New High Polarity bis (Cyanopropyl) Siloxane Stationary Phase for GC Resolution of Positional and Geometric Isomers of Fatty Acid Methyl Esters.

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Abstract

Very high percentage cyanopropyl (80-100%) containing polysiloxane stationary phases are used for the capillary GC analysis of fatty acid methyl esters (FAME) when characterization of geometric and positional isomers of fats and oils is required. The high polarity of these stationary phases is necessary to better resolve the potentially numerous cis/trans FAMEs in these samples.

High cyanopropyl content polysiloxanes have always presented problems with film stability both during initial coating of the capillary column and later, with use at higher temperatures as the viscosity of the polymer decreases. This is aggravated by the fact that extremely long columns of at least 100 meters are typically required to generate the separating power needed to adequately resolve positional isomers. To address these issues, an approximately 88% cyanopropyl polysiloxane stationary phase is stabilized by the incorporation arylene bridges into the polymer backbone and otherwise "tuned" by structural modifications to behave properly as a capillary GC stationary phase. This column has distinct advantages in temperature limits and separation quality relative to other columns commonly used for FAMES applications. The elution of sixtyseven individual FAMEs have been characterized on HP-88, and an algorithm has been developed to allow the prediction of elution order changes with chromatographic temperature changes.

Characterizing Elution of 67 FAMEs

Analysis of FAMEs (Fatty Acid Methyl Ester) found in edible oils, processed foods, conventional foods, and biological samples is now better enabled by the rugged characterization of over 67 important saturated, unsaturated, and cis and trans-FAMES on Agilent's HP-88 GC Column (Table 1). This represents the most extensive characterization of FAMES published by any column manufacturer to date, and allows analysts to more confidently confirm the identification of specific FAMES of interest in new or unusual samples, or to switch from another manufacturer's previous generation column to Agilent's HP-88 column.

HP-88 is a more stable, more efficient arylene cyanopropyl stationary phase version compared to previous generation non-arylene cyanopropyl columns used for this analysis. Because of it's higher upper temperature limit, analysts using HP-88 should enjoy longer lifetime and better resolution of FAMEs than conventional cyanopropyl columns.

No one column can resolve all possible FAME permutations of, say, a highly polyunsaturated edible oil which has been partially hydrogenated. However, HP-88 has a feature that can allow a more complete characterization: temperature dependent selectivity [1]. Temperature dependent selectivity means that you can, just by changing the average chromatographic temperature the compounds experience, improve the separation order of some compounds of interest. Practically, this means that more FAMEs can be identified in very complex samples just by changing the temperature conditions (see Table 1 and explanation to follow). The temperature change required to get meaningful selectivity changes however is a large (30°C), so analysts do not have to worry about elution order changes over minor deviations in temperature that normally result from routine column maintenance or slight changes in column flow for temperature programmed runs.

Temperature dependant selectivity is sometimes counter intuitive. Normally, one would think that to improve a separation you simply lower the temperature. It is not always the case. To aid in maximizing the resolution between any two FAMEs Agilent provides an Excel tool that enables the analyst to determine whether to increase or decrease the average chromatographic temperature in order to improve the resolution, and also will indicate at what temperature the two FAMEs of interest will co-elute. This tool can be downloaded from the Agilent web site. Visit www.agilent.com/chem, click Columns & Accessories then All Column Phases then HP-88 for a downloadable spreadsheet that will allow you to determine the elution order of the listed FAMEs at a given temperature and unretained peak time."

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Table 1. Elution order of 67 FAMEs on HP-88 at 155°C and 180°C. Elution order reversals are in bold

Isothermal Temp (C)	тт 155 вт	5.67 180
CHAIN	Γί I	rt I
C08:0	6.47	6.03
C11:0	8.13	6.67
C11:1	9.11	7.07
C12:0	9.28	7.09
C12:1	10.48	7.53
C13:0	10.66	7.53
C13:1	12.49	8.21
C14:0	12.78	8.24
C15:1n5 - trans	13.12	8.35
C14:1n5 - trans	14.01	8.66
C14:1	14.73	8.92
C15:0	15.48	9.03
C15:1n5	18.19	9.96
C15:1n1	18.65	10.05
C16:0	19.24	10.10
C16:1 - trans	21.66	11.03
C16:1	22.69	11.40
C17:0	25.15	12.05
C17:1n7 - trans	27.83	12.91
C17:1	29.16	13.39
C18:0	32.41	14.00
C16:3	34.16	15.11
C18:1n12 - trans	35.21	14.89
C18:1n9 - trans	35.38	14.97
C18:1n7 - trans	35.96	15 10
C18:1n12	36.51	15.22
C18:1n9	36.89	15.35
C18:1n7	37.78	15.57
C18:2n6_trans	41.62	16.66
018.210 - traits	45.20	10.00
C18:2n6	45.30	18.20
C19:1n12 - trans	45.00	10.22
C19:1n9 - trans	48.25	18.64
C18:3n6	53.08	20.70
C20:0	55.85	20.64
C18:3n3	58.99	22.28
C19:2n6	59.81	22.48
C20:1n9 - trans	61.02	22.26
C18:2-d10 trans,d12 trans (conjugated)	62.64	23.30
C18:2- d9 cis, d11 trans (conjugated)	63.35	23.36
C20:1n9	63.45	23.09
C18:2-d10 cis,d12 trans (conjugated)	64.63	23.88
C18:2- d10 trans, d12 cis (conjugated)	65.50	24.01
C18:4n3	68.23	25.37
C21:0	75.55	25.14
C20:2n6	79.30	27.55
C20:3n9	82.90	28.86
C21:1n9	85.70	28.24
C20:3n6	91.81	31.24
C22:0	100.24	31.50
C20:4n6	101.91	34.25
C20:3n3	103.03	33.96
C21:2n6	106.08	34.43
C22:1n9 - trans	110.80	33.84
C22:1n9	111.68	35.61
C20;4n3	119.89	38.74
C20:5n3 (DPA)	131.26	42.94
C22:2n6	135.27	42 61
022.2110	1/2 10	42.01
C23.1N9	176.01	52 10
022:300	170.01	53.19
022:416	1/8.91	54.93
C24:0	182.04	50.00
C22:5n6	195.05	59.45
C24:1n9	197.65	56.34
C22:5n3 (EPA)	233.41	69.01
	055 40	75 26
C22:6n3 (DHA)	255.42	75.20
C22:6n3 (DHA) C24:5n3	409.85	110.29

program.

Example: Looking at the table, a run at 155°C gives the elution order of 18:2n6 (45.30 min) followed by C19:1n12-trans (45.66 min). If there is very large amount of 18:2n6 present and a small amount of C19:1n12trans, the 18:2n6 peak will "front" and the C19:1n12-trans peak will be lost in the fronting. By RAISING the temperature to 180°C, the C19:1n12-trans peak will actually elute before the 18:2n6 peak, and resolution will be regained.

How can the direction of elution order change be predicted?

Temperature dependent selectivity can predicted by characterizing the elution of different FAMEs at multiple temperatures (See Figure 1), and then plotting curves according to the following equation:

-T (Kelvin) x ln (k) vs Elution Temperature,

where k = (Retention Time of FAME – Unretained Peak Time)/Unretained peak time

It is the differing slopes (m) that indicate whether or not two given compounds will potentially change resolution or even elution order by varying the chromatographic temperature. They also indicate which direction in temperature you have to go, increased or decreased, relative to where you are in order to improve resolution. The following graph demonstrates the previous example.

-200140 -400 -600 -800 -1000

-TIn(k)



-1200



Elution orders and resolutions can change with a change in chromatographic temperature. This is not "new news." If you look hard enough, you can find a pair of compounds that reverse elution orders on any capillary GC column. What is less commonly understood and counter intuitive is that resolutions can be improved by increasing chromatographic temperature. The practical benefit of this is that for a complex sample that has co-elution at one temperature, it is possible to achieve complete resolution of all FAMEs simply by changing the temperature and using data from both runs to more fully characterize the sample, or simply modifying the current temperatur

This allows a linear curve to be fit of y = mx+b.

C18:2n6 and C19:1n12-trans Elution Order Change with Chromatographic Temp Change



Figure 1. – Tln(k) v Chromatographic Temperature curve for C18:2n6 and C19:1n12-trans. These curve fit equations for each allow the prediction of elution order at any given temperature and the exact co-elution temperature. Additionally, one can predict retention times if the temperature and un-retained peak times are known.

While difficult to see graphically, note the two different slopes of the plots (in green) ... this indicates the possibility for an elution order change by going higher or lower in temperature. By setting the the equations equal to each other and solving for x, one can also determine from the equations describing the two curves the temperature at which these two compounds exactly co-elute.

19:1n12-trans = 18:2n6

19.054x - 3789.6 = 18.419x - 3687.4

x (coelution temp) = 160.95° C

If we wanted the 19:1n12-trans to elute before the 18:2n6, we would have to go up in chromatographic temperature from 160.95C. Referring to Table 1. retention times highlighted in green we note elution order reversal is achieved.

Conclusion

The following figures are a number of edible oil and fish oil chromatograms on HP-88, demonstrating that HP-88 is the most comprehensively characterized commercially high cyanopropyl column for FAMEs analysis available today. No other manufacturer has characterized and published the temperature dependent selectivity of their phase. As such, with HP-88, the analyst has much greater flexibility in achieving resolution between coeluting pairs simply by changing the chromatographic temperature, and greater confidence in the identification of their FAMEs under a variety of chromatographic conditions. Combine this with the HP-88's higher upper temperature limit and you have a flexible and robust solution for identifying your FAMEs of interest.

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1.	C6:0	16.	C16:1 trans	31.	C20:0
2.	C8:0	17.	C16:1	32.	C18:3n3
3.	C9:0	18.	C17:0	33.	C20:1n9 trans
4.	C10:0	19.	C17:1	34.	C20:1 (8)
5.	C11:0	20.	C18:0	35.	C20:1 (11)
6.	C12:0	21.	C18:1n9 trans	36.	C20:2n6
7.	C11:1	22.	C18:1n7 trans	37.	C20:3n6
8.	C12:1	23.	C18:1n12	38.	C20:0
9.	C13:0	24.	C18:1n9	39.	C20:4n6
10.	C13:1	25.	C18:1n7	40.	C20:3n3
11.	C14:0	26.	C18:2n6 trans	41.	C22:1n9
12.	C14:1	27.	C19:0	42.	C20:5n3
13.	C15:0	28.	C18:2n6	43.	C22:2n6
14.	C15:1n1	29.	C19:1	44.	C22:3n6
15.	C16:0	30.	C18:3n6	45.	C22:4n6
				46.	C24:0

1.	C6:0	16.	C17:0	31.	C18:3
2.	C8:0	17.	C17:1	32.	C20:1 (8)
3.	C9:0	18.	C18:0	33.	C20:1 (11)
4.	C10:0	19.	C18:1T (9)	34.	C20:2 (11,14)
5.	C11:0	20.	C18:1T (11)	35.	C22:0 + C20:3n6
6.	C12:0	21.	C18:1C	36.	C20:3n3
7.	C12:1 + C13:0	22.	C18:1C (9)	37.	C20:4
8.	C13:1	23.	C18:1 (11)	38.	C22:1
9.	C14:0	24.	C19:0	39.	C22:2 + C20:5
10.	C14:1	25.	C18:2TT	40.	C24:0
11.	C15:0	26.	C18:2	41.	C22:3n6
12.	C15:1	27.	C18:3	42.	C22:4n6
13.	C16:0	28.	C20:0	43	C24·1
14.	C16:1T	29.	C18:3 (6,9,12 gamma)	44	C22.5n3
15.	C16:1	30.	C20:1 (5)	45	C22.6n3

