FM system, at least to achieve adequate separation power, slightly limits
386 system performances resulting either in an equivalent separation power at the cost of sensitivity [33] or in a
387 sensitivity and quantitation consistency at the cost of ~20 % separation power.

388

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509
510

511 **Figure Captions:**

512 **Figure 1:** MMix calibration solution at 10 mg/L analyzed with the different configurations. **(1A)** reference TM-
513 GC×GC-TOFMS/FID; **(1B)** – FM Set-up #1a [DB1 10 m × 0.10 mm d_c × 0.10 μm d_f + OV17 1.8 m × 0.18 mm d_c ×
514 0.18 μm d_f]; **(1C)** – FM Set-up #1b [DB1 10 m × 0.10 mm d_c × 0.10 μm d_f + OV17 2.5 m × 0.25 mm d_c × 0.25 μm
515 d_f]; **(1D)** – FM Set-up #2a [DB1 10 m × 0.10 mm d_c × 0.40 μm d_f + OV17 1.8 m × 0.18 mm d_c × 0.18 μm d_f]; **(1E)**
516 – FM Set-up #2b [DB1 10 m × 0.10 mm d_c × 0.40 μm d_f + OV17 2.5 m × 0.25 mm d_c × 0.25 μm d_f]; **(1F)** FM Set-
517 up #3a [DB1 20 m × 0.18 mm d_c × 0.18 μm d_f + OV17 1.8 m × 0.18 mm d_c × 0.18 μm d_f]; **(1G)** – FM Set-up #3b
518 [DB1 20 m × 0.18 mm d_c × 0.18 μm d_f + OV17 2.5 m × 0.25 mm d_c × 0.25 μm d_f].

519
520 **Figure 2:** separation performances for the reference TM-GC×GC-TOFMS/FID method (red bars) compared to
521 translated FM- GC×GC-MS/FID set-up (#1a and b – grey; #2a and b blue; #3a and b green). Performances
522 refer to **(1A)** re-injection pulse width ($^1\sigma$); **(1B)** net separation measure ($S_{GC\times GC}$); **(1C)** ^1D peak-width expressed
523 as standard deviation ($^1\sigma$); **(1D)** ^1D separation measure (S_1); **(1E)** ^2D peak-width expressed as standard
524 deviation ($^2\sigma$); **(1F)** ^2D separation measure (S_2).

525
526 **Figure 3:** **(3A)** scatter diagram referring of linearity of calibration models (coefficient of determination R^2)
527 obtained with the FM-GC×GC-MS/FID method and set-up #3a; red marks report mean and median of the
528 reference methodology. **(3B)** shows accuracy results for the two tested raw materials spiked at 1 and 10 mg/L
529 level. Accuracy is reported as relative error % - see section 2.6 for details.

530
531 **Figure 4:** Histograms showing LOD values ($\mu\text{g/L}$) estimated for the TM- GC×GC-TOFMS/FID (reference – red
532 bars) and FM-GC×GC-MS/FID method and set-up #3a (green bars) on FID signal **(4A)** and TICMS signal **(4B)**.

533

534

535 **Table Captions:**

536 **Table 1:** List of analytes included in the MMix together with FM-GC×GC-MS/FID precision data on ¹D and ²D
537 retention times (¹*t_R* and ²*t_R*), 2D peak absolute volumes and normalized volumes on FID and MS channels;
538 linearity (*R*²) and accuracy (relative error %) at two spiking levels. “\$” refers to accuracy data calculated on
539 the TIC-MS signal instead of FID.

540

541 **Table 2:** Reference and translated methods settings, including: columns characteristics, initial head-pressure
542 (*p*_{*i*}), helium volumetric flows, and hold-up times on the basis of reference equations. Oven temperature
543 programming and total analysis time (*t_A*) are also reported. Operative conditions include also modulation
544 parameters.

545

Table 1

Compound Name	Precision - Repeatability								Linearity		Accuracy – Relative error %					
	¹ D Retention (¹ t _R)			² D Retention (² t _R)			FID – Responses %RSD		MS TIC – Responses %RSD		Citrus-like TS1		Flowery-like TS2			
	min	Stdev	%RSD	sec	Stdev	%RSD	Volumes	Norm. Vol.	Volumes	Norm. Vol.	R ² FID	R ² MS	+1 mg/L	+10 mg/L	+1 mg/L	+10 mg/L
1,4-Dibromobenzene	15.17	0.08	0.50	1.35	0.03	1.87	3.69	0.00	2.55	0.00	-	-	-	-	-	-
4,4'-Dibromobiphenyl	33.55	0.00	0.00	2.00	0.00	0.25	3.57	0.00	1.68	0.00	-	-	-	-	-	-
Benzaldehyde	8.70	0.00	0.00	1.21	0.01	0.63	0.45	1.63	2.07	4.39	0.998	0.994	-7.21	-2.27	-15.07	-12.29
α-Pinene	8.80	0.00	0.00	0.38	0.00	0.00	1.21	0.03	2.95	9.66	0.998	0.989	-5.06	-9.36	-0.22	-6.16
β-Pinene	9.85	0.00	0.00	0.51	0.00	0.57	2.02	0.84	0.90	0.07	0.996	0.999	-5.80	3.16	-0.11	-2.75
Benzyl alcohol	10.63	0.03	0.27	1.34	0.02	1.14	0.24	1.42	1.33	1.41	0.998	0.998	15.26	-6.18	-8.44	2.25
α-Terpinene	10.83	0.03	0.27	0.52	0.02	3.87	1.10	0.08	1.40	4.39	0.998	0.997	-21.40	-2.51	12.23	-2.78
Salicylaldehyde	10.88	0.03	0.26	1.34	0.01	0.65	0.70	1.88	3.32	2.60	0.998	0.998	19.74	22.04	-1.86	5.47
Limonene	11.15	0.00	0.00	0.51	0.01	2.03	1.81	0.63	2.59	2.06	0.996	0.990	-6.44	-7.62	-0.87	16.91
Terpinolene	12.75	0.00	0.00	0.64	0.01	1.20	14.58	13.41	2.11	2.91	0.993	0.998	-6.79	-0.10	-7.41	-13.09
Linalool	12.83	0.03	0.22	0.65	0.01	1.55	8.66	9.84	1.81	0.80	0.996	0.996	9.43	-15.61	1.62	-9.05
Camphor	13.95	0.00	0.00	1.13	0.01	0.89	3.24	2.06	0.72	1.10	0.998	0.997	6.39	2.05	-2.60	2.74
Menthol	14.90	0.00	0.00	0.72	0.01	1.44	2.73	1.55	0.69	3.33	0.995	0.996	-8.86	-1.21	-21.80	-0.30
Folione	15.17	0.03	0.19	1.11	0.01	0.45	2.61	1.43	5.63	5.58	0.994	0.997	-9.91	5.22	-6.26	-6.95
Methyl salicylate	15.23	0.03	0.19	1.28	0.01	0.98	2.51	1.33	4.29	4.42	0.997	0.998	-11.74	-0.67	-0.64 ^s	-13.38 ^s
α-Terpineol	15.33	0.03	0.19	0.88	0.01	1.19	3.13	1.95	8.65	1.31	0.997	0.997	-5.16	0.50	-3.82	-13.03
Citronellol	16.27	0.03	0.18	0.72	0.01	1.44	2.10	0.92	3.28	0.33	0.998	0.993	-2.79	-2.75	-8.83	-4.81
Neral	16.47	0.03	0.18	0.97	0.01	0.79	2.63	1.45	3.16	3.96	0.998	0.997	-1.36 ^s	6.28 ^s	-1.59	-5.68
Carvone	16.50	0.00	0.00	1.20	0.01	0.84	1.22	0.04	4.90	6.15	0.998	0.996	-8.43	0.36	0.60	-0.88
Cinnamaldehyde	16.90	0.05	0.30	1.76	0.01	0.72	3.78	2.60	4.32	6.27	0.998	0.997	-4.59	15.87	-6.79	8.98
Geraniol	16.93	0.03	0.17	0.84	0.01	1.19	0.67	0.51	2.82	3.90	0.998	0.995	17.64	7.77	9.97	8.58
Linalyl acetate	17.10	0.00	0.00	0.66	0.02	2.30	2.66	3.84	4.91	1.61	0.998	0.998	17.12	-6.75	-7.48	-1.31
Geranial	17.18	0.03	0.17	0.98	0.01	0.78	2.14	0.96	0.55	0.42	0.998	0.998	-16.86	11.12	-0.58 ^s	-5.43 ^s
Anise alcohol	17.30	0.05	0.29	1.81	0.02	1.12	1.24	2.42	4.67	8.44	0.998	0.995	-9.85	1.08	-13.22	-10.00
Hydroxycitronellal	17.47	0.03	0.17	1.03	0.01	1.28	2.02	0.84	0.51	0.86	0.997	0.997	-1.03	-3.02	-20.49	-3.19
Anethole trans	17.72	0.03	0.16	1.22	0.01	0.71	4.70	3.52	4.78	1.31	0.998	0.998	-8.64	-0.18	-10.81	-6.72
Cinnamyl alcohol	17.97	0.03	0.16	1.67	0.02	0.91	0.73	0.45	1.34	5.23	0.997	0.998	4.06	13.18	-15.09	8.44
DMBCA	18.65	0.00	0.00	1.07	0.01	1.18	1.03	0.15	3.73	1.81	0.999	0.998	5.08	1.92	-20.04	-6.82
Eugenol	19.47	0.03	0.15	1.34	0.01	0.43	3.28	2.10	1.68	4.40	0.998	0.998	0.03	5.80	-11.21	-10.68
Vanillin	20.05	0.05	0.25	2.15	0.03	1.40	11.32	10.15	11.65	1.31	0.997	0.996	15.05	16.41	12.39	4.13
δ-Damascone	20.22	0.03	0.14	0.94	0.00	0.31	11.86	10.69	5.32	4.68	0.978	0.997	0.31	-8.10	-7.76	0.42
Geranyl acetate	20.23	0.03	0.14	0.87	0.03	3.04	7.85	9.02	4.19	0.19	0.996	0.997	-3.15	13.68	16.80	-6.11
β-Damascenone	20.38	0.03	0.14	1.09	0.01	0.80	4.10	2.92	7.46	8.32	0.997	0.997	-4.00	2.41	-14.15	-4.19
α-Damascone	20.65	0.00	0.00	1.01	0.01	1.25	3.70	2.52	0.22	0.47	0.991	0.992	-6.62	-2.16	-11.71	6.89
Coumarin	21.00	0.05	0.24	2.59	0.03	1.16	2.49	1.31	3.93	3.14	0.997	0.994	-9.81	9.51	-12.50	-17.43
Majantol	21.02	0.03	0.14	1.19	0.01	1.11	4.08	2.91	6.62	1.70	0.998	0.995	-4.25	6.74	-7.89	4.30
β-Damascone	21.17	0.03	0.14	1.03	0.01	0.56	3.41	2.23	1.14	5.97	0.998	0.991	-6.38	-5.46	-14.72	-15.45
Isoeugenol (E)	21.75	0.00	0.00	1.43	0.01	0.73	3.17	1.99	3.03	2.75	0.998	0.998	-19.77	9.51	-14.49	3.96
β-Caryophyllene	21.87	0.03	0.13	0.70	0.01	1.43	3.54	2.36	4.12	7.26	0.993	0.996	-6.30	-1.75	-4.24	-1.37
Ebanol (Z isomer)	22.10	0.00	0.00	0.72	0.01	1.40	3.82	2.64	3.99	1.37	0.998	0.998	4.60	3.64	-13.60	-9.55
Ebanol (E isomer)	22.30	0.00	0.00	0.73	0.01	1.73	3.46	2.28	3.19	0.06	0.997	0.998	-2.12	3.69	-16.47	-8.40
Isomethylionone alpha	22.92	0.03	0.13	0.87	0.01	0.58	4.63	3.45	2.25	0.80	0.996	0.997	-4.56	-1.99	-5.61	-1.88

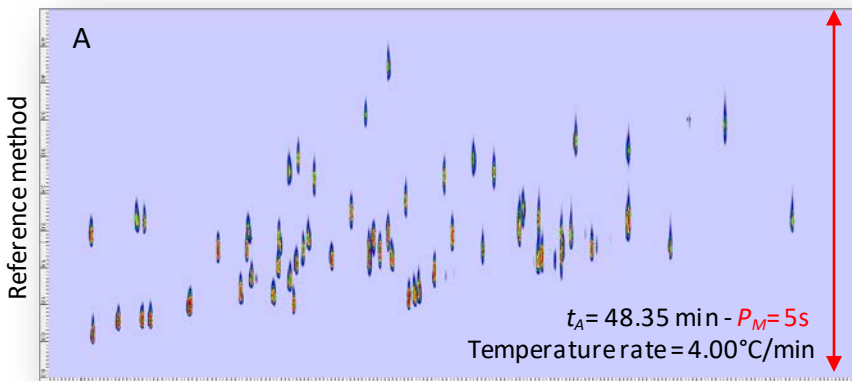
Eugenyl acetate	23.35	0.05	0.21	1.63	0.01	0.31	4.13	2.95	1.13	3.74	0.997	0.999	-9.11	10.74	-7.44	15.63
Lilial	23.67	0.03	0.12	1.19	0.00	0.24	4.18	3.00	2.51	4.43	0.997	0.996	4.33	-0.18	-5.39	-0.46
Propylidene phtalide	24.57	0.03	0.12	1.79	0.01	0.32	2.71	1.53	0.81	2.08	0.998	0.998	-27.26	9.69	-3.70	10.25
Amyl salicylate	24.93	0.03	0.12	1.03	0.01	0.84	0.28	0.90	6.05	2.63	0.995	0.994	-5.19	1.27	-14.88	-8.85
Isoeugenyl acetate	25.38	0.03	0.11	1.65	0.01	0.46	4.20	3.02	5.88	3.67	0.998	0.992	-9.74	13.06	-6.90	-2.71
Amylcinnamaldehyde alpha	26.47	0.03	0.11	1.24	0.02	1.68	0.21	1.39	5.26	5.58	0.984	0.993	-3.74	22.29	3.02	4.89
Lyr al (minor isomer)	26.48	0.03	0.11	1.34	0.01	0.65	11.57	10.40	3.63	5.56	0.996	0.999	3.32	-22.34	-9.54	-4.87
Lyr al (major isomer)	26.63	0.03	0.11	1.36	0.01	0.85	3.33	2.16	1.08	0.23	0.997	0.996	-11.96 ^s	14.81 ^s	-12.89	5.80
ISO E Super (major isomers)	27.23	0.03	0.11	0.97	0.01	1.07	3.99	2.81	2.33	1.08	0.998	0.996	-12.23	12.79	-10.56	10.33
Amylcinnamyl alcohol alpha	27.28	0.03	0.11	1.24	0.01	1.01	4.08	2.90	3.02	7.75	0.997	0.990	-5.37	10.41	-17.93	1.20
α-Santalol	27.42	0.03	0.11	0.98	0.01	0.51	2.87	1.69	2.28	5.97	0.996	0.994	-4.36	5.60	-23.17	-4.82
Farnesol	28.22	0.03	0.10	0.86	0.00	0.34	0.47	0.71	4.35	4.58	0.997	0.994	-2.05	9.18	5.50	-14.12
β-Santalol	28.25	0.00	0.00	1.07	0.01	1.17	3.50	2.32	6.66	2.70	0.997	0.998	-3.83	15.37	-12.40	-17.09
α-Hexylcinnamaldehyde	28.63	0.03	0.10	1.17	0.01	0.89	4.83	3.65	6.24	0.05	0.998	0.997	1.03	8.23	-9.73	5.06
Benzyl benzoate	28.78	0.03	0.10	1.88	0.01	0.53	5.25	4.07	7.76	3.91	0.997	0.997	-11.89	8.91	-19.23	-1.93
Acetylcedrene	29.48	0.03	0.10	1.08	0.01	0.71	3.93	2.75	0.09	0.60	0.997	0.999	-3.30	7.53	-11.61	6.86
Benzyl salicylate	31.00	0.05	0.16	1.76	0.01	0.59	1.87	3.04	1.32	0.40	0.997	0.997	2.85	12.59	2.01	10.91
Galaxolide (major isomers)	31.50	0.05	0.16	1.22	0.01	0.47	3.38	2.20	1.53	1.61	0.997	0.997	-4.21	10.25	-8.28	13.56
Hexadecanolactone	32.73	0.03	0.09	1.08	0.01	0.71	3.31	2.13	1.64	1.31	0.993	0.985	8.05	12.62	-10.55	2.86
Benzyl cinnamate	35.03	0.03	0.08	1.92	0.01	0.30	3.09	1.91	0.12	5.82	0.997	0.998	-5.41	19.90	-4.13	19.67
Sclareol	37.82	0.03	0.08	1.23	0.00	0.00	1.87	3.05	3.58	11.29	0.998	0.986	0.15	24.33	-8.06	15.02
Average	/	/	0.12	/	/	0.98	3.51	2.71	3.30	3.20	0.996	0.996	-3.07	4.58	-7.44	-0.69

Table 2

	¹ D	² D	Connections and capillaries	Oven programming	Modulation parameters
Reference method TM-GC×GC-TOFMS/FID	DB1 60 m × 0.25 mm d_c × 0.25 μm d_f He @ 2.0 mL/min - constant flow Initial head-pressure (p_i relative) 254.7 kPa Outlet pressure (p_{mid} absolute) 163.7 kPa Hold-up 3.52 min - Outlet velocity 46.97 cm/s	OV17 1.8 m × 0.18 mm d_c × 0.18 μm d_f He @ 2.0 mL/min - constant flow Initial head-pressure (p_{mid} absolute) 163.7 kPa Hold-up 1.8 sec - Outlet velocity 106.6 cm/s	Loop-capillary deactivated silica: 1.0 m, 0.10 mm d_c MS/FID split ratio 70:30 to MS: 0.7 m, 0.10 mm d_c to FID: 1.1 m, 0.18 mm d_c	60°C(1') to 280°C (10') @ 4°/min t_A = 48.35 min	P_M = 5s hot-jet pulse: 250 ms
Translated methods FM-GC×GC-MS/FID					
Set-up #1a	DB1 10 m × 0.10 mm d_c × 0.10 μm d_f He @ 0.27 mL/min - constant flow Initial head-pressure (p_i relative) 305.27 kPa Outlet pressure (p_{out} absolute) 278 kPa Hold-up 0.89 min - Outlet velocity 18.80 cm/s	OV17 1.8 m × 0.18 mm d_c × 0.18 μm d_f He @ 8.0 mL/min - constant flow Initial head-pressure (p_{out} relative) 177 kPa Hold-up 0.6 sec - Outlet velocity 292.57 cm/s	MS/FID split ratio 70:30 to MS: 0.5 m, 0.10 mm d_c to FID: 1.1 m, 0.18 mm d_c bleeding capillary: 6.37 m, 0.10 mm d_c	60°C(0.25') to 280°C (2.52') @ 15.89°/min t_A = 12.37 min; t_A % reduction: 25.6%	P_M = 2s pulse time: 150 ms
Set-up #1b	DB1 10 m × 0.10 mm d_c × 0.10 μm d_f He @ 0.27 mL/min - constant flow Initial head-pressure (p_i relative) 288.54 kPa Outlet pressure (p_{out} absolute) 253 kPa Hold-up 0.83 min - Outlet velocity 19.95 cm/s	OV17 2.5 m × 0.25 mm d_c × 0.25 μm d_f He @ 11.0 mL/min - constant flow Initial head-pressure (p_{out} relative) 151.94 kPa Hold-up 2.58 sec - Outlet velocity 225.65 cm/s	MS/FID split ratio 70:30 to MS: 0.5 m, 0.10 mm d_c to FID: 1.1 m, 0.18 mm d_c bleeding capillary: 5.11 m, 0.10 mm d_c	60°C(0.24') to 280°C (2.37') @ 16.87°/min t_A = 11.67 min; t_A % reduction: 24.1%	P_M = 4s pulse time: 150 ms
Set-up #2a	DB1 10 m × 0.10 mm d_c × 0.40 μm d_f He @ 0.27 mL/min - constant flow Initial head-pressure (p_i relative) 307.9 kPa Outlet pressure (p_{out} absolute) 278 kPa Hold-up 0.88 min - Outlet velocity 18.95 cm/s	OV17 1.8 m × 0.18 mm d_c × 0.18 μm d_f He @ 8.0 mL/min - constant flow Initial head-pressure (p_{out} relative) 177 kPa Hold-up 0.6 sec - Outlet velocity 292.57 cm/s	MS/FID split ratio 70:30 to MS: 0.5 m, 0.10 mm d_c to FID: 1.1 m, 0.18 mm d_c bleeding capillary: 6.37 m, 0.10 mm d_c	60°C(1.01') to 280°C (10.08') @ 3.97°/min t_A = 48.80 min; t_A % increase: 100.9%	P_M = 3s pulse time: 150 ms
Set-up #2b	DB1 10 m × 0.10 mm d_c × 0.40 μm d_f He @ 0.27 mL/min - constant flow Initial head-pressure (p_i relative) 291.29 kPa Outlet pressure (p_{out} absolute) 253 kPa Hold-up 0.83 min - Outlet velocity 20.01 cm/s	OV17 2.5 m × 0.25 mm d_c × 0.25 μm d_f He @ 11.0 mL/min - constant flow Initial head-pressure (p_{out} relative) 151.94 kPa Hold-up 2.58 sec - Outlet velocity 225.65 cm/s	MS/FID split ratio 70:30 to MS: 0.5 m, 0.10 mm d_c to FID: 1.1 m, 0.18 mm d_c bleeding capillary: 5.11 m, 0.10 mm d_c	60°C(0.95') to 280°C (9.5') @ 4.21°/min t_A = 46.05 min; t_A % reduction: 95.2%	P_M = 4.5s pulse time: 150 ms
Set-up #3a	DB1 20 m × 0.18 mm d_c × 0.18 μm d_f He @ 0.5 mL/min - constant flow Initial head-pressure (p_i relative) 227.73 kPa Outlet pressure (p_{out} absolute) 278 kPa Hold-up 2.72 min - Outlet velocity 13.34 cm/s	OV17 1.8 m × 0.18 mm d_c × 0.18 μm d_f He @ 8.0 mL/min - constant flow Initial head-pressure (p_{out} relative) 177 kPa Hold-up 0.6 sec - Outlet velocity 292.57 cm/s	MS/FID split ratio 70:30 to MS: 0.5 m, 0.10 mm d_c to FID: 1.1 m, 0.18 mm d_c bleeding capillary: 6.06 m, 0.10 mm d_c	60°C(0.77') to 280°C (7.74') @ 5.17°/min t_A = 37.85 min; t_A % reduction: 78.3%	P_M = 3s pulse time: 150 ms
Set-up #3b	DB1 20 m × 0.18 mm d_c × 0.18 μm d_f He @ 0.5 mL/min - constant flow Initial head-pressure (p_i relative) 207.12 kPa Outlet pressure (p_{out} absolute) 253 kPa Hold-up 2.52 min - Outlet velocity 13.21 cm/s	OV17 2.5 m × 0.25 mm d_c × 0.25 μm d_f He @ 11.0 mL/min - constant flow Initial head-pressure (p_{out} relative) 151.94 kPa Hold-up 2.58 sec - Outlet velocity 225.65 cm/s	MS/FID split ratio 70:30 to MS: 0.5 m, 0.10 mm d_c to FID: 1.1 m, 0.18 mm d_c bleeding capillary: 2.76 m, 0.10 mm d_c	60°C(0.72') to 280°C (7.16') @ 5.58°/min t_A = 34.95 min; t_A % reduction: 72.3%	P_M = 4.5s pulse time: 150 ms

Figure 1

TM-GC×GC-TOF MS/FID



FM-GC×GC-MS/FID

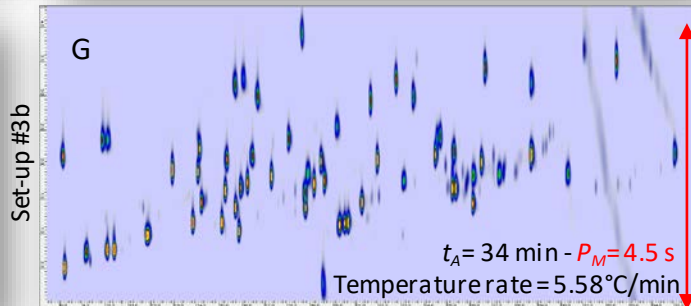
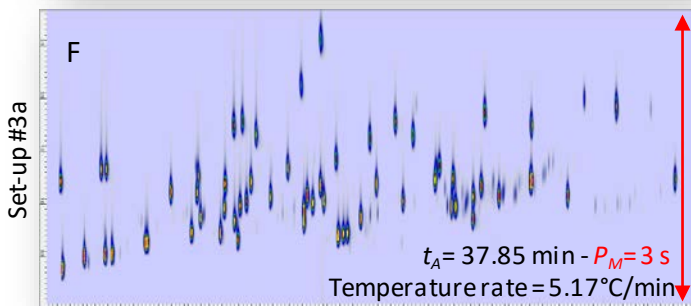
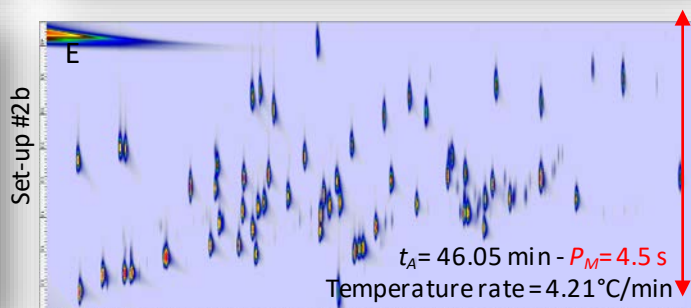
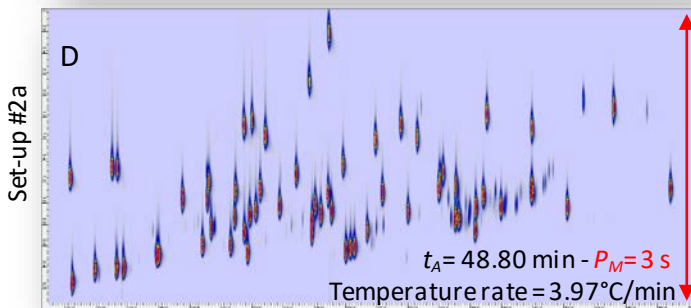
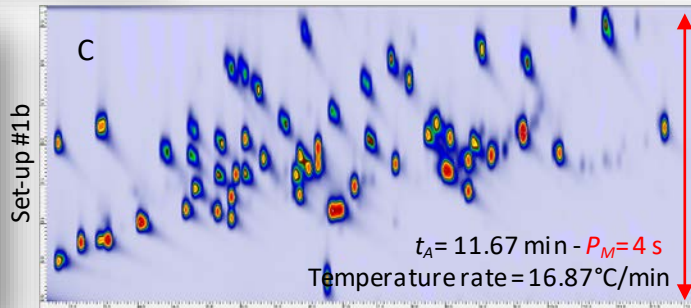
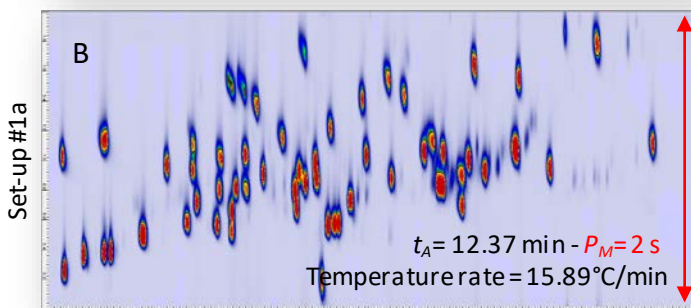


Figure 2

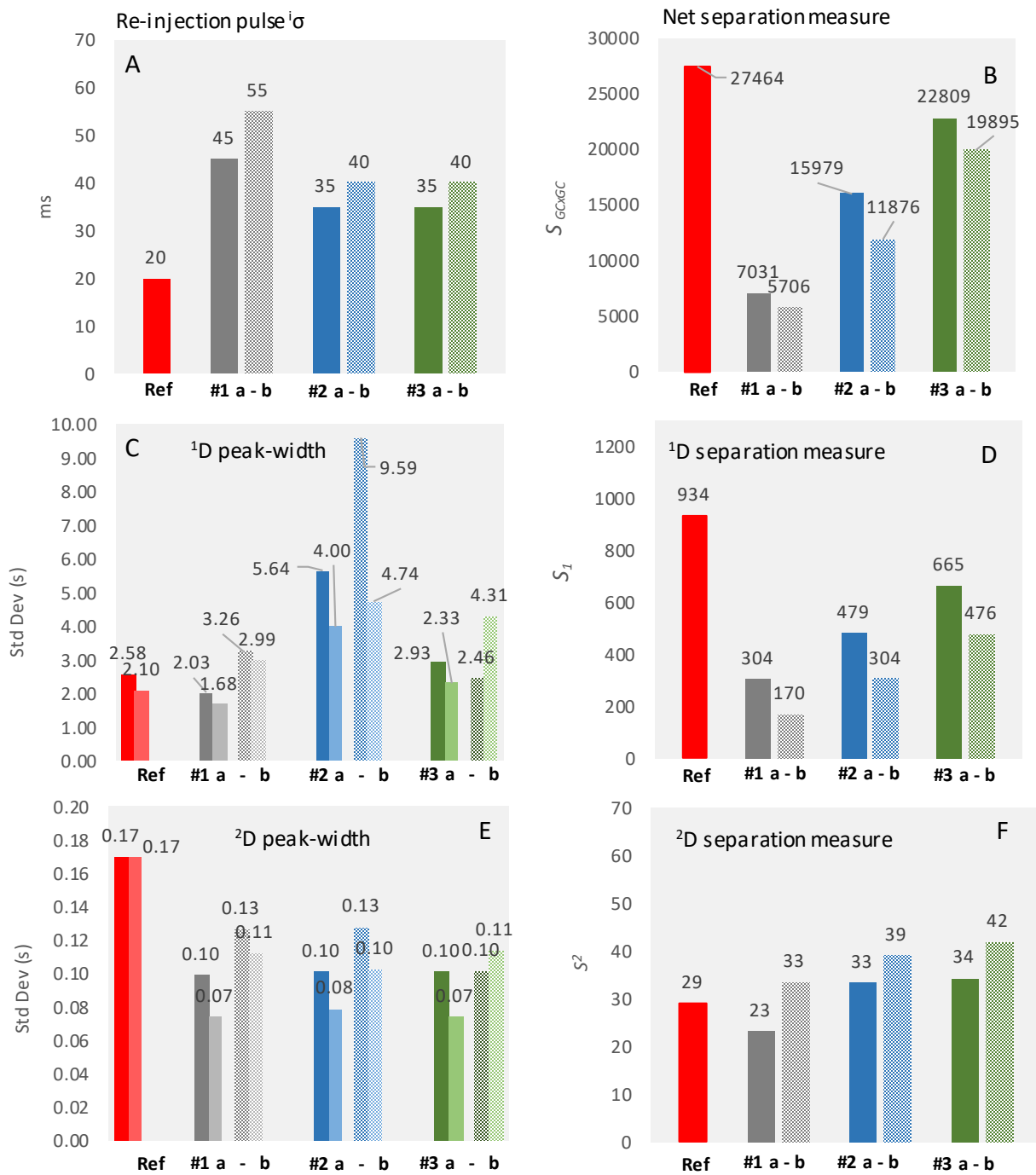


Figure 3

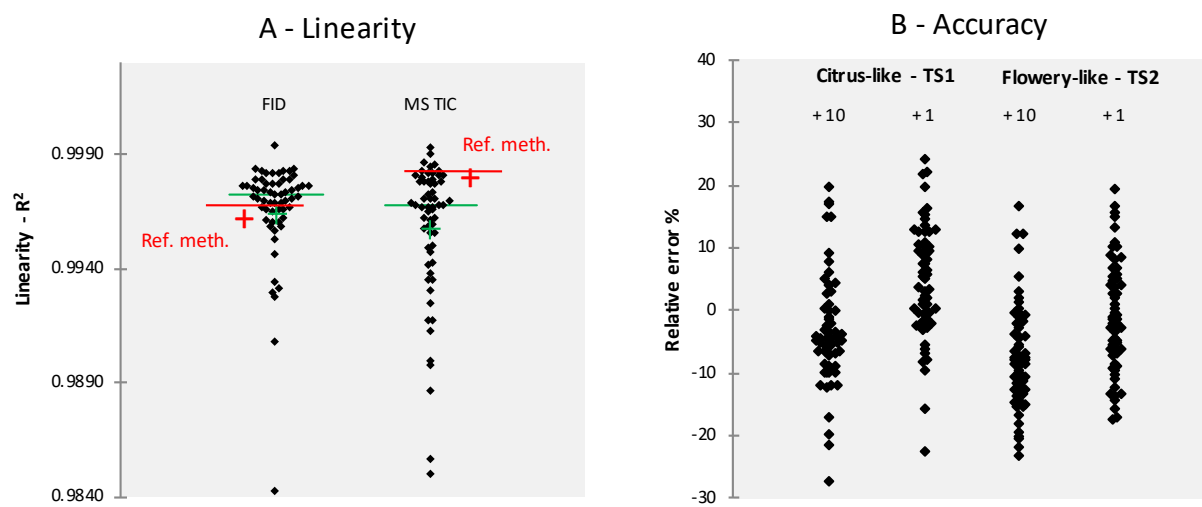
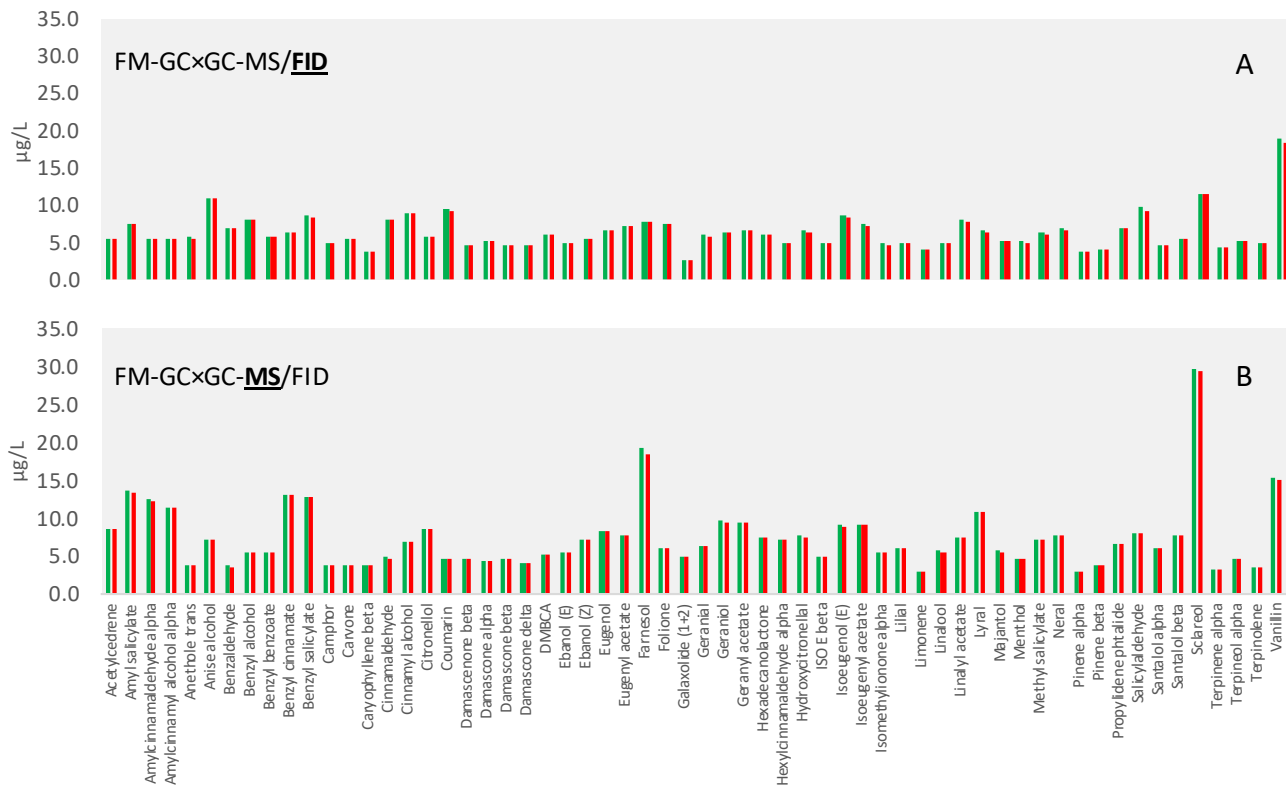


Figure 4



Supplementary Material

A step forward in the equivalence between thermal and differential-flow modulated comprehensive two-dimensional gas chromatography methods

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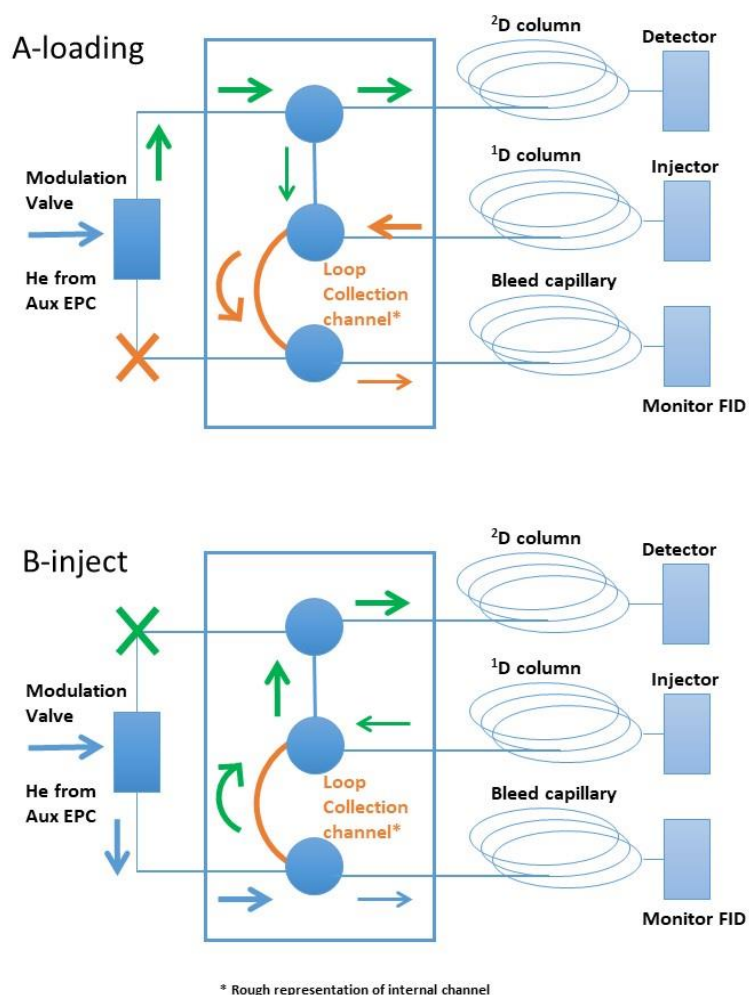
4. GC Image LLC, Lincoln, NE USA

5. Agilent Technologies, Gas Phase Separations Division, Wilmington DE, USA

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Figure SF1: schematic diagram of the differential-flow modulator implementing the reverse fill/flush (RFF) dynamics.



Analyses separated by the ^1D column enter at the center port of the modulator plate (^1D column in) and fill the fixed size collection channel, which is connected to a bleeding capillary port (bottom port). The length and diameter of the bleeding capillary are chosen according to the pressure/flow conditions of the columns to provide a minimal flow increase of about 10% to the output of the first column [1].

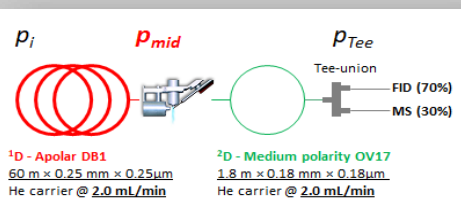
After loading the collection channel, the three-way solenoid micro-valve switches EPC module flow to the bottom post, the channel is flushed, typically for 0.10-0.20 seconds, in the reverse direction of the fill flow into the ^2D column at a suitable volumetric flow. The band enters into the ^2D columns and undergoes separation in a few seconds. The modulation cycle is then repeated.

[1] M. Giardina, J.D. McCurry, P. Cardinael, G. Semard-Jousset, C. Cordero, C. Bicchi, Development and validation of a pneumatic model for the reversed-flow differential flow modulator for comprehensive two-dimensional gas chromatography, *J. Chromatogr. A* 1577 (2018) 72–81. doi:10.1016/j.chroma.2018.09.022.

Figure SF2: step-by-step procedure for chromatographic parameters translation from TM-GC×GC to FM-GC×GC.

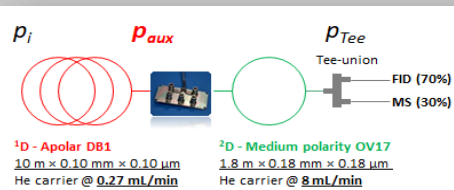
Step-1 Reference method TM-GC×GC

Calculation of initial head-pressure (p_i) and mid-point pressure (p_{mid}) at the junction of the two columns - use oven programming initial temperature as reference temp.



Step-2 Translated method FM-GC×GC

Calculation of initial head-pressure (p_i) and auxiliary carrier pressure (p_{aux}) at the modulator port feeding the ²D column. Pay attention to flow restrictions to avoid loop collection channel overloading.



Step-3 Translatable parameters calculation by method translation software

Column dimensions (blue box), initial head-pressures (p_i) and mid-point pressure (p_{mid}) or auxiliary carrier pressure (p_{aux}) at the modulator port are inputted in the dialog box. Reference method temperature programming (yellow box) is inputted in the corresponding dialog box. The model calculates the normalized temperature programming to be used (green dotted-line box).

Agilent Technologies Method Translator

Speed gain: 1,2921

Translate

Best Efficiency

Last file imported:

Original Method Parameters		Calculated Method Parameters	
Gas: He		Gas: He	
Length (m)	60 m	20 m	
Inner Diameter (µm)	250 µm	180 µm	
Film Thickness (µm)	0,25 µm	0,18 µm	
Phase Ratio	249,25	249,25	
Inlet Pressure (gauge)	254,7 kPa	227,73 kPa	
Outlet Flow (mL/min)	2 mL/min	0,5 mL/min	
Average Velocity (cm/s)	28,408 cm/sec	12,235 cm/sec	
Outlet Pressure (abs)	163,7 kPa	278 kPa	
Holdup Time	3,5202 min	2,7243 min	
Outlet Velocity (cm/s)	46,966	13,337	

Original Method Parameters				Calculated Method Parameters			
#	Ramp Rate (°C/min)	Final Temp (°C)	Final Time (min)	#	Ramp Rate (°C/min)	Final Temp (°C)	Final Time (min)
Init		60	1,00	Init		60	0,77
1	4,0000	280	10,00	1	5,1685	280	7,74

Total Run Time: 66,00 min (Original) / 51,08 min (Calculated)

Pressure Units: kPa

Original Column Capacity: 2,42

Translated Column Capacity: 0,61

The column capacity of the translated method is 25% of the original column capacity. You may need to adjust your injection volume.

(<https://www.agilent.com/en/support/gas-chromatography/gcmethodtranslation>)

Figure SF3: relative retention (RR) calculated for the two chromatographic dimensions and taking as reference centroid methyl salicylate and sclareol as last eluting peak. In the ²D the relative retention is normalized to P_M . RR reference equations:

$${}^1D RR = ({}^1D Rt_i - {}^1D Rt_{\text{methyl salicylate}}) / {}^1D Rt_{\text{sclareol}}$$

$${}^2D RR = ({}^2D Rt_i - {}^2D Rt_{\text{methyl salicylate}}) / P_M$$

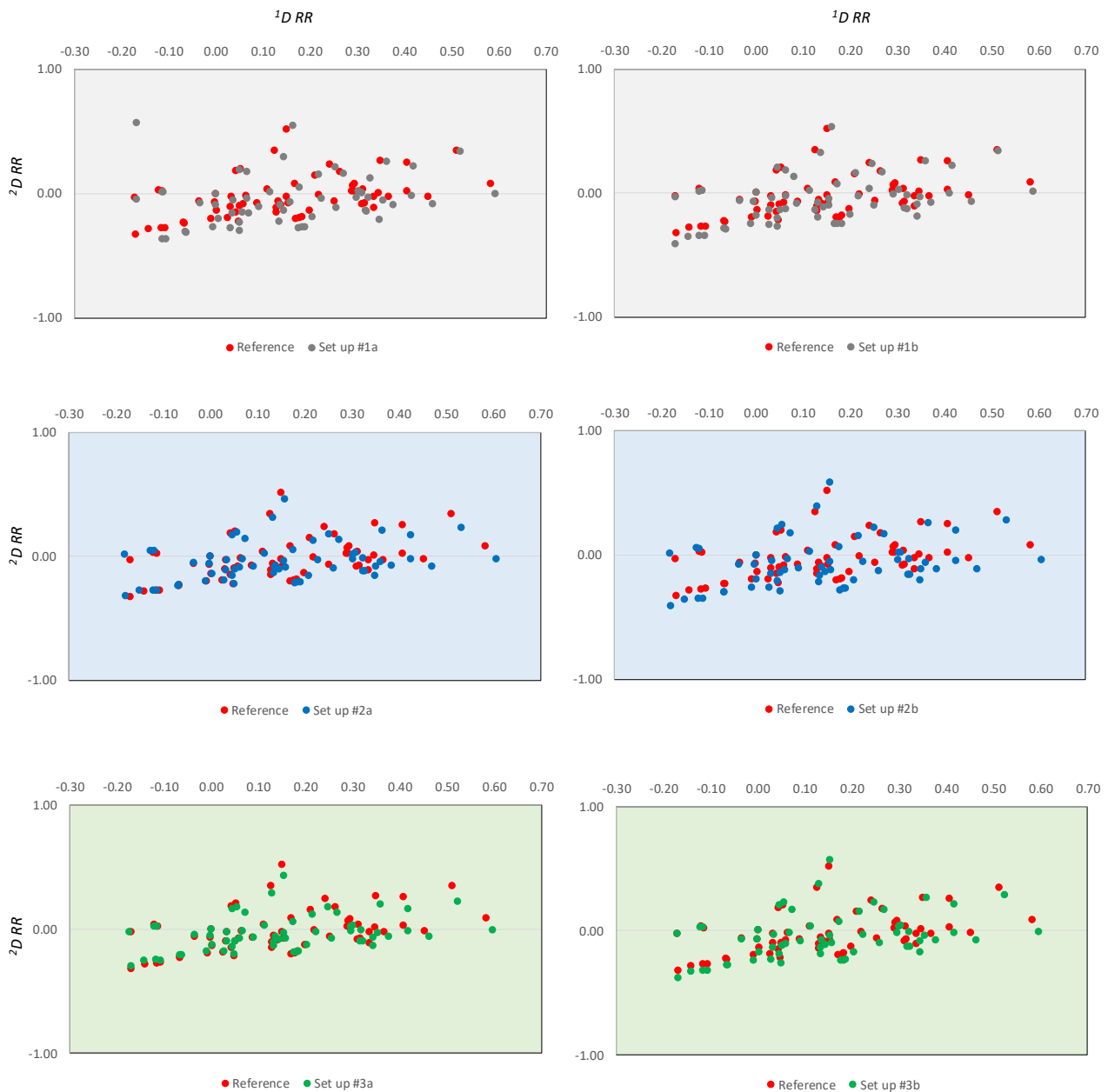
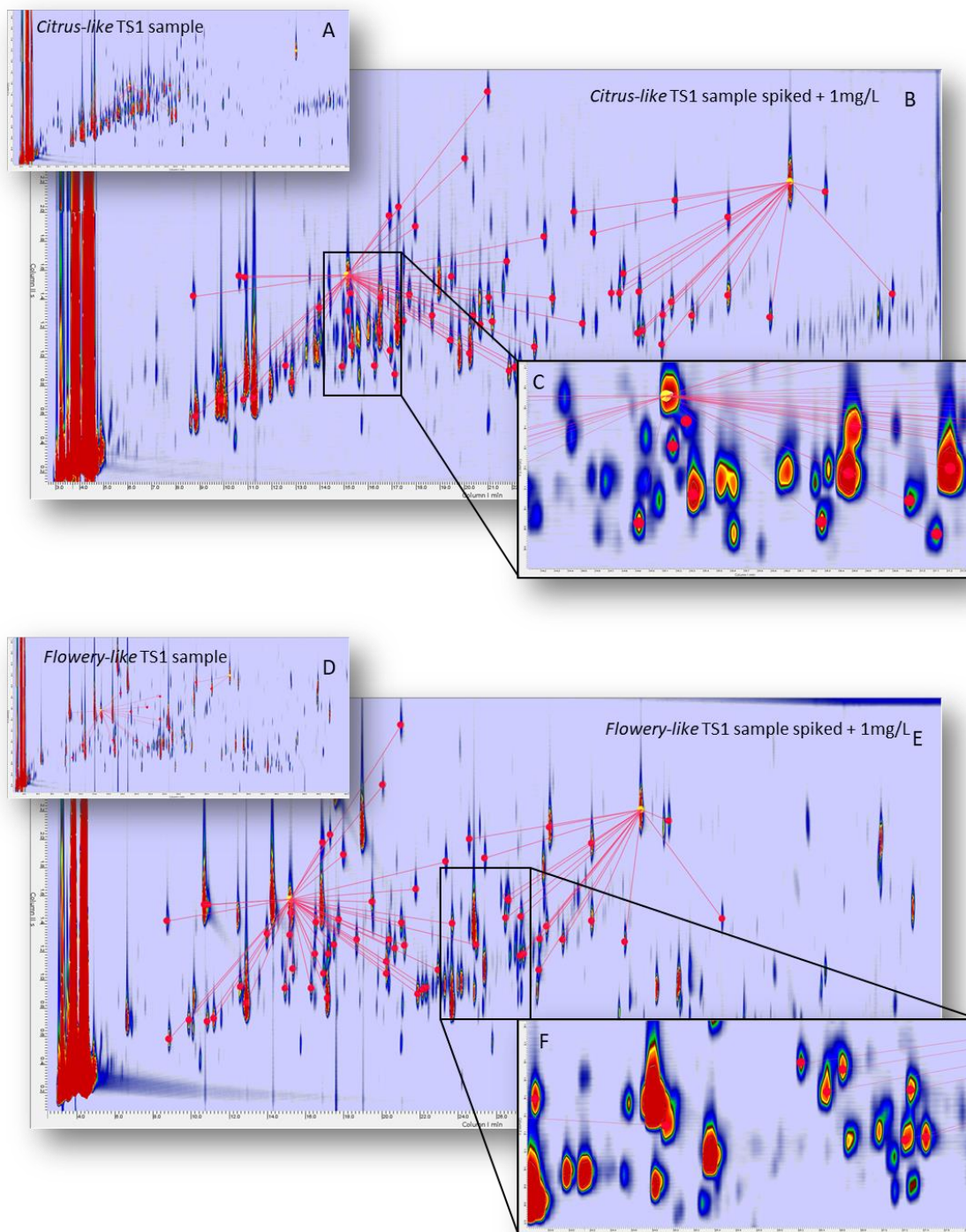


Figure SF4: contour plots of the tested raw fragrance materials (dilution 20% w/v). *Citrus-like* sample TS1 (A) and spiked at 1 mg/L level (B). *Flowery-like* sample TS2 (D) and spiked at 1 mg/L level (E). Enlarged areas in C and D show in higher detail some elution regions on the 2D patterns.

Analyses were by translated method conditions including a ¹D DB1 20 m × 0.18 mm d_c × 0.18 μm d_f and a ²D OV17 1.8 m × 0.18 mm d_c × 0.18 μm d_f .



Supplementary Table 1: list of analytes included in the MMix together with peak-widths expressed as standard deviation (σ) for all tested set ups. Retention times (1t_R and 2t_R) are reported for Reference TM and Set up #3a. A graphical visualization of the coherent relative retention between the two configurations is visualized in Supplementary Figure SF3.

Compound Name	Chromatographic performance – Peak standard deviation σ														Pattern coherence - t_R			
	Reference TM		Set up #1b		Set up #1b		Set up #2a		Set up #2b		Set up #3a		Set up #3b		Reference TM	Set up #3a		
	$^1\sigma$ sec	$^2\sigma$ sec	$^1\sigma$ sec	$^2\sigma$ sec	$^1\sigma$ sec	$^2\sigma$ sec	$^1\sigma$ sec	$^2\sigma$ sec	$^1\sigma$ sec	$^2\sigma$ sec	$^1\sigma$ sec	$^2\sigma$ sec	$^1\sigma$ sec	$^2\sigma$ sec	1t_R min	2t_R sec	1t_R min	2t_R sec
Acetylcedrene	2.94	0.17	2.25	0.07	3.19	0.11	2.55	0.07	2.47	0.10	1.79	0.08	2.68	0.09	37.92	1.96	29.50	1.07
Amyl salicylate	3.66	0.35	1.77	0.07	2.91	0.11	4.20	0.08	4.65	0.09	2.10	0.08	3.00	0.09	32.33	1.77	24.95	1.03
Anethole trans	2.87	0.13	1.68	0.06	2.44	0.09	5.18	0.08	6.59	0.10	2.39	0.10	2.63	0.10	23.25	2.00	17.75	1.21
Anise alcohol	4.11	0.19	2.41	0.05	2.45	0.10	4.61	0.14	5.83	0.15	3.16	0.11	3.59	0.12	22.75	3.10	17.35	1.79
Benzaldehyde	2.58	0.17	2.03	0.10	3.26	0.13	5.64	0.10	9.59	0.13	2.93	0.10	2.46	0.10	11.92	1.94	8.70	1.20
Benzyl alcohol	2.32	0.31	1.56	0.10	3.89	0.16	3.09	0.11	3.00	0.12	2.09	0.12	2.10	0.11	14.33	2.24	10.65	1.33
Benzyl benzoate	4.37	0.19	1.55	0.09	3.36	0.15	4.30	0.09	5.74	0.12	2.48	0.09	2.01	0.11	37.08	3.41	28.85	1.87
Benzyl cinnamate	4.06	0.18	1.83	0.10	2.31	0.11	5.10	0.10	5.50	0.13	2.70	0.09	1.91	0.13	44.92	3.81	35.05	1.92
Benzyl salicylate	3.77	0.35	1.39	0.07	3.44	0.15	4.67	0.09	5.78	0.12	2.40	0.09	3.57	0.12	39.83	3.36	31.05	1.75
Camphor	2.62	0.17	1.34	0.08	3.41	0.11	4.24	0.09	5.72	0.11	1.98	0.08	1.30	0.10	18.50	1.79	13.95	1.12
Carvone	2.51	0.16	1.92	0.08	3.05	0.11	4.08	0.09	4.41	0.11	2.44	0.09	2.08	0.10	21.75	1.96	16.50	1.19
Cinnamaldehyde	4.51	0.22	2.28	0.05	2.72	0.13	4.48	0.12	4.46	0.12	2.61	0.12	3.15	0.12	22.25	3.00	16.95	1.75
Cinnamyl alcohol	4.67	0.40	2.40	0.11	3.76	0.16	6.35	0.11	7.94	0.15	4.04	0.13	3.49	0.12	35.25	2.26	18.00	1.66
Citronellol	2.80	0.31	1.63	0.05	2.25	0.07	4.55	0.08	6.36	0.09	2.43	0.09	1.94	0.09	21.42	1.13	16.30	0.72
Coumarin	5.61	0.21	2.25	0.08	2.30	0.13	6.27	0.14	7.76	0.17	4.10	0.13	3.86	0.15	27.42	4.67	21.05	2.56
DMBCA	2.80	0.14	1.27	0.08	3.44	0.07	3.81	0.09	5.49	0.10	2.37	0.08	1.30	0.09	24.42	1.73	18.65	1.06
Ebanol (E isomer)	3.71	0.27	1.39	0.07	3.34	0.06	5.50	0.08	9.51	0.10	2.03	0.08	2.61	0.09	29.00	1.17	22.30	0.71
Ebanol (Z isomer)	3.12	0.18	0.96	0.07	3.34	0.06	2.62	0.08	3.39	0.10	2.03	0.07	2.61	0.09	28.75	1.11	22.10	0.71
Eugenol	3.53	0.45	2.15	0.09	3.64	0.12	4.65	0.09	5.36	0.11	2.64	0.10	2.61	0.10	25.50	2.26	19.50	1.34
Eugenyl acetate	2.69	0.32	1.71	0.07	2.22	0.08	3.26	0.09	6.19	0.12	2.14	0.09	1.30	0.11	30.33	2.84	23.40	1.62
Farnesol	4.33	0.09	1.92	0.05	6.26	0.09	4.27	0.05	7.70	0.08	3.92	0.05	3.04	0.08	36.42	1.53	28.25	0.86
Folione	2.72	0.07	1.89	0.05	3.83	0.09	2.88	0.05	9.35	0.09	2.39	0.05	1.98	0.08	20.08	1.74	15.20	1.11

Chromatographic performance – Peak standard deviation σ														Pattern coherence - t_R				
	Reference TM		Set up #1b		Set up #1b		Set up #2a		Set up #2b		Set up #3a		Set up #3b		Reference TM		Set up #3a	
Galaxolide (major isomers)	3.85	0.17	1.91	0.07	3.05	0.11	4.78	0.07	7.35	0.11	2.70	0.07	2.90	0.10	39.83	2.21	31.05	1.22
Geranial	2.82	0.14	1.83	0.08	1.43	0.08	3.37	0.09	3.65	0.10	2.41	0.09	2.08	0.09	22.58	1.60	17.20	0.98
Geraniol	2.71	0.13	1.55	0.04	3.32	0.07	3.63	0.10	5.84	0.09	3.12	0.09	2.31	0.08	22.25	1.33	16.95	0.83
Geranyl acetate	3.33	0.07	1.49	0.04	3.98	0.07	3.20	0.08	7.81	0.07	2.05	0.04	1.89	0.07	26.42	1.34	20.25	0.87
Hexadecanolactone	4.33	0.27	1.46	0.07	2.86	0.11	4.15	0.07	7.07	0.10	1.88	0.07	3.31	0.11	42.00	1.99	32.75	1.08
Hydroxycitronellal	3.07	0.17	2.10	0.05	4.98	0.11	4.18	0.09	8.44	0.11	2.44	0.09	1.36	0.10	23.00	1.69	17.55	1.03
ISO E Super (major isomers)	3.10	0.08	1.36	0.06	2.18	0.08	2.59	0.06	2.43	0.11	1.70	0.06	1.81	0.08	35.17	1.67	27.25	0.97
Isoeugenol (E)	3.22	0.36	2.17	0.10	4.01	0.12	4.34	0.10	7.49	0.13	2.54	0.09	3.17	0.11	28.33	2.50	21.80	1.43
Isoeugenyl acetate	3.07	0.28	1.90	0.07	3.14	0.12	4.32	0.08	6.83	0.12	2.40	0.08	2.14	0.11	32.92	2.97	25.40	1.65
Isomethylionone alpha	5.84	0.10	1.63	0.08	3.86	0.10	2.92	0.08	5.02	0.09	1.97	0.08	2.07	0.09	29.75	1.43	22.95	0.87
Lilial	3.70	0.20	1.70	0.06	3.26	0.10	4.37	0.08	7.18	0.11	2.23	0.08	1.33	0.10	30.75	2.04	23.70	1.19
Limonene	1.87	0.05	1.39	0.07	5.31	0.10	3.77	0.08	4.76	0.07	2.22	0.08	1.30	0.09	15.00	0.73	11.15	0.51
Linalool	3.53	0.19	0.98	0.07	1.15	0.07	2.09	0.07	8.70	0.10	1.84	0.10	1.30	0.08	17.00	0.91	12.85	0.64
Linalyl acetate	2.58	0.10	1.65	0.04	6.79	0.09	4.21	0.06	6.41	0.08	2.66	0.05	1.78	0.08	22.50	0.99	17.10	0.65
Lyrar (major isomer)	2.85	0.29	2.00	0.08	2.24	0.09	3.92	0.08	2.80	0.10	2.31	0.08	2.26	0.10	34.42	2.49	26.65	1.36
Lyrar (minor isomer)	2.34	0.29	1.93	0.09	2.81	0.02	2.86	0.08	5.34	0.11	2.21	0.09	1.77	0.09	34.25	2.41	26.50	1.32
Majantol	3.10	0.34	1.48	0.07	1.77	0.09	2.60	0.08	5.57	0.10	1.84	0.08	2.67	0.10	27.42	1.97	21.05	1.18
Menthol	2.93	0.14	1.89	0.06	4.40	0.09	5.10	0.07	9.55	0.11	2.34	0.07	1.30	0.09	19.75	1.10	14.90	0.72
Methyl salicylate	3.46	0.52	1.94	0.09	2.90	0.10	5.71	0.08	6.30	0.10	2.92	0.10	1.88	0.10	20.17	2.09	15.25	1.27
Neral	2.23	0.09	1.75	0.05	2.54	0.07	3.67	0.05	4.23	0.08	2.21	0.05	1.33	0.08	21.67	1.57	16.50	0.97
Propylidene phtalide	2.93	0.22	1.97	0.09	2.44	0.13	3.82	0.09	6.89	0.12	2.27	0.10	1.47	0.11	31.83	3.29	24.60	1.78
Salicylaldehyde	3.63	0.52	2.34	0.10	1.15	0.11	4.01	0.11	10.79	0.15	3.03	0.11	3.92	0.11	14.67	2.19	10.90	1.33
Sclareol	2.10	0.17	1.68	0.07	2.99	0.11	4.00	0.08	4.74	0.10	2.33	0.07	4.31	0.11	48.33	2.50	37.85	1.23
Terpinolene	1.44	0.04	1.10	0.08	6.00	0.10	5.19	0.09	2.46	0.09	1.80	0.07	2.23	0.09	16.92	0.94	12.75	0.63
Vanillin	3.75	0.26	2.44	0.11	2.90	0.13	5.57	0.11	8.28	0.17	3.61	0.11	2.97	0.13	26.25	3.81	20.10	2.13
α -Amylcinnamaldehyde	2.83	0.08	1.54	0.06	3.48	0.07	3.74	0.05	3.96	0.08	2.32	0.05	2.25	0.08	34.17	2.19	26.45	1.22
α -Amylcinnamyl alcohol	2.83	0.08	1.98	0.09	3.03	0.14	4.41	0.09	6.05	0.11	3.12	0.09	2.50	0.10	34.33	2.20	27.30	1.24
α -Damascone	3.17	0.17	1.41	0.04	3.43	0.08	3.91	0.08	4.93	0.10	2.28	0.08	1.45	0.08	26.92	1.64	20.70	1.02

Chromatographic performance – Peak standard deviation σ														Pattern coherence - t_R				
	Reference TM		Set up #1b		Set up #1b		Set up #2a		Set up #2b		Set up #3a		Set up #3b		Reference TM		Set up #3a	
α -Hexylcinnamaldehyde	4.64	0.19	2.19	0.08	3.82	0.10	4.02	0.09	4.46	0.10	2.85	0.08	2.32	0.10	36.92	2.13	28.65	1.17
α -Pinene	1.44	0.10	1.36	0.07	7.19	0.10	4.70	0.07	11.28	0.10	2.04	0.08	1.30	0.08	12.00	0.46	8.80	0.38
α -Santalol	3.52	0.12	1.51	0.05	2.42	0.08	3.70	0.06	4.77	0.09	2.58	0.06	1.47	0.11	35.42	1.71	27.45	0.98
α -Terpinene	2.86	0.06	1.14	0.07	1.15	0.04	3.38	0.08	3.20	0.07	2.05	0.08	1.52	0.08	14.58	0.71	10.85	0.53
α -Terpineol	2.08	0.13	1.65	0.05	3.16	0.07	2.56	0.07	3.04	0.08	2.00	0.06	2.78	0.08	20.25	1.40	15.35	0.87
β -Caryophyllene	3.80	0.17	1.32	0.07	6.52	0.09	2.82	0.07	2.61	0.10	2.38	0.07	1.50	0.09	28.42	1.09	21.90	0.71
β -Damascenone	3.58	0.14	2.10	0.06	3.23	0.06	3.27	0.07	3.75	0.10	2.25	0.07	3.74	0.09	26.58	1.80	20.40	1.08
β -Damascone	2.91	0.25	1.73	0.04	4.14	0.06	4.72	0.08	7.50	0.08	1.96	0.09	2.12	0.06	27.58	1.70	21.20	1.03
β -Pinene	2.37	0.13	1.54	0.07	2.03	0.09	3.43	0.07	5.71	0.09	1.63	0.07	2.61	0.08	13.33	0.67	9.85	0.51
β -Santalol	3.75	0.45	2.33	0.05	3.99	0.07	3.85	0.08	7.17	0.11	2.70	0.08	3.07	0.10	36.42	1.96	28.25	1.06
δ -Damascone	2.80	0.14	1.58	0.07	2.96	0.10	4.72	0.07	4.04	0.10	1.92	0.09	3.18	0.09	26.42	1.54	20.25	0.94
Mean	3.22	0.20	1.75	0.07	3.33	0.10	4.06	0.08	5.92	0.11	2.43	0.08	2.33	0.10				
Median	3.07	0.17	1.71	0.07	3.19	0.10	4.08	0.08	5.74	0.10	2.34	0.08	2.23	0.10				