



Analysis of Dioxins

Part 2 – How are Dioxins analysed?

Due to the highly toxic nature of dioxins it is essential that they are carefully monitored down to extremely low concentrations. The standard, low resolution GCMS systems routinely used for the determination of environmental contaminants like PAHs, Phenols and Pesticides are neither

sensitive nor selective enough to detect these very low concentrations in the presence of potential interferences. The detection limits required for the common organic contaminants range in the ppm (mg/kg) to ppb (ug/kg) levels for soils and in the ppb (ug/L) for waters.

For dioxins, however, the levels of concern are ppt (ng/kg) for soils and ppq (pg/L) for waters. One instrument capable of detecting these ultra-trace concentrations is a High Resolution, Magnetic Sector, Mass Spectrometer (HRMS).

As mentioned above, the standard low resolution GCMSs are not suitable for dioxin analysis and the reason is that they operate with “unit mass resolution”.

In other words, they can only resolve the mass of a fragment to the nearest atomic mass unit (amu) whereas the HRMS can separate peaks having the same nominal mass on the low resolution GCMS system.

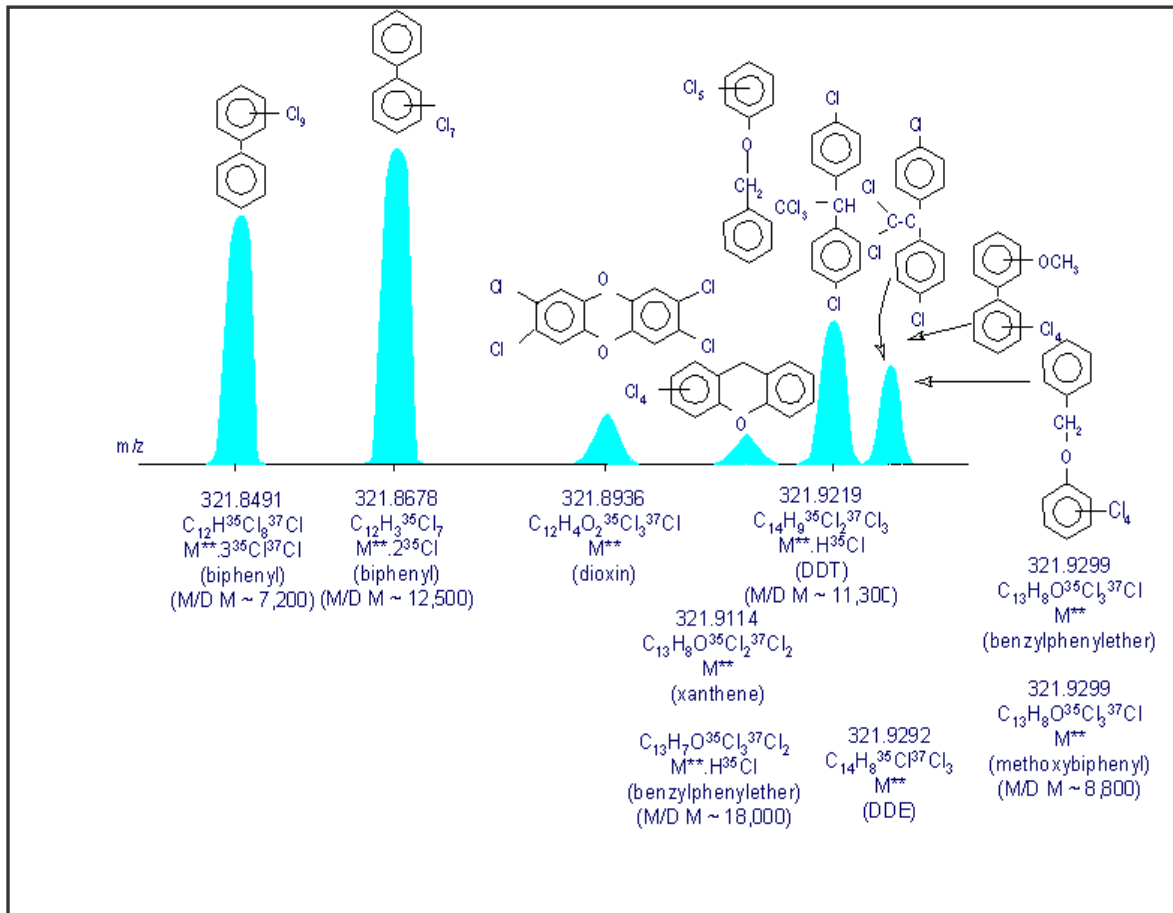
For example, all masses between 321.5 and 322.5amu would be seen by a standard GCMS as 322 but the HRMS can easily resolve these as two separate peaks. (See diagram on next page.)

The significant increase in selectivity offered by HRMS results in more accurate identification of analyte fragments and lower detection limits by eliminating interferences caused by co-eluting compounds with similar mass fragments.



GC/High Resolution, Magnetic Sector, Mass Spectrometer

The extremely sensitive HRMS requires that the sample extract is very clean prior to analysis and extensive clean-up procedures are undertaken. Acidic/basic/neutral silica gel and florisil are used to remove co-extracted organics compounds which may interfere with the operation of the GC/HRMS analysis.



This example shows how ions with similar masses are resolved by a high resolution mass spectrometer and the resolution required for separation. On a low resolution system these fragments would all have a nominal mass of 322.

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