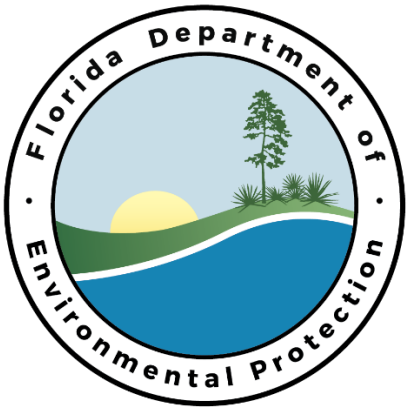
Standard Operating Procedure for:

ANALYSIS OF PESTICIDES AND PCBs IN WATER, SOIL AND TISSUE SAMPLES USING GC/MS/MS



DEPARTMENT OF ENVIRONMENTAL PROTECTION
CHEMISTRY SECTION
TALLAHASSEE FLORIDA

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1. SCOPE AND APPLICATION

1.1. This method is applicable to the determination of selected organonitrogen and organophosphorus pesticides in water and soil samples as listed in Tables 1A-WATER and 1A-SOIL/WASTE, selected organochlorine pesticides in soil as listed in Table 1B and PCB Aroclors in soil as listed in table 1C, and selected organochlorine pesticides and PCB congeners in fish tissues as listed in table 1D. Method Detection Limits and Practical Quantitation Limits yielded by this method are also provided in Tables 1A, 1B, 1C, and 1D

1.2. This method is based on EPA 8270E mod. (ref 15.1) Laboratory Information Management System (LIMS) tests: W-PSNP-TQ, SPLP-NP-TQ, S-PSCL-TQ, S-PCB-TQ, WS-PSCL-TQ, WS-PCB-TQ, S-PSNP-TQ, WS-PSNP-TQ, T-PCBCL-TQ and T-PCB-TQ.

1.3. This Standard Operation Procedure is restricted to use by an analyst experienced in the use of an Agilent 7010 GC/MS/MS triple quadrupole system, and in the use of appropriate computer programs. The minimum qualifications required:

- B.S. in Chemistry or Biochemistry with minimum one year of professional chemical or biochemical experience
- Knowledge of principles and practice of gas chromatography/mass spectrometry
- Ability to perform basic laboratory mathematics
- Knowledge of the Masshunter GC/MS/MS software and DEP LIMS.

2. SUMMARY OF THE METHOD

2.1 General description.

Water and soil samples are extracted using the appropriate procedures listed in the Preparation SOP- GC-002 (ref 15.2). Tissue samples are extracted according to preparation SOP GC-004-1. (ref 15-15). The extract is analyzed using an Agilent 7010 GC/MS/MS triple quadrupole system operating in the Multiple Reaction Monitoring (MRM) mode. Qualitative identification of the parameters in the extract is performed using the retention time and the relative abundance of the characteristic MRM transitions. Quantitative analysis is performed using an internal standard technique.

2.2 Agilent Masshunter Optimizer.

Agilent Masshunter Optimizer software (ref. 15.6) is used to perform MRM optimization to find the most suitable transitions for target analytes for GC analysis. The Optimizer is a version of the Agilent acquisition software. An individual standard of a pesticide is prepared at a suitable concentration and used for the MRM study. In fully automated mode the software runs a full scan analysis and picks precursor ions, follows with a SIM mode analysis to determine the product ions and then finally performs the MRM optimization for all the transitions for collision energies. Since the final result can be a very large table summarizing all the transitions arranged by abundance, for practical purposes the procedure is usually done stepwise to select the most promising precursor ions for further study to save on time and limit the amount of data generated. Once the final MRM table is obtained several of the most abundant transitions are further tested for possible interferences from the instrument background and to get an estimation of the MDL.

Typically, the most abundant transition is used as a quantifier and the second one as a qualifier. The transitions are also tested for interferences from real environmental samples. Once all these steps are completed, the MDL validation is performed.

2.3 Modifications to EPA 8270E.

The analysis uses analyte protectants (Ethoxyglycerin, Gulonolactone and Sorbitol at 25,000ppm/2500ppm/5000ppm respectively). Those compounds are co-injected with the samples using the sandwich technique. Analyte protectants are necessary to suppress matrix induced response enhancement effects. The 7010 GC/MS/MS seem to be especially sensitive to those kinds of effects.

The degradation /tailing factor mix is run at lower concentration (5 ppm instead of 50 ppm) to reduce carry-over effects with DDT-p,p'. Only pentachlorophenol peak is used to determine the tailing factors. Benzidine peak is not detected in

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the presence of the analyte protectants. Since the absence of Benzidine peak does not have any bearing on the analysis of the target analytes it is considered inconsequential for the purpose of this analysis.

The method uses different internal standards and a different surrogate that suggested in EPA 8270E due to their closer similarity to the target analytes.

3. INTERFERENCES

3.1. Raw GC/MS/MS data from all blanks, samples, and spikes must be evaluated for interferences. Determine if the source of interference is in the preparation and/or cleanup of the samples and take corrective action to eliminate the problem.

3.2. Contamination by carryover can occur whenever high-level and low-level samples are analyzed sequentially. To reduce carryover, rinse the syringe several times with solvent between samples. It may be necessary to analyze one or more solvent blanks between samples and even change out the syringe in extreme cases.

3.3 Method interferences may be caused by contaminants in solvents, reagents, glassware, and other sample processing hardware that lead to discrete artifacts and/or elevated baselines in gas chromatograms. All these materials must routinely demonstrate to be free from interferences under the conditions of the analysis by running laboratory reagent blanks. Glassware must be scrupulously cleaned. Clean all glassware as soon as possible after use by rinsing with the last solvent used in it. Solvent rinsing should be followed by rinsing with DI water. The glassware should then be drained dry and heated in a muffle furnace at 550 °C for 8 hours. Some thermally stable materials may not be eliminated by this treatment. Solvent rinses with acetone and pesticide quality hexane may supplement the muffle furnace heating. Volumetric glassware should not be heated in a muffle furnace. After drying and cooling, glassware should be sealed and stored in a clean environment to prevent any accumulation of dust or other contaminants. Store inverted or capped with aluminum foil. The use of high purity reagents and solvents helps to minimize interference problems. Purification of solvents by distillation in all-glass systems may be required or irradiation with UV light. Matrix interferences may be caused by contaminants that are co-extracted from the sample. The extent of matrix interferences will vary considerably from source to source, depending upon the sample characteristics.

4. DEFINITIONS

4.1. ACCURACY: The closeness of agreement between an observed value and an accepted reference value. When applied to a set of observed values, accuracy will be a combination of a random component and of a common systematic error (or bias) component.

4.2. BATCH: A group of samples, which behave similarly with respect to the sampling or the testing procedures being employed, that are processed as a unit. For QC purposes, if the number of samples in a group is greater than 20, then each group of 20 samples or less will all be handled as a separate batch.

4.3. BIAS: The deviation due to matrix effects of the measured value (Xs - Xu) from a known spiked amount. Bias can be assessed by comparing a measured value to an accepted reference value in a sample of known concentration or by determining the recovery of a known amount of contaminant spiked into a sample (matrix spike). Thus, the bias (B) due to matrix effects based on a matrix spike is calculated as:

$$B = (Xs - Xu) - K$$

where:
Xs = measured value for spiked sample,
Xu = measured value for unspiked sample, and
K = known value of the spike in the sample.

Using the following equation yields the percent recovery (%R).

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$$\%R = 100 (Xs - Xu) / K$$

4.4. PRACTICAL QUANTITATION LIMIT (PQL): The lowest concentration that can be reliably achieved within specified limits of precision and accuracy during routine laboratory operating conditions. The PQL is generally 3 to 5 times the MDL. However, it may be nominally chosen within these guidelines to simplify data reporting. For many analytes, the PQL concentration is selected as the lowest non-zero standard in the calibration curve. Sample PQLs are highly matrix dependent.

4.5. FIELD DUPLICATES: Independent samples which are collected as close as possible to the same point in space and time. They are two separate samples taken from the same source, stored in separate containers, and analyzed independently. These duplicates are useful in documenting the precision of the sampling process.

4.6. INTERNAL STANDARD: A pure compound added to a sample extract in known amounts and used to calibrate concentration measurements of other compounds that are sample components. The internal standard must be a compound that is not a sample component.

4.7. LABORATORY FORTIFIED BLANK/LABORATORY CONTROL SAMPLE (LFB/LCS): A known matrix material spiked with compound(s) representative of the target analytes. The LFB is analyzed exactly the same way as other samples. This is used to determine whether the methodology is in control, and whether the laboratory is capable of making accurate and precise measurements.

4.8. MATRIX: The component or substrate (e.g., surface water, drinking water) which contains the analyte of interest.

4.9. MATRIX SPIKE: An aliquot of sample spiked with a known concentration of target analyte(s). The spiking occurs prior to sample preparation and analysis. A matrix spike is used to document the bias of a method in a given sample matrix.

4.10. MATRIX SPIKE DUPLICATES: A second aliquot of the same sample used for matrix spike spiked with identical concentrations of target analyte(s). The spiking occurs prior to sample preparation and analysis. They are used to document the precision and bias of a method in a given sample matrix.

4.11. METHOD BLANK: An analyte-free matrix to which all reagents are added in the same volumes or proportions as used in sample processing. The method blank must be carried through the complete sample preparation and analytical procedure. The method blank is used to document contamination resulting from the analytical process. For a method blank to be acceptable for use with the accompanying samples, the concentration in the blank of any analyte of concern shall not be higher than the method detection limit

4.12. METHOD DETECTION LIMIT (MDL): The minimum concentration of a substance that can be measured and reported with 99% confidence that the analyte concentration is greater than zero and is determined from analysis of a sample in a given matrix type containing the analyte. For operational purposes, when it is necessary to determine the MDL in the matrix, the MDL should be determined by multiplying the appropriate one-sided 99% t-statistic by the standard deviation obtained from a minimum of seven analyses of a matrix spike containing the analyte of interest at a concentration one to five times the estimated MDL.

4.13. ORGANIC-FREE REAGENT WATER: All references to water in the method refer to water in which interference is not observed at the method detection limit of the compounds of interest. Organic-free reagent water can be generated by passing tap water through a carbon filter bed containing about 1 pound of activated carbon. A water purification system may be used to generate organic-free de-ionized water.

4.14. PRECISION: The agreement among a set of replicate measurements without assumption of knowledge of the true value. Precision is estimated by means of duplicate analyses. These samples should contain concentrations of analyte above the MDL and involve the use of matrix spikes or laboratory fortified blanks. The estimates of precision are based on the relative percent difference (RPD).

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$$RPD = 100 [2 (X1 - X2) / (X1 + X2)]$$

where X1 and X2 are the two measurements

4.15. INITIAL CALIBRATION VERIFICATION (ICV): A standard solution from a source, other than normal calibration standards, that is certified and traceable. These standards are used to check the accuracy of a calibration curve immediately after the calibration standards are run.

4.16. CONTINOUS CALIBRATION VERIFICATION (CCV): A standard solution from a source that is certified and traceable. These standards are used to check the accuracy of a calibration curve.

4.17. SPIKE SOLUTION (SS): A solution of method analytes of known concentrations that is used to fortify an aliquot of laboratory reagent water or sample matrix.

4.18. STANDARD CURVE: A plot of concentrations of known analyte standards versus the instrument response to the analyte. Calibration standards are prepared by successively diluting a standard solution to produce working standards, which cover the working range of the instrument. Standards should be prepared at the frequency specified in section six (6) of this SOP. The calibration standards should be prepared using the same type of solvent as the final sample preparation solvent.

4.19. SURROGATE: An organic compound which is similar to the target analyte(s) in chemical composition and behavior in the analytical process, but which is not normally found in environmental samples. Surrogates are used to monitor the preparation and are added to each field and QC sample prior to extraction.

5. APPARATUS AND EQUIPMENT

5.1 Apparatus.

Agilent 7010 GC/MS/MS triple quadrupole system or equivalent. Must be temperature programmable with an injector port designed for cold splitless injection. A Multi-Mode Inlet (MMI) may be used if available. The GC, GC Automatic Sampler and MSD operating parameters are illustrated in Tables 2, 3 and 4. The analytical column is an HP-5MS UI or equivalent, fused silica capillary, 20 m x 0.25 mm x 0.25 um or similar column with Ultimate Union placed after the initial 5 m of the column (5m-15m mid-column backflash configuration).

5.2 Data system

5.2.1 A computer system is interfaced to the GC/MS/MS that allows the continuous acquisition and storage on machine-readable media of all chromatographic measurements obtained throughout the duration of the chromatographic run sequence program.

5.2.2 This system currently uses the Masshunter software from Agilent Technologies Inc. For reporting data, the system currently uses DEP LIMS.

5.3 Gases

5.3.1 Helium, UPC Grade or higher, is used as the carrier and collision cell gas. The helium is passed through an oxygen and a hydrocarbon filters before it enters the GC.

5.3.2 Nitrogen, UPC Grade or higher, is used as a collision cell gas. The N_2 is passed through a hydrocarbon filter before entering the GC.

6. REAGENTS AND CHEMICALS

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6.1. Solvents

6.1.1. Methylene Chloride, Fisher Scientific, GC-Resolve, Pesticide, HPLC or OPTIMA grade.

6.1.2. Isooctane, Fisher Scientific, Pesticide, HPLC or OPTIMA grade.

6.1.3. Acetone, Fisher Scientific, Pesticides, HPLC or Optima grade.

6.2. Standards

6.2.1. For detailed standard preparation see APPENDICES 1 and 2

6.3. Stock and Intermediate Standards

6.3.1. Custom made stock standards and/or neat standards for individual analytes available) are purchased from commercial suppliers. The concentrations of (two different sources or two different lot numbers if only one vendor is currently purchased) custom made standards are listed in the appendix 1: "Preparation of pesticides standards".

6.3.2. Intermediate standard solutions are mixtures of individual standards used to prepare working standards. They are prepared in our lab from stock standards by mixing / diluting with isooctane or acetone. They can also be purchased from a certified manufacturer (ISO 9000 or EPA certified). The concentrations of the components in the intermediate standard are typically several mg/L. Intermediate standards are replaced once per year. New standard is checked vs. a second source (QC Standard), after diluting it to one of the working standard levels. The criterion of acceptance is +/- 10% difference. All standard preparations and verifications have to be recorded in the Standard Preparation Tracker located in DEP LIMS. A list containing all standards with their serial numbers used in the analysis must be part of analysis documentation folder. Currently standard serial numbers are entered in the analysis run sequence.

6.4. Working Standard Solutions (Calibration standards)

6.4.1. Working standard solutions are a series of diluted individual or mixture standards in isooctane - acetone 4:1 v/v, pure isooctane is used for chlorinated pesticides. and PCBs. They are used for calibration and are prepared by diluting intermediate standard solutions. The internal standard mixtures listed below are added to every working standard at 100 µg/L.

Internal Standard Mixture for NP analytes:

EPTC-d14
Tributyl Phosphate-d27
Atrazine-d5
Hexazinone-d6
Parathion Ethyl–d10
Metribuzin-d3
Caffeine-d9
Azoxystrobin-d4

Internal Standard Mixture for CL analytes and PCBs:

Alpha-BHC-d6
2,5-Dichlorobiphenyl-2',3',4',5',6'-d5 (DCB-d5)
2,3,5,6-Tetrachlorobiphenyl-2',3',4',5',6'-d5 (TCB-d5)
2,3,3',4,4'5-Hexachlorobiphenyl-2',6,6'-d3 (HCB-d3)

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DDT-p,p'-d8
Trifluralin-d14
Dicofol-d-8

6.4.2. The concentrations for each analyte in the working (calibration) standards are listed in Table 5A for Nitrogen Phosphorus analytes, in Table 5B for chlorinated pesticides, in Table 5C for PCB Aroclors, and in table 5D for chlorinated pesticides/ PCB congeners for tissue analysis. The second source/CCV standard is prepared at midpoint level.

6.5. Spiking Solution

6.5.1. These solutions are used when fortifying sample matrix spikes or lab fortified blanks at extraction. These fortified samples are used to verify the accuracy and precision of the sample preparation and analysis.

6.5.2. Spike solutions are prepared by diluting stock or intermediate standards with acetone. Concentrations of the parameters in these solutions are listed in tables 5A,5B, 5C and 5D.

6.5.3. Freshly prepared spike solutions are checked vs. valid working standards. The acceptance criterion is ± 20% difference.

6.6. Initial Calibration Verification (ICV). A standard solution from a source, other than normal calibration standards, that is certified and traceable. These standards are used to check the accuracy of a calibration curve immediately after the calibration standards are run. The acceptance criterion is ± 30%.

6.7. Continuous Calibration Verification (CCV). A mid-level calibration standard solution from a source that is certified and traceable. These standards are used to check the accuracy of a calibration curve on daily bases.

6.7.1 The acceptance criterion is ± 20% difference.

6.7.2 The Analyst must ensure that the calibration standards are checked with the corresponding CCV with every initial calibration and then in 12 hrs intervals thereafter.

6.8 Analyte protectants.
The use of analyte protectants was proposed by Anastassiades et al. (ref 15-3 and 15-4) and it has become an established practice for pesticides analysis in food products analysis, where triple quad GC/MS/MS technology has found the widest use. Agilent 7010 GC/MS/MS instrument is very sensitive to matrix induced response enhancements which makes exact quantitation problematic. Analyte protectants are generally very polar organic compounds injected at very high concentrations along with every standard and sample in the analytical run sequence. Due to their polarity, they are thought to deactivate all the active sites in the system, and, due to their very high concentration, to render all the other matrices in the samples basically insignificant. In effect, all the samples and standards injected into the GC/MS/MS system have effectively the same matrix – the analyte protectants – and therefore matrix induced response differences are greatly reduced. This method uses a mixture of three specific analyte protectant compounds: Ethoxyglycerin, Gulonolactone and Sorbitol at 25000 ppm, 2500 ppm and 5000 ppm respectively. Due to solubility considerations, the working solution is prepared in MeOH containing 5% of DI water. It is injected along with every standard and sample using a "sandwich injection" technique. 0.4 ul of the above analyte protectants mixture is injected, which corresponds to 10 ug, 1 ug and 2 ug of the corresponding analyte protectants on column.

7. SAMPLE COLLECTION, PRESERVATION, AND HANDLING

7.1. Samples must be collected in glass containers with Teflon-lined screw caps.

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7.2. All samples and sample extracts must be refrigerated at plus 6 degrees C or less from time of collection until extraction.

7.3. All samples must be extracted within 7 days of collection (waters) or 14 days of collection (soils, wastes) or 365 days (tissue samples) and completely analyzed within 40 days of extraction. If the water samples are to be analyzed for Aldrin and residual Chlorine is present, then add 80 mg of Sodium Thiosulfate per 1 L of sample and mix well.

8. SAMPLE PREPARATION PROCEDURE

8.1. For preparation see DEP SOP GC-002: (ref 15.2). Also refer to Appendix 6: "Preparations Flowcharts"

8.2. For test W-PSNP-TQ 1L water samples are extracted with Methylene Chloride (3×60 mL) to a final volume of 0.25 ml. 0.2 ml is submitted for analysis to account for the addition of 50 ul of 500 ug/L NPTQ internal standard solution.

8.3. For soil samples (S-PSNP-TQ, S-PSCL-TQ and S-PCB-TQ) 30 g of sample is extracted with 1:1 methylene chloride/acetone (sonication), solvent exchanged to isooctane and then concentrated to 2 ml of final volume.

8.4. Tissue samples (test ID T-PCBCL-TQ, T-PCB-TQ) are extracted according to SOP GC-004-1 (ref 15-15); 5 g samples are extracted with methylene chloride using Dionex ASE350 machine. The extracts are solvent exchanged to isooctane and blown down to 2 mL.

8.5. Both soil and tissue extracts are further cleaned up by using GPC (NP pesticides) or GPC/Florisil (chlorinated pesticides and PCBs). 1ml sample is typically vialed for GPC clean-up; 0.8 ml is then injected, and 0.7 ml is submitted to allow for the ISTD addition (80 ul of 1000 ppb solution).

8.6. Extreme care must be exercised by all the laboratory staff involved in preparation and analysis to limit background contamination due to ultralow detection limits achievable with the Agilent 7010 GC/MS/MS system. DI water should be used to perform both method blanks and Laboratory Fortified Blanks due to low level pesticide contamination usually found in both tap water and well water.

9. GENERAL DESCRIPTION OF GC/MS/MS ANALYSIS

9.1. GC/MS/MS Maintenance and Tuning

9.1.1 DFTPP tune is not applicable for GC/MS/MS methods. Instead, as recommended by 8270E paragraph 11.3.1, this SOP follows manufacturer's tuning instructions. GC/MS/MS tuning includes periodically performed autotune as well as a daily tune check.

9.1.2 Initial checking and maintenance of the instrument consists mainly of the following steps:

9.1.2.1 Check the vacuum operation and periodically run an air/water leak test. Oxygen, nitrogen and water must be found at below 5% of mass 69 level. Air/water leak test must be run each time the vacuum system is vented. It may take several hours (even overnight) of pumping down to bring the air/water content below 5%!

CAUTION: In order to properly perform the air/water leak test nitrogen gas flow to the collision cell has to be turned manually off at the source! After the test, nitrogen gas must be turned back on!

9.1.2.2 Perform the triple quadrupole GC/MS/MS system verification (tune check) before each run sequence. Print the tune check report and include with the documentation. The tune check requirements are listed in appendix 3. Periodically perform the EI high sensitivity autotune of the GC/MS/MS triple quadrupole system and save the current settings in the autotune file. The autotune has to be perform, however, every time the tune check fails. The report is printed

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automatically, and it should be placed in the autotune reports log. If the autotune criteria are not met repeat the autotune. If still failing, run the autotune from the default values. If that fails, the ion source may have to be cleaned. **It is not recommended to attempt manual tune of the instrument without the assistance of the Agilent Technologies' triple quad trained specialist!**

9.1.2.3 Replace the injector liner (Agilent's 2 mm dimpled liner part no: 5190-2296 is recommended for cold splitless injection), cut 1-3 inch of the column after running contaminated samples or encountering unusually heavy matrix. Occasional trimming of the column is still necessary even if backflush technology is used.

9.1.2.4 Run an Instrument Blank and look for instrument contamination.

9.1.2.5 In case the instrument is contaminated raise the furnace temperature to 260ºC and leave it overnight.

9.1.2.6 To perform maintenance of the MMI inlet replace the liner and septum and clean the inside of the inlet body with cotton swabs soaked with methanol and methylene chloride. **Do not use a harsh brush to clean the inside of the inlet body!** To complete the MMI inlet cleaning perform an inlet bake out procedure. Set the inlet mode to split (split ratio 200:1) and let the gas flow for a couple of minutes. Then raise the inlet temperature to 330 ºc. and the oven temperature to 300 ºc. Bake for 1-2 hrs. It is beneficial and recommended to bake the ion source at 350 ºc. at the same time.

9.1.2.7 The autosampler syringe has to be frequently and thoroughly cleaned to avoid injection repeatability problems. A dirty plunger will cause reproducibility problems, bad injections occurring randomly, and poor peak shapes and calibration problems. Replacing the syringe on regular, frequent basis is highly recommended.

9.1.2.8. Re-check for instrument contamination and if needed repeat the procedure until the instrument is contamination free.

9.1.2.9. Following column trimming and/or column replacement the retention times may need to be adjusted in the dMRM acquisition method. For that purpose, a high-level calibration standard is run for each method. The data file for that single run is then added to the most recent Masshunter Quant batch file and quantitated (quantitate single sample option is strongly preferred here). Peak assignments for each analyte, internal standard and surrogate need to be verified carefully. When done, the entire batch is saved under different name indicating RT adjustment. In some cases, it is desirable to adjust the retention times in the quant method and save the quant method under different name, again indicating RT adjustment. That, RT adjusted quant method, can then be used (copied) to process the next batch of samples.

In order to adjust the acquisition times in the dMRM method the single run data file with RTs verified above is used. In the MS acquisition screen go to Method/Update RTs, browse to the quant file to be used and hit "update". Even with the retention times correctly assigned in Quant, the automated adjustment in the dMRM method is, occasionally, error prone, The software may confuse some closely eluting, isomeric or chemically very similar compounds assigning the same RT to both, Therefore, the RT assignments in the acquisition method must be carefully verified. Special attention needs to be paid to the following compounds: all BHCs, especially Beta and Gamma-BHC, Gamma-Chlordane and Alpha-Chlordane, Dieldrin and Endrin, as well as Phorate, Terbufos and Disulfoton.

Analysts may elect to type in all the retention times in the acquisition method instead if using the automated procedure.

PCB peaks get easily confused by the Quant software. If in doubt, refer to the peak assignments in this SOP. It is typically not necessary to adjust the retention times for the PCB aroclor transition in

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the dMRM method, since wide acquisition windows are used. However, internal standards and surrogates still need to be adjusted carefully.

9.2 GC/MS/MS System Initial Calibration

9.2.1. Analyze the calibration standards at the following levels listed in Tables 5A, 5B and 5C, 5D. At each level, the internal standards should be present at 100 µg/L. The linearity of the calibration curve is defined by an RSD that is less than or equal to 20% of the Response Factors of the calibration curve, or by a correlation coefficient R^2 not smaller than 0.99. If a higher order curve is to be used the correlation coefficient R^2 has to be at least 0.99. When new calibration is inspected linear fit is usually tried first, followed by average response factor (%RSD which is equivalent to weighted linear forced through origin), then followed by quadratic fit and finally higher order curves. Do not use the "include" origin option in the Masshunter software. "Ignore" origin is preferable to "force" through origin in most cases. Forcing the curve through origin is acceptable whenever ignoring origin produces nonsensical results for small peaks close to MDL (like negative values). When calibration curve fit is selected in the Masshunter software the % calibration drift has to be monitored in order to have all the calibration levels within 70-130% of the expected value. Special care has to be taken to carefully fit the curves at the lower end of the calibration range where the vast majority of problems occur. All calibration curves should be weighted curves (1/x or 1/x2); do not use equal weighing. It is permissible to remove individual analyte calibration levels from either the lowest and/or highest levels of the curve (the PQL may have to be adjusted). Removal of interior levels is forbidden. An entire single standard calibration level may be removed from the interior of the curve whenever the standard was not correctly injected or a wrong standard was injected. If more than 10% of the total number of analytes fail the calibration fit criteria or more than 20% of analytes fail the % calibration drift criteria, then the instrument system must be corrected. Some possible problems include standard mixture degradation, injection port inlet contamination, analytical column contamination, and active sites in the column or chromatographic system.

9.2.2. Approximate retention times, the primary quantitation transitions and confirmatory, secondary transitions (if available) are given, along with MRM acquisition time windows, in Table 4A, 4B, 4C, and 4D, The primary and secondary ions should all be present and the relative intensities should agree within ±30% (absolute) of the reference mass spectrum after background subtraction is performed. In cases where the qualifier has higher intensity than quantifier ions, relative ±30% is used.

9.2.3 Initial calibration curve is always immediately checked with the second source initial calibration verification standard (ICV). The acceptance criterion is ±30%. If the Initial Calibration is not run with the batch, the CCV acceptance criterium is +/- 20% (see 9.3.2).

9.3 Daily GC/MS/MS Performance and Calibration Check

The initial calibration curve and instrument performance must be verified on each day of analysis by the measurement of one or more check standards.

9.3.1 Degradation/tailing factor check

A modified GC/MS tuning standard is used to perform this task. The standard contains 5 mg/L each of DDT-p,p' and Pentachlorophenol. Benzidine, which is also recommended by method 8270E, is usually not detectable in the presence of analyte protectants. Since the absence of benzidine peak in the chromatograms has no bearing on the chromatographic behavior of the target analytes and surrogates, only pentachlorophenol is used for the tailing factor determination. The degradation check/tailing factor standard is run at the beginning of the analytical run sequence to verify injection port inertness and GC column performance. A full scan version of the acquisition method is used for this purpose. Degradation of DDT to DDD and DDE should not exceed 20%.

The percent breakdown calculation is performed using the following formula (EPA method 8081)

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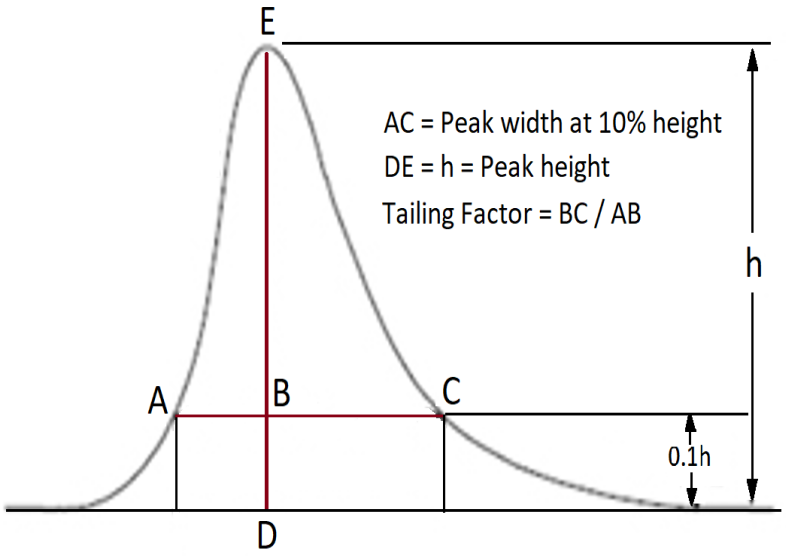
%Dec. DDT = Sum Peak Area (DDE + DDD) / Sum Peak Area (DDE + DDD + DDT) × 100%

The following are the Relative Retention Times for DDD-p,p' and DDE-p,p' (relative to DDT-p,p'):
DDE-p,p' RRT = 0.885
DDD-p,p' RRT = 0.949

Usually it is necessary to perform spectral deconvolution of the chromatograms to remove the analyte protectants "hump" and obtain correct integration values and clean spectra for target analytes. Deconvolution for GC/MS data is the process of computationally separating co-eluting components and creating a pure spectrum for each component. Specifically, for each observed EIC that results from two or more components, deconvolution calculates the contribution of each component to EIC.

The tailing factor for pentachlorophenol should not be higher than 2 according to the following equation:

Tailing Factor = BC / AB



Where the peak is defined as follows: AC is the width at 10% height; DE is the height of peak and B is the height at 10% of DE. This equation compares the width of the back half of the peak to the width of the front half of the peak at 10% of the height. If DDT-p,p' degradation and or tailing factors are excessive the injection port maintenance has to be performed until proper chromatographic performance is restored.

9.3.2 Analyze midpoint level standards as continuing calibration check (CCV) standards. These calibration check standards must be analyzed at the start of each run and at 12-hour intervals thereafter. The acceptance criteria for all components are 80-120% recovery. If multiple CCV failures are observed corrective action must be taken prior to the analysis of samples. When compounds fail, they may still be reported as non-detects (with a "J" qualifier) if it can be demonstrated that there was adequate sensitivity to detect the compounds at the applicable quantitation limit. For situations when the failed compound is present, the concentrations in the affected samples must be reported as estimated.

9.3.3 Calibration verification standard must also meet the following criteria:

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9.3.3.1 Internal standard responses: the peak area for each of the internal standards may not change beyond the factor of two (-50% to +100%) from that of the average internal standard response of all the levels in the most recent initial calibration.

9.3.3.2 Internal standards retention times: the retention times of the internal standards in the calibration verification standard must not drift by more than 30seconds from that of the mid-point standard level of the most recent initial calibration.

9.3.3.3 If any of the requirements mentioned in 9.3.3 are not met, the system must be evaluated, and corrective action must be taken before sample analysis begins. Some possible problems are standard mixture degradation, injection port inlet contamination, contamination at the front end of the analytical column, active sites in the column or chromatographic system, and a contaminated MS source.

9.4 GC/MS/MS Sample Analysis.

9.4.1 Quantitative analysis of all analytes is accomplished by the internal standard calibration method. All target component positives found must be quantified using at least a five-point calibration curve (for linear fit), at least six points for quadratic and at least seven points for higher order curves. Each sample extract MUST contain 100 µg/L of each internal standard. Any extract that is determined, in initial analysis, to contain high concentrations of any of the target analytes should be diluted as deemed necessary. **The concentration of internal standard must remain at 100 µg/L when diluting samples by adding additional internal standard to the extract.**

9.4.2 Analysis Run Sequence.

The analyst will set up an analysis run sequence by placing the GC vials containing the sample extracts and standards on the autosampler tray in the following order or similar:

- isooctane (to clean the system)
- degradation/performance check
- Instrument Blank (containing internal standards at 100 ug/L)
- pesticides calibration set (when initial calibration is run, levels 1-8)
- ICV initial calibration verification check (when initial calibration is run)
- CCV continuing calibration check
- Instrument Blank (containing internal standards at 100 ug/L)*extraction blank
- diatomaceous earth blank (tissues only)
- laboratory fortified blank (LFB)
- laboratory fortified blank duplicate
- sample matrix spike,
- sample matrix spike duplicate
- samples (for up to 12hrs)
- CCV continuing calibration check
- Instrument Blank (containing internal standards at 100 ug/L)
- samples (for up to 12 hours)

* If a CCV is directly followed by the method blank, then the instrument blank is not needed.

9.4.3 Print a hard copy of the run sequence and place it in the final data folder.

9.5 Analysis of PCB Aroclors using GC/MS/MS

9.5.1 The acquisition method for PCB Aroclors (AR_MRM_yymmdd) contains, in one single acquisition segment, 21 individual PCB transitions along with transitions for internal standards (three deuterated

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PCB congeners are used). The list of PCB transitions includes, at least, one transition for each level of chlorination, plus a number of other transitions prominent in specific Aroclors. The use of single acquisition window ensures that the entire PCB pattern can be recreated by summing up all the different transitions. All the individual transitions used in the acquisition method are listed in Table 4C. The individual PCB transitions listed in the acquisition method each reconstruct parts of the Aroclors pattern, over certain RT spans; they will each show as clusters of PCB peaks at different RTs in different parts of the chromatogram. Those peaks would, usually, be common for two or more individual Aroclors. Therefore, correlation between the acquisition transitions, and the analytical Aroclor peaks is not straightforward. The typical Aroclor analytical peaks with their quantifier and qualifier transitions are listed in Table 1C. Analyst will select 5 analytical peaks for each Aroclor that cover the entire RT range and include major transitions for that specific PCB aroclor.

9.5.2 Identification of PCB Aroclor pattern is accomplished by visual comparison of the sample chromatogram to that of the most similar Aroclor standard. A choice must be made by the analyst whether that standard is truly representative of the PCBs in the sample. Individual Aroclor standards are run for PCBs 1221, 1232, 1242, 1248, 1254 along with PCB 1016/1260 mixture (also referred to as PCB-1060). The visual comparison is accomplished in Qualitative Software by extracting the relevant chromatograms in the EIC-MRM mode. Once the identification is made the relevant chromatograms are printed out and included with the documentation. Refer to appendix 6 for PCB Aroclor patterns and analytical peaks.

9.5.3 Although this SOP is based on EPA method 8270E the quantitation algorithm of the PCBs Aroclors analysis essentially follows EPA method 8082A (Polychlorinated Biphenyls (PCBs) by Gas Chromatography) (ref 15.14). Method 8270E (ref 15.1) states in paragraph 11.7.5 that quantitation of multicomponent compounds such as Aroclors is beyond its scope and refers to GC/ECD methods (i.e.; 8082).

9.5.4 The analytical run sequence for the PCB Aroclors analysis includes a full six-point calibration for PCB 1016/1260 mix along with single standards for the five, remaining individual Aroclors, for pattern identification purposes. During the days after the initial calibration and PCB patterns are run, it is sufficient to run only PCB-1060 CCV, provided that no retention time changes occurred (no column cutting!). If the CCV fails or other factors occur (such as ion source cleaning, column cutting or replacement) the entire initial calibration must be run again. If no PCBs are identified in the sample, non- detects are reported. Positive hits for PCB 1016 and 1260 can also be reported, provided their concentrations do not exceed the calibration range. If any of the remaining Aroclor is identified, the samples must be rerun along with a full calibration for that specific Aroclor. Surrogates are included in the PCB 1016/1260 mix and therefore they may be analyzed in the original PCB analytical run sequence.

9.5.5 Once the Aroclor pattern has been identified the quantitation of Aroclors is accomplished by using 5-major peaks characteristic for each individual Aroclor (see table 1C). For the best results those peaks should be evenly spread over the entire Aroclor pattern. A separate calibration curve is built for each of the individual analytical peaks. The concentration for the total Aroclor is then assigned to each analytical peak. The amount of the Aroclor is calculated using the individual calibration factors for each of the 5 analytical peaks and the calibration model established (linear or non-linear) from the multi-point calibration. Different calibration models may be used for each selected peak. The concentrations obtained for those five analytical peaks are then, finally, averaged to determine the concentration of that Aroclor.

9.5.6 Weathering of PCBs in the environment and changes resulting from waste treatment processes may significantly alter the PCB patterns. Averaging of five, carefully chosen, analytical peaks provides for some ability to overcome weathering effects and still obtain acceptable quantitation results. To accomplish that, it is essential not to attempt to" reverse match" the analytical peaks used for calibration to those identified in the degraded sample pattern. Instead, the individual concentrations calculated for

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the analytical peaks are summed up and still divided by five, even if some peaks are missing in the sample.

9.5.7 In some cases, it may be advisable to use the total area approach to calculate the concentration in a weathered Aroclor sample. Great care must be exercised, however, to ensure that no interfering compounds elute in the same portion of the chromatogram.

9.5.8 Additional PCB aroclor standard called PCB-1268 maybe be run in some cases, especially when there is a reasonable suspicion that PCB congeners higher than those commonly found in PCB-1260 are present in the sample. PCB-1268 is not currently a target analyte in S-PCB-TQ test. However, the presence of PCB-1268 pattern indicates the presence of Decachlorobiphenyl (PCB-209, a component of PCB-1268 pattern) in the sample. Since Decachlorobiphenyl is used as a surrogate, such samples will typically have that surrogate failing high. It is therefore not necessary to report Decachlorobiphenyl surrogate in such samples.

9.5.9 In case when two overlapping PCB aroclors are present in the sample, it is permissible to select different peaks for quantitation. This includes situations when an estimate of the Total Aroclor concentration is requested by the client.

9.6 Data Processing using the Mass hunter software.

9.6.1 Using the Qual software, examine the degradation/performance check sample. Calculate DDT decomposition and the tailing factor for pentachlorophenol.

9.6.2 Examine the quantitation reports soon after the samples have been analyzed. Check all the calibration check standards analyzed during the run sequence and ensure that they met the minimum criteria given above.

9.6.3 The concentration reported for an identified hit in the sample extract, expressed in ug/L, is quantitated using the initial calibration curve. However, the analyst must ensure that all identification criteria are fulfilled, and the peak area integration was correctly done. If not, the integration must be re-done by choosing a new set of integration parameters or by manual integration (see SOP CM-018.1 for manual integration, ref 15.12).

9.6.4 If the response for any of the compounds exceeds the calibration curve, the extract must be diluted so that the response will be within the limits of the curve, and then reanalyzed. Make sure when performing dilutions to use isooctane spiked with the appropriate levels of internal standard so that their response will be the same in the dilution as it was in the original extract.

9.6.5 The internal standard responses and retention times in the calibration check standard must be evaluated immediately after data acquisition. If the retention time for any internal standard changes by more than 0.05 minutes from the last calibration, then the chromatographic system must be evaluated for either a) chromatographic matrix induced shift or inspected for malfunctions (such as leaks) and corrections must be made. The m/z abundances for all of the internal standards must be within a factor of two (50% to 200%) from the abundance in the daily calibration standard check. Corrective action is indicated if the m/z abundance is outside of these limits. If the holding time for a sample has expired and the internal standard areas are out of the acceptance range, then the final report must be commented, and any positives detected must be qualified with a "J" to indicate that the result is an estimate.

9.6.6 Analysis of surrogates.

9.6.6.1 The analyst should monitor the performance of the extraction, cleanup, analytical system, and effectiveness of the method by spiking each sample, QC samples and Method Blanks with the NP-TQ surrogate spike solution currently containing Simazine-d10 and Terbufos-d10 at 100

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ug/L, or PSCL surrogate spike solution currently containing Decachlorobiphenyl and Tetrachloro-m-xylene at 200 ug/L. Both chlorinated surrogates are used for tests, S-PSCL-TQ, S-PCB-TQ and T-PCBCL-TQ. The surrogate compounds are expected to be found at 20 µg/L in all the sample extracts, Blanks, LFBs, and Matrix Spikes.

9.6.6.2 To determine the acceptance accuracy limits for a surrogate the following procedure should be used (ref 15.5): (1) for each sample analyzed, calculate the percent recovery of each surrogate in the sample, (2) once a minimum of twenty samples of the same matrix has been analyzed, calculate the average percent recovery (p), and standard deviation of the percent recoveries (s), for each of the surrogates, (3) for a given matrix, calculate the upper and lower control limit for method performance for each surrogate standard as follows:

Upper Control Limit (UCL) = p + ts
Lower Control Limit (LCL) = p – ts
Where "t" stands for Student's coefficient for 99% confidence level for n-1 degrees of freedom (n = number of measurements).

The control limits are supposed to be checked once per year if enough measurements have been conducted. For new surrogates, the initial acceptance limits of about 50-150 % will be used until enough statistical data is acquired to perform the necessary calculations.

9.6.6.3 If a surrogate recovery fails, and there is a reasonable suspicion that instrument related factors may be responsible, the sample maybe re-analyzed and the rerun reported if passing. If the surrogate fails again, and recovery is biased low, the sample must be re-extracted and re-analyzed, even if the holding time for extraction is already exceeded. If the recovery is biased high, the re-extraction is not required, and the reported hits must be qualified as estimated (J). An automatic comment will be generated by LIMS.

9.6.7 Analysis of matrix spikes and LFBs

Check the Matrix Spike and Lab Fortified Blank recoveries. They must be within the current acceptance ranges. A comment must be added to the final report explaining any deviation from the routine recoveries whenever the spikes or surrogates are out of range. Matrix spikes and LFBs recovery and precision limits should be calculated based on available in-house data once enough data points are collected. See ref 15.8, chapter 5.3 for details. LFBs and Matrix spikes recovery limits are calculated independently; see Table 6 for details. In case LFB failures are observed the LFBs may be rerun and reanalyzed. All the associated samples that have positives (above PQL) for the analytes failing in the LFBs must be re-run and reanalyzed as well. Similarly, if the number of matrix spikes failure is deemed excessive matrix spikes (along with the background sample) may be rerun and reanalyzed. Refer to ref 15.8 chapter 5.3 for details on disposition of QC failures.

9.6.8 Blank contamination

In the event a positive identification is found in both the sample(s) and the instrument blank, the instrument must be cleaned and the sample(s) rerun/reanalyzed.

In the event a positive identification is found in both the sample(s) and the extraction blank then the sample set must be re-extracted and reanalyzed. If samples passed the holding time, the results will be reported with a "V" qualifier up to ten times the amount found in the blank.

In the event a positive identification is found in a field blank, but method blank(s) pass, the field blank detection only affects the samples in the same job. If those samples do not show any detections for the analyte found in the field blank, the field blank does not need to be re-extracted. If the detections are found up to 10x the level in the field blank, all samples with such detections and the field blank must be re-extracted. If the detections are above the 10x field blank level, no re-extractions are necessary.

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9.6.9 Continuing Calibration

9.6.9.1 After initial calibration, the GC/MS/MS response is checked immediately by running an Initial Calibration Verification standard (ICV) and then, on a continuing basis (every 12 hours), by using a continuing calibration check (CCV), middle range pesticides standard. Criterion of acceptance for continuing calibration check is +/-20 % of initial calibration. If a CCV fails, all the samples run after this standard, must be re-run for all positive hits found at concentrations higher than PQL level. If the samples have exceeded the analysis holding time, then all hits must be flagged as estimated.

9.6.9.2 If CCVs do not meet method requirements but the associated analytical results are below the detection limit or below the quantifiable threshold (PQL) and no systematic failure is observed (i.e., the failure is deduced to be due to a statistical outlier in a multi-component analysis where results from other CCV components and LFB results do not indicate a systematic bias in the analysis or detector response), an appropriate test comment and result qualifier (J) shall be provided to indicate the CCVs are outside control limits. However, when a systematic or system failure is detected, or the affected analytical data are above the quantifiable threshold, the analysis shall be re-run if possible. If re-analysis is not an option, the analytical results shall be qualified as estimates (see 15.7 for more details).

9.6.10. Quantitation of positives.

Positives are quantified based on their peak area. The concentration reported for an identified hit in the sample extract, expressed in ug/L, is based on calibration curve of the initial calibration. The Masshunter software used to process data will do the interpolation for the sample extract. However, the analyst must ensure that all identification criteria are fulfilled, and the peak area integration was correctly done. If not, the integration has to be corrected by choosing a new set of integration parameters or by manual integration (for manual integration procedure see 15.12). Only extract concentrations are calculated by the processing software. The final analyte concentrations in sample are calculated in the QC Manager during the data upload process software. This is done as follows:

- C_{sample} (ug/kg) = (C_X) × ($V_{extract}$) × (DF)/(W_{sample}) for sediment and waste and tissue
- C_{sample} (ng/L) = (Cx) × ($V_{extract}$) × (DF)/(V_{sample}) for water samples

where:

- C_X - The concentration, in ug/L, of the analyte in the sample extract determined by the processing software.
- $V_{extract}$ -The volume of the extract, in mls (usually 0.25 or 10 or 2 mls) recorded in the preparation report.
- DF - The dilution of the sample extract recorded in the dilution report.
- W_{sample} - For sediment it is the dry weight of the sample that was extracted. For waste and tissue it is the weight of the sample taken for extraction. The weights are expressed in grams and are recorded in the preparation report.
- V_{sample} -This is the volume of the water sample taken in extraction, expressed in mLs (usually 1000 mL).

9.7 Analysis if caffeine by isotope dilution. Caffeine is considered a tracer of human activity since it is contained in coffee, tea, and other drinks and finds its way into environment. Due to its polarity, it may extract from water poorly. To offset the possible extraction loses, the isotope dilution approach is used using caffeine d-9 as an

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extracted internal standard. Caffeine-d9 is spiked into samples with other surrogates at a concentration that results in the theoretical final volume concentration of 100 ppb, assuming 100% recovery. The concentration of caffeine-d9 in calibration standards (as internal standard) is also 100 ppb. Regardless of the actual recovery, the concentration of caffeine-d9 as internal standard in samples is assumed to be 100 ppb, therefore offsetting the loses. In order to also assess the recovery of caffeine-d9 as surrogate it is additionally quantitated as surrogate against "injection" internal standard -atrazine-d5.

9.8 Caffeine is often present at detectable levels in method blanks and other kinds of blanks. It is therefore highly recommended that field blanks and equipment blanks are collected and analyzed along with samples scheduled for caffeine analysis.

10 REPORTING AND DOCUMENTATION

10.1 When analysis is complete, generate a .txt file in the Masshunter software for all the reported samples, QC samples and CCVs. The QC Manager is then used to download the final sample results into the Laboratory Information Management System (LIMS). If a sample has been diluted, then make sure that the information was entered properly into the QC Manager. The following convention should be used in QC calculator:

NP_CCV or CL_CCV or PCB_CCV for CCV
SURNP_CCV or SURSNP_CCV or SURCL_CCV or SURRPCB for surrogate in CCV
SURNP_1234567 or SURSNP_1234567 or SURCL_1234567 or SURRCLT_1234567 or SURPCB_1234567 for surrogate in sample

10.2 The QC manager will convert the data from ug/L to ng/L (LIMS reporting units, water samples only; not applicable for soils and tissues) and also it will add MDLs for all analytes not included in the text file (non-detects). The converter will also average the PCB aroclors result and report the average as the corresponding aroclor.

10.3 Add the appropriate qualifiers and comments to the sample data in the QC Manager after performing a complete review of the sample data and QC data. Follow DEP SOP GC-001- (ref 15.8) for details of data review and reporting, See DEP SOP LB-027, (ref 15-7) for guidelines for qualifying data when quality control results are outside established control limits and re-analysis is not a viable or desired option. Definitions of the available qualifying codes are listed in DEP SOP LB-027.

10.4 All quantitation reports for samples and QC should be placed in a results folder labeled with the job number, the sample numbers, and the type of analysis.

10.5 Enter the results for each sample in the analysis results form. Print out QC results from the QC Manager. Include a copy of dilutions page if any. Also include a printout of sample positives from the data review (a scrollable report) and file it in the data folder.

10.6 Submit the result folder to the GC pesticides section supervisor. The supervisor will review results and then authorize the sample. The supervisor will then file the folders in the GC-pesticides filing cabinets.

11 QUALITY CONTROL

11.1 See DEP SOP GC-001, (ref 15.8) for detailed information on quality control, definitions and interferences. See DEP SOP LB-027, (ref 15.7) for guidelines for qualifying data when quality control results are outside established control limits and re-analysis is not a viable or desired option.

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11.2 All data generated by a chemistry analyst are subjected to supervisory review and authorization. The supervisor is assessing the validity of data generated by assuring that all QA/QC criteria are met by checking the following review/authorization checklist:

- Check sample preparation report
  - procedure
  - surrogate and spiking solutions
  - preparation holding time
- Check project log-in folder for special requests
- Check initial calibration for linearity and fit
- Check continuing calibration check standards
- Check surrogate recoveries
- Check accuracy and precision for LFB and Matrix Spikes
- Check internal standard recoveries
- Check retention time drift
- Check for blanks contamination
- Check for positives:
  - Proper integration of the peaks (baseline)
  - Retention time confirmation
  - Amount confirmation
  - If response is within the calibration range
  - Calculations
  - Qualifiers
  - Proper identification of Aroclor patterns
- Check information in the Mass hunter Report Header:
  - SOP #
  - Instrument ID
  - Analyst name
- Evaluate the data against any field information
- Check field preservation record
- Check LIMS report:
  - Preparation and analysis dates
  - MDLs
  - Amounts reported for positives
  - Qualifiers
  - Comments

12 DATA ARCHIVAL

12.1 All raw data are retained in electronic or hard copy format. All paper formats are maintained either in the laboratory office or in a State warehouse for at least ten years. Electronic chromatographic raw data are archived by analysis file ID and instrument ID on dual CDs by the Laboratory Support Section.

12.2 The valid data files (tune, ICALS, CCVs, QC and sample data files) are moved soon after collection from the hard disk of the instrument computers to the network drive \\TLHLAB3\GC\BACKUP_GC_TQ-1 (or TQ-2, or TQ-3 or TQ-4). Raw data files on the hard disk of each instrument may be deleted after 3 to 4 months or whenever they are no longer needed. This process is now automated with backup executable files that run automatically every 24 hrs.

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12.3 Upload files are generated by a macro and stored automatically (as .txt files) into \\TLHLAB3\GC\UPLOAD_GC_TQ-1 (or TQ-2, or TQ-3 or TQ-4). They are then converted in QC Manager for reporting in LIMS.

13. DETERMINATION OF METHOD DETECTION LIMITS

13.1 The MDLs were established using procedures given in EPA Chapter 40 Part 136, Appendix B of the Federal Register (ref 15.13). Also refer to references 15.9 and 15.10**.**

13.2 At least seven replicate samples are analyzed near the MDL. The MDL is the concentration of analyte at which there is analyte present with 99% confidence. The validation exercise is split into at least three extraction batches performed on three separate days. The samples are run in all the instruments that are considered identical for the purpose of this analysis. Along with the spikes an equal number of blanks is extracted.

13.3 The results of the (at least) seven replicate data sets are tabulated and the statistical calculations are performed electronically to establish or update the MDLs and PQLs for each analyte and matrix. The MDL results calculated based on the blanks and spikes data are compared and the MDL is set at the higher value (at least).

13.4 For PCB aroclors a mixture 1016+1260, which covers the entire PCB range, is used for MDL determination. The higher of the two calculated MDLs is the applied to all seven PCB aroclors.

13.5 MDLs are verified quarterly and recalculated annually. At least one spike is run in each instrument per quarter in which samples are analyzed. The spike is prepared at concentration between MDL and PQL and it is also considered a PQL verification. The PQL acceptance criteria are specified in the QCM limits tables for each analyte and are typically up to 20% wider than the corresponding LFB recovery limits. The MDLs are recalculated annually (at least) based on the last 24 months of data. Both spikes and blanks are used in calculations. If the calculated MDL is within a factor of 2 of the current MDL, the current MDL may be kept unchanged. Otherwise, the MDL has to be changed to the new calculated value. MDL/PQL verification spikes are reported to LIMS as QC type SRM. The LIMS statistics module is used for the annual re-calculation of MDLs.

14. SAFETY/HAZARDOUS WASTE MANAGEMENT

See SOP OG-001, (ref 15.11) for specific details on safety and hazardous waste management.

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15. REFERENCES

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15.2 GC SOP GC-002: Extraction of Pesticides, Environmental Tracers and Polychlorinated Biphenyls (PCBs) from Water, Wastes, and Soil/Sediments Samples for Subsequent Analysis by GC/MS Techniques.

15.3 Anastassiades, M., Mastovska, K., Lehotay, S.J., “Evaluation of analyte protectants to improve gas chromatographic analysis of pesticides” Journal of Chromatography A, 1015 (2003) 163-184.

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15.5 EPA 8000D Determinative Chromatographic Separation; Test Methods for Evaluating Solid Wastes, Physical/Chemical Methods, SW 846; 3rd Edition, Update 5, revision 4, July 2014.

15.6 Agilent Masshunter Optimizer software. Agilent Masshunter Workstation Optimization Tools B.10.00 (10.0.706.2). 11/05/2020.

15.7 DEP SOP LB-027. Reporting Qualified Data and Correcting Quality Control Problems.

15.8 DEP SOP GC-001. Quality Assurance/Quality Control and Data Review Authorization in the GC Pesticides Laboratory

15.9 DEP SOP LB-007 *Procedure and Policy for Demonstration of Capability for Methods, Instruments and Laboratory Staff.*

15.10 DEP SOP LB-031 Method Detection *Limit Verification.*

15.11 DEP SOP OG-001. Safety and Waste Management Practices in the Organic Analysis Groups (Volatile, Semi-Volatile and Pesticide Laboratories).

15.12 DEP SOP CM-018-1 Laboratory Policy Regarding Manual Chromatographic Peak Integration.

15.13 Code of Federal Regulations, Title 40, Part 136, Appendix B.

15.14 Test Methods for Evaluating Solid Wastes, Third Edition, SW-846, Method 8082A, Polychlorinated Biphenyls (PCBs) By Gas Chromatography

15.15 DEP SOP GC-004: Extraction of Organophosphorus, organonitrogen, organohalide pesticides, PAHs and PCBs from Fish Tissue Using Pressurized Fluid Extraction Technique.

15.16 Wylie, P., Meng, Chin-Kai, "A Method for the Trace Analysis of 175 Pesticides Using Agilent Triple Quadrupole GC/MS/MS" Agilent Technologies Application Note.

15.17 Mastovska, K. "Rugged GC/MS/MS Pesticide Residue Analysis Fulfilling the USDA Pesticide Data Program (PDP) Requirements." Agilent Technologies Application Note

15.18 Foch, I., Ciceri, E., Huebschmann, H., "Fast GC-MS/MS for High Throughput Pesticides Analysis" Thermo Fisher Scientific Application Note 52027

15.19 Walker, D., "Analyzing PCB Aroclors by Agilent's 7000B GCMS tandem quadrupole Mass Spectrometer" Agilent presentation.

16. TABLES

TABLE 1A-Water: Internal standard associations, quantifier and qualifier transitions, MDLs, PQLs and approximate RTs for Nitrogen Phosphorus pesticides included in LIMS test W-PSNP-TQ. **LIMS reporting units are ng/L (ppts)**

Analyte	Approximate Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	MDL (ug/L)	MDL (ng/L)	PQL (ug/L)	PQL (ng/L)
					extract	sample	extract	sample
Simazine-d10 surrogate	6.13	Atrazine-d5	211.3-179.1	179.2-144				

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Analyte	Approximate Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	MDL (ug/L)	MDL (ng/L)	PQL (ug/L)	PQL (ng/L)
Terbufos-d10 surrogate	6.00	Tributyl Phosphate- d27	241.1-130.9	163.0-98.9				
EPTC	4.30	EPTC-d14	189.1-128.1	128.1-86.1	5.0	1.30	20	5.0
Butylate	4.58	EPTC-d14	217.1-156.1	174.1-146.1	1.6	0.40	6.4	1.6
Mevinphos	4.64	Tributyl Phosphate- d27	192-127	127-95	4.2	1.0	17	4.2
Etridiazole	4.76	Atrazine-d5	210.9-240.0	210.9-182.9	0.60	0.15	2.4	0.60
Molinate	5.09	EPTC-d14	187-126	187-158	1.2	0.30	4.8	1.2
Demeton*	5.44 –"O" 6.09 - "S"	Tributyl Phosphate- d27	171.0-115.0 171.0-115.0	171. 97.0 171.0-97.0	6.0	1.5	24	6.0
Ethoprop	5.57	Tributyl Phosphate- d27	158.0-97.0	158.0-114.0	0.40	0.10	1.6	0.40
Naled*	3.98 "peak 1" 5.65 "peak2"	Tributyl Phosphate- d27	185.0-93.0 184.9-93.0	109.0-79.0 144.9-109	6.0	1.5	24	6.0
Atrazine Desethyl	5.78	Atrazine-d5	186.0-172.1	187.0110.1	6.0	1.5	24	6.0
Phorate	5.90	Tributyl Phosphate- d27	231.0-174.9	231.0-128.9	2.1	0.53	8.4	2.1
Simazine	6.17	Atrazine-d5	185.6-90.9	201.1-138.1	2.0	0.50	8.0	2.0
Prometon	6.18	Atrazine-d5	225.2-183.1	225.2-210.2	3.6	0.90	14	3.6
Atrazine	6.21	Atrazine-d5	200.1-104	200.1-122.1	1.0	0.25	4.0	1.0
Terbuthylazine	6.37	Atrazine-d5	213.9-104	213.9-132	1.7	0.43	6.8	1.7
Terbufos	6.36	Tributyl Phosphate- d27	231.0-128.9	213.0-174.9	0.40	0.10	1.6	0.40
Pronamide	6.39	Atrazine-d5	172.9-145.1	172.9-109.1	0.60	0.15	2.4	0.60
Fonofos	6.41	Tributyl Phosphate- d27	246.0-137.0	246.0-109.0	0.80	0.20	3.2	0.80
Diazinon	6.49	Atrazine-d5	304.1-179.1	179.1-121.1	0.50	0.13	2.0	0.50
Disulfoton	6.56	Tributyl Phosphate- d27	185.9-108.9	185.9-97	2.0	0.50	8.0	2.0
Caffeine	6.80	Caffeine-d9	194.0-109.1	194.0-137.1	20	5.0	80	20
Dimethenamid	6.94	Atrazine-d5	230-154	154-111	0.40	0.10	1.6	0.40
Propanil	6.94	Atrazine-d5	161.0-99.0	161.0-90.0	0.50	0.13	2.0	0.50
Metribuzin	6.95	Metribuzin-d3	198-82	198-55	10	2.5	40	10
Acetochlor	6.99	Atrazine-d5	223-132	223-147.1	1.0	0.25	4.0	1.0
Chlorpyrifos Methyl	7.01	Tributyl Phosphate- d27	286-93	286-270.9	0.20	0.050	0.80	0.20
Alachlor	7.08	Atrazine-d5	188.1-160.1	161.1-146.1	1.0	0.25	4.0	1.0
Fipronil Desulfinyl	7.09	Atrazine-d5	387.9-332.9	387.9-280.9	0.50	0.13	2.0	0.50

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Analyte	Approximate Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	MDL (ug/L)	MDL (ng/L)	PQL (ug/L)	PQL (ng/L)
Ametryn	7.10	Atrazine-d5	227.1-58.3	227.1-155.2	2.4	0.60	9.6	2.4
Prometryn	7.13	Atrazine-d5	241.1-58.2	241.1-184.2	0.80	0.20	3.2	0.80
Metalaxyl	7.13	Atrazine-d5	234.1-174.1	249.1-190.1	3.0	0.75	12	3.0
Dithiopyr	7.21	Atrazine-d5	354.1-306	354.1-286	0.70	0.18	2.8	0.70
Prodiamine	7.25	Atrazine-d5	321.0-279.0	321.0-203.0	0.70	0.18	2.8	0.70
Parathion Methyl	7.25	Parathion Ethyl-d10	262.9-109.0	262.9-124.9	2.2	0.55	8.8	2.2
Bromacil	7.31	Atrazine-d5	205-132	231-188	2.0	0.50	8.0	2.0
Malathion	7.35	Tributyl Phosphate- d27	173.1-99.0	173.1-117	1.0	0.25	4.0	1.0
Thiobencarb	7.37	Atrazine-d5	125.0-89.0	257.1-100	2.4	0.60	9.6	2.4
Metolachlor	7.38	Atrazine-d5	162.1-133.1	238.0-162.0	1.4	0.35	5.6	1.4
Chlorpyrifos Ethyl	7.44	Tributyl Phosphate- d27	196.9-168.9	196.9—107.0	1.0	0.25	04.0	1.0
Cyanazine	7.47	Atrazine-d5	225.1-198.1	225.1-189.1	13	3.2	52	13
Parathion Ethyl	7.65	Parathion Ethyl-d10	291.0-109.0	291.0-137.0	1.0	0.25	4.0	1.0
Tridimefon	7.67	Atrazine-d5	208.1-111.0	208.1-181.1	1.0	0.25	4.0	1.0
Cyprodinil	7.79	Atrazine-d5	224.0-118.0	224.0-208.1	0.40	0.10	2.0	0.50
Pendimethalin	7.70	Parathion Ethyl-d10	252.1-162.1	252.1-191.1	4.0	1.0	16	4.0
Fipronil Sulfide	7.72	Tributyl Phosphate- d27	350.9-255	419.9-351	0.60	0.15	2.4	0.60
Fipronil	7.78	Atrazine-d5	367-213	367-255	1.0	0.25	4.0	1.0
Stirophos	8.00	Tributyl Phosphate- d27	329.0-109.0	329.0-79.0	0.50	0.13	2.0	0.50
Fenamiphos	8.07	Tributyl Phosphate- d27	154-139	303-195	2.0	0.50	8.0	2.0
Napropamide	8.08	Atrazine-d5	271.1-128.1	271.1-71.1	1.6	0.40	6.4	1.6
Flutolanil	8.09	Atrazine-d5	173.0-145.1	173.0-95.0	0.40	0.10	1.6	0.40
Fludioxonil	8.16	Atrazine-d5	248.0-127.0	248.0-182.0	0.50	0.13	2.0	0.50
Oxadiazon	8.17	Atrazine-d5	174.9-112	301.9-175.0	1.20	0.30	4.8	1.2
Imazalil	8.20	Atrazine-d5	214.9-173.0	173.0-145	3.0	0.75	12	3.0
Oxyfluorfen	8.22	Atrazine-d5	252.0-146.0	252.0-196.1	0.60	0.15	2.4	0.60
Myclobutanil	8.23	Atrazine-d5	179.0-125.0	179.0-152.0	1.0	0.25	4.0	1.0
Fipronil Sulfone	8.25	Tributyl Phosphate- d27	382.9-255	255-228	0.60	0.15	2.4	0.60
Fluazifop-P-butyl	8.32	Atrazine-d5	383-282.1	282.0-238.1	0.40	0.10	1.6	0.40

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Analyte	Approximate Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	MDL (ug/L)	MDL (ng/L)	PQL (ug/L)	PQL (ng/L)
Chlorfenapyr	8.34	Tributyl Phosphate- d27	247.1-227.1	326.0-247.0	0.70	0.18	2.8	0.70
Ethion	8.49	Tributyl Phosphate- d27	231.0-128.9	231-174.9	0.60	0.15	2.4	0.60
Carfentrazone Ethyl	8.57	Atrazine-d5	330.0-310.1	340.0312.1	0.40	0.10	1.6	0.40
Carbophenothion	8.60	Tributyl Phosphate- d27	341.9-159.0	343.9-158.9	0.80	0.20	3.2	0.80
Norflurazon	8.74	Atrazine-d5	303.3-145	303.3-173.1	2.0	0.50	8.0	2.0
Pyraflufen Ethyl	8.77	Atrazine-d5	349.0-307.0	412.0-349.0	1.0	0.25	4.0	1.0
Propiconazole**	8.79	Atrazine-d5	259.0-173.0	172.9-144.9	2.0	0.50	8.0	2.0
Hexazinone	8.82	Hexazinone-d6	171.1-85.1	128-83	2.0	0.50	8.0	2.0
Tebuconazole	9.00	Atrazine-d5	250.0-125.0	252.0-127.0	2.0	0.50	8.0	2.0
Propargite	9.02	Atrazine-d5	173.1-107.1	173.1-135.1	6.0	1.5	24	6.0
Phenytoin	9.04	Atrazine-d5	209.0-180.0	180.0-76.9	14	3.5	56	14
Iprodione	9.10	Atrazine-d5	313.9-56.0	316.0-56.0	2.4	0.60	9.6	2.4
Fluxapyroxad	9.15	Atrazine-d5	381.0-159.0	159.0-139.0	0.40	0.10	1.6	0.40
Sulfentrazone	9.18	Atrazine-d5	385.9-307.1	385.9-351.1	2.0	0.50	8.0	2.0
Pyriproxyfen	9.33	Atrazine-d5	136.1-78.0	136.1-96.0	0.50	0.13	2.0	0.50
Azinphos Methyl	9.35	Atrazine-d5	160.1-77.1	160.1-132.1	8.0	2.0	32	8.0
Pyridaben	9.77	Tributyl Phosphate- d27	147.0-117.0	147.0-132.0	1.8	0.45	9.0	2.2
Coumaphos	9.91	Tributyl Phosphate- d27	361.9-109.0	361.9-81.0	2.0	0.50	8.0	2.0
Fenbuconazole	10.20	Atrazine-d5	198.0-129.0	129.0-102	0.50	0.13	2.0	0.50
Flumioxazin	10.79	Atrazine-d5	354.0-326.0	354.0-312.0	7.0	1.8	28	7.0
Difenoconazole**	11.30	Atrazine-d5	323.0-265.0	265.0-139.0	2.4	0.60	9.6	2.4
Azoxystrobin	11.73	Azoxystrobin-d4	388.1-345.2	344.1-329.1	2.0	0.50	8.0	2.0
Dimethomorph*	11.77	Azoxystrobin-d4	300.9-165.0	303.0-165.0	0.70	0.18	4.2	1.1
Loratadine	12.13	Azoxystrobin-d4	382.1-292.0	382.1-245.1	0.40	0.10	1.6	0.40
EPTC-d14	4.25	Internal Standard	203.1-94.1	142.1-94.1				
Tributyl Phosphate- d27	5.51	Internal standard	103.1-83.0	103.1-63.0				
Atrazine-d5	6.19	Internal standard	205.1-105.1	205.1-127.1				

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Analyte	Approximate Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	MDL (ug/L)	MDL (ng/L)	PQL (ug/L)	PQL (ng/L)
Caffeine-d9	6.75	Internal standard***	203.1-60.1	203.1-115.1				
Metribuzin-d3	6.90	Internal standard	202.0-118.0	216.8-201.0				
Parathion Ethyl-d10	7.63	Internal standard	301.0-115.0	301.0-147.0				
Hexazinone-d6	8.82	Internal standard	177.2-77.1	177.2-91.1				
Azoxystrobin-d4	11.70	Internal Standard	348.0-292.0	382.1-245.1				

- *Summary peak is used to report Demeton, Dimethomorph and Naled
- ** "Sum all" approach is used to report Propiconazole and Difenoconazole. Both have two closely eluting isomers.
- *** Caffeine-d9 is used as internal standard/surrogate for isotope dilution analysis of caffeine.

Organophosphate analytes are associated to terbufos-d10 surrogate, while organonitrogen analytes are associated to simazine-d10 surrogate. Caffeine is associated to caffeine-d9 surrogate.

TABLE 1A-Soil/Waste: Internal standard associations, Quantifier and qualifier transitions, as well as MDLs, PQLs and approximate RTs for Nitrogen Phosphorus pesticides included in LIMS test S-PSNP-TQ/WS-PSNP-TQ. **LIMS reporting units are ug/Kg**

Analyte	Appr. Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	MDL ug/L	MDL ug/Kg soil	MDL ug/Kg waste	PQL ug/L	PQL ug/Kg soil	PQL ug/Kg waste
					extract	sample	sample	extrac t	sample	sample
Simazine-d10 surrogate	6.13	Atrazine-d5	211.3-179.1	179.2-144						
Terbufos-d10 surrogate	6.32	Tributyl Phosphate-d27	241.1-130.9	163.0-98.9						
Methamidophos	4.05	Tributyl Phosphate-d27	141.0-95.0	141.0-79.0	24	1.6	240	96	6.4	960
EPTC	4.30	EPTC-d14	189.1-128.1	128.1-86.1	5.0	0.33	50	20	1.3	200
Butylate	4.58	EPTC-d14	217.1-156.1	174.1-146.1	4.0	0.27	40	16	1.1	160
Mevinphos	4.64	Tributyl Phosphate-d27	192-127	127-95	5.0	0.33	50	20	1.3	200
Molinate	5.09	EPTC-d14	187-126	187-158	1.5	0.10	15	6.0	0.40	60

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Analyte	Appr. Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	MDL ug/L	MDL ug/Kg soil	MDL ug/Kg waste	PQL ug/L	PQL ug/Kg soil	PQL ug/Kg waste
Demeton*	5.44 –"O" 6.09 - "S"	Tributyl Phosphate-d27	171.0-115.0 171.0-115.0	171. 97.0 171.0-97.0	14	0.93	140	56	3.7	560
Ethoprop	5.57	Tributyl Phosphate-d27	158.0-97.0	158.0-114.0	0.5	0.033	5	2.0	0.13	20
Naled*	3.98 "peak 1" 5.65 "peak2"	Tributyl Phosphate-d27	185.0-93.0 184.9-93.0	109.0-79.0 144.9-109	10	0.67	100	40	2.7	400
Atrazine Desethyl	5.78	Atrazine-d5	186.0-172.1	187.0110.1	6.0	0.40	60	24	1.6	240
Phorate	5.90	Tributyl Phosphate-d27	231.0-174.9	231.0-128.9	1.0	0.067	10	4.0	0.27	40
Monocrotophos	6.06	Tributyl Phosphate-d27	192.0-127.0	192.0-164.0	25	1.7	250	100	6.7	1000
Simazine	6.17	Atrazine-d5	185.6-90.9	201.1-138.1	2.0	0.13	20	8.0	0.53	80
Prometon	6.18	Atrazine-d5	225.2-183.1	225.2-210.2	3.6	0.24	0.90	14	0.96	3.6
Atrazine	6.21	Atrazine-d5	200.1-104	200.1-122.1	1.0	0.067	10	4.0	0.27	40
Terbuthylazine	6.37	Atrazine-d5	213.9-104	213.9-132	1.0	0.067	10	4.0	0.27	40
Terbufos	6.36	Tributyl Phosphate-d27	231.0-128.9	213.0-174.9	1.0	0.067	10	4.0	0.27	40
Pronamide	6.39	Atrazine-d5	172.9-145.1	172.9-109.1	1.0	0.067	10	4.0	0.27	40
Fonofos	6.41	Tributyl Phosphate-d27	246.0-137.0	246.0-109.0	0.80	0.053	8.0	3.2	0.21	3.2
Diazinon	6.49	Atrazine-d5	304.1-179.1	179.1-121.1	1.0	0.067	10	4.0	0.27	40
Disulfoton	6.56	Tributyl Phosphate-d27	185.9-108.9	185.9-97	2.0	0.13	20	8.0	0.53	80
Dimethenamid	6.94	Atrazine-d5	230-154	154-111	0.20	0.013	2.0	0.80	0.053	8.0
Metribuzin	6.95	Metribuzin-d3	198-82	198-55	5.0	0.33	50	20	1.3	200

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Analyte	Appr. Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	MDL ug/L	MDL ug/Kg soil	MDL ug/Kg waste	PQL ug/L	PQL ug/Kg soil	PQL ug/Kg waste
Acetochlor	6.99	Atrazine-d5	223-132	223-147.1	3.0	0.20	30	12	0.80	120
Chlorpyrifos Methyl	7.01	Tributyl Phosphate-d27	286-93	286-270.9	1.0	0.067	10	4.0	0.27	40
Alachlor	7.08	Atrazine-d5	188.1-160.1	161.1-146.1	2.0	0.13	20	8.0	0.53	80
Fipronil Desulfinyl	7.09	Atrazine-d5	387.9-332.9	387.9-280.9	0.70	0.047	7.0	2.8	0.19	28
Ametryn	7.10	Atrazine-d5	227.1-58.3	227.1-155.2	2.0	0.13	20	8.0	0.53	80
Prometryn	7.13	Atrazine-d5	241.1-58.2	241.1-184.2	3.0	0.20	30	12	0.80	120
Metalaxyl	7.13	Atrazine-d5	234.1-174.1	249.1-190.1	3.0	0.20	30	12	0.80	120
Dithiopyr	7.21	Atrazine-d5	354.1-306	354.1-286	0.60	0.080	6.0	2.4	0.16	24
Prodiamine	7.25	Atrazine-d5	321.0-279.0	321.0-203.0	0.60	0.080	6.0	2.4	0.16	24
Parathion Methyl	7.25	Parathion Ethyl-d10	262.9-109.0	262.9-124.9	1.0	0.067	10	4.0	0.27	40
Bromacil	7.31	Atrazine-d5	205-132	231-188	4.0	0.27	40	16	1.1	160
Malathion	7.35	Tributyl Phosphate-d27	173.1-99.0	173.1-117	2.0	013	20	8.0	0.53	80
Metolachlor	7.38	Atrazine-d5	162.1-133.1	238.0-162.0	1.2	0.080	12	4.8	0.32	48
Chlorpyrifos Ethyl	7.44	Tributyl Phosphate-d27	196.9-168.9	196.9—107.0	1.0	0.067	10	4.0	0.27	40
Cyanazine	7.47	Atrazine-d5	225.1-198.1	225.1-189.1	4.0	0.27	40	16	1.1	160
Parathion Ethyl	7.65	Parathion Ethyl-d10	291.0-109.0	291.0-137.0	1.0	0.067	10	4.0	0.27	40
Pendimethalin	7.70	Parathion Ethyl-d10	252.1-162.1	252.1-191.1	4.0	0.27	40	16	1.1	160
Fipronil Sulfide	7.72	Tributyl Phosphate-d27	350.9-255	419.9-351	1.4	0.093	14	5.6	0.37	56
Fipronil	7.78	Atrazine-d5	367-213	367-255	1.0	0.067	10	4.0	0.27	40

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Analyte	Appr. Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	MDL ug/L	MDL ug/Kg soil	MDL ug/Kg waste	PQL ug/L	PQL ug/Kg soil	PQL ug/Kg waste
Fenamiphos	8.07	Tributyl Phosphate-d27	154-139	303-195	4.1	0.27	41	16	1.1	160
Oxadiazon	8.17	Atrazine-d5	174.9-112	301.9-175.0	0.50	0.033	5.0	2.0	0.13	20
Fipronil Sulfone	8.25	Tributyl Phosphate-d27	382.9-255	255-228	1.3	0.090	13	5.2	0.35	53
Ethion	8.49	Tributyl Phosphate-d27	231.0-128.9	231-174.9	3.0	0.20	30	12	0.80	120
Carbophenothion	8.60	Tributyl Phosphate-d27	341.9-159.0	343.9-158.9	1.0	0.067	10	4.0	0.27	40
Norflurazon	8.74	Atrazine-d5	303.3-145	303.3-173.1	4.0	0.27	40	16	1.1	160
Propiconazole**	8.79	Atrazine-d5	259.0-173.0	172.9-144.9						
Hexazinone	8.82	Hexazinone-d6	171.1-85.1	128-83	8.0	0.20	80	32	0.80	320
Tebuconazole	9.00	Atrazine-d5	250.0-125.0	252.0-127.0	1.0	0.067	10	4.0	0.27	40
Sulfentrazone	9.18	Atrazine-d5	385.9-307.1	385.9-351.1	1.2	0.080	12	4.8	0.32	48
Azinphos Methyl	9.35	Atrazine-d5	160.1-77.1	160.1-132.1	12	0.80	120	48	3.2	480
Flumioxazin	10.79	Atrazine-d5	354.0-326.0	354.0-312.0	12	0.80	120	48	3.2	480
EPTC-d14	4.25	Internal Standard	203.1-94.1	142.1-94.1						
Tributyl Phosphate-d27	5.51	Internal standard	103.1-83.0	103.1-63.0						
Atrazine-d5	6.19	Internal standard	205.1-105.1	205.1-127.1						
Metribuzin-d3	6.90	Internal standard	202.0-118.0	216.8-201.0						
Parathion Ethyl-d10	7.63	Internal standard	301.0-115.0	301.0-147.0						
Hexazinone-d6	8.82	Internal standard	177.2-77.1	177.2-91.1						

- *Summary peak is used to report Demeton and Naled

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- ** "Sum all" approach is used to report Propiconazole. Propiconazole has two closely eluting isomers.

Organophosphate analytes are associated to terbufos-d10 surrogate, while organonitrogen analytes are associated to simazine-d10 surrogate.

TABLE 1B: Internal standard associations, quantifier and qualifier transitions, MDLs, PQLs and approximate RTs for Chlorinated pesticides included in LIMS tests S-PSCL-TQ and WS-PSCL-TQ. **LIMS reporting units are ug/kg**

Analyte	**Approx. Retention Time (min)**	**Internal standard**	**Quantifier transition**	**Qualifier transition**	**MDL ug/L**	**MDL ug/kg soil**	**MDL Ug/kg waste**	**PQL ug/L**	**PQL ug/kg soil**	**PQL ug/kg waste**
					extract	sample	sample	extract	sample	sample
Tetrachloro-m-xylene surrogate	5.99	DCB-d5	206.9-136.0	206.9-171.9						
Decachlorobiphenyl surrogate	16.25	HCB-d3	497.6-427.9	497.6-462.7						
Ethalfluralin	6.56	Trifluralin-d14	276.0-202.0	316.0-276.0	1.0	0.067	10	4.0	0.27	40
Trifluralin	6.69	Trifluralin-d14	306.1-264.0	306.1-160.0	2.0	0.13	20	8.0	0.53	80
Alpha-BHC	6.92	Alpha-BHC-d6	181.0-145.0	181.0-109.0	0.25	0.017	2.5	1.0	0.067	10
Hexachlorobenzene	7.08	DCB-d5	283.7-213.9	283.7-248.8	1.0	0.067	10	4.0	0.27	40
Beta-BHC	7.42	Alpha-BHC-d6	181.0-145.0	181.0-109.0	0.50	0.033	5.0	2.0	0.13	20
Gamma-BHC	7.53	Alpha-BHC-d6	181.0-145.0	181.0-109.0	0.50	0.033	5.0	2.0	0.13	20
Delta-BHC	7.94	TCB-d5	181.0-145.0	181.0-109.0	5.0	0.33	50	20	1.3	80
Chlorothalonil	8.04	TCB-d5	265.9-230.9	265.9-133.0	5.0	0.33	50	20	1.3	200
Heptachlor	8.84	TCB-d5	271.9-236.8	271.9-234.8	0.50	0.033	5.0	2.0	0.13	20
Aldrin	9.52	TCB-d5	260.9-190.9	262.9-192.9	2.2	0.15	22	8.8	0.59	88
Dacthal	9.90	TCB-d5	300.8-222.9	300.8-257.8	0.25	0.017	2.5	1.0	0.067	10
Heptachlor Epoxide	10.32	TCB-d5	352.9-262.8	352.9-281.9	1.0	0.067	10	4.0	0.27	40
Gamma-Chlordane	10.82	TCB-d5	271.7-236.9	372.9-263.9	0.50	0.033	5.0	2.0	0.13	20
Prallethrin	10.92	TCB-d5	168.1-123.1	153.9-90.9	6.0	0.40	60	24	1.6	240
Endosulfan I	11.07	TCB-d5	240.9-205.9	206.8-172.0	2.5	0.17	25	10	0.67	100

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Analyte	Approx. Retention Time (min)	Internal standard	Quantifier transition	Qualifier transition	MDL ug/L	MDL ug/kg soil	MDL Ug/kg waste	PQL ug/L	PQL ug/kg soil	PQL ug/kg waste
Alpha-Chlordane	11.13	TCB-d5	271.7-236.9	372.9-263.9	0.50	0.033	5.0	2.0	0.13	20
Trans-Nonachlor	11.24	TCB-d5	408.7-299.8	408.7-372.7	1.0	0.067	10	4.0	0.27	40
DDE-p,p’	11.60	TCB-d5	246.0-176.1	246.0-175.1	0.50	0.033	5.0	2.0	0.13	20
Dieldrin	11.61	HCB-d3	262.9-192.9	260.9-190.9	4.0	0.27	40	16	1.1	160
Endrin	12.06	HCB-d3	262.8-192.8	262.7-191.1	4.0	0.27	40	16	1.1	160
Endosulfan II	12.27	HCB-d3	241.0-206.0	206.9-172.1	5.0	0.33	50	20	1.3	200
DDD-p,p’	12.49	HCB-d3	235.0-165.1	235.0-199.1	0.50	0.033	5.0	2.0	0.13	20
Cis-Nonachlor	12.56	HCB-d3	408.7-299.8	408.7-372.7	1.0	0.067	10	4.0	0.27	40
Endrin Aldehyde	12.67	HCB-d3	344.8-280.9	344.8-244.9	4.0	0.27	40	16	1.1	160
Carbophenothion	13.06	HCB-d3	341.9-157.0	343.9-158.9	1.5	0.10	15	6.0	0.40	60
Endosulfan Sulfate	13.18	HCB-d3	271.7-236.8	269.7-234.9	2.0	0.13	20	8.0	0.53	80
DDT-p,p’	13.28	DDT-p,p’-d8	235.0-165.1	235.0-199.1	1.5	0.10	15	6.0	0.40	60
Endrin Ketone	14.03	HCB-d3	316.9-280.9	316.9-101.1	4.0	0.27	40	16	1.1	160
Methoxychlor	14.28	DDT-p,p’-d8	227.1-169.1	227.1-141.1	0.50	0.033	5.0	2.0	0.13	20
Bifenthrin	14.28	HCB-d3	181.1-165.1	181.1-166.1	0.30	0.020	3.0	1.2	0.080	12
Dicofol	14.30	Dicofol-d8	251.0-139.0	253.0-141.0	11	0.73	110	44	2.9	440
Phenothrin	14.58	HCB-d3	183.1-153.1	183.1-168.1	2.0	0.13	20	8.0	0.53	80
Mirex	14.73	HCB-d3	271.9-236.9	271.9-234.8.	1.0	0.067	10	4.0	0.27	40
Lambda-Cyhallothrin*	14.85	HCB-d3	181.1-152.1	208.0-127.1	2.0	0.13	20	8.0	0.53	80
Permethrin*	15.35	HCB-d3	183.1-168.1	183.1-153.1	3.0	0.20	30	12	0.80	120
Beta-Cyfluthrin*	15.81	HCB-d3	226.1-206.1	163.0-127.1	2.0	0.13	20	8.0	0.53	80
Cypermethrin*	15.97	HCB-d3	180.9-152.1	208.9-169.2	2.5	0.17	25	10	0.67	100
Deltamethrin	17.22	HCB-d3	181.1-152.1	253.0-93.0	3.0	0.20	30	12	1.6	120
Trifluralin-d14	6.64	Internal standard	315.0-267.1	266.9-163.1						
DCB-d5	6.69	Internal standard	226.9-157.1	226.9-192.1						

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Analyte	Approx. Retention Time (min)	Internal standard	Quantifier transition	Qualifier transition	MDL ug/L	MDL ug/kg soil	MDL Ug/kg waste	PQL ug/L	PQL ug/kg soil	PQL ug/kg waste
Alpha-BHC-d6	6.92	Internal standard	223.8-187.0	223.8-150.0						
TCB-d5	9.42	Internal standard	296.8-225.0	296.8-262.0						
DDT-p,p'-d8	13.30	Internal standard	243.0-172.6	243.0-206.1						
Dicofol-d8	13.74	Internal standard	142.9-115.1	142.9-78.0						
HCB-d3	14.22	Internal standard	362.7-362.7	362.7-292.9						
Octachloronaphthalene	15.80	Internal standard	354.9-267.0	354.9-351.0						

- **Sum-all integration used due to closely eluting peaks**

All target analytes are associated to both surrogates.

TABLE 1C: Internal standard associations, RTs, quantifier and qualifier transitions for analytical peaks, as well as MDLs and PQLs for PCB Aroclors included in LIMS tests S-PCB-TQ and WS-PCB-TQ. **LIMS reporting units are ug/kg**

Analyte	Approximate Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	matrix	MDL ug/L	MDL ug/kg	PQL ug/L	PQL ug/kg
						extract	sample	extract	sample
Tetrachloro-m-xylene surrogate	5.99	DCB-d5	206.9-136.0	206.9-171.9					
Decachlorobiphenyl surrogate	16.25	HCB-d3	497.6-427.9	497.6-462.7					
PCB-1016					s	21	1.4	84	5.6
PCB-1016					ws	21	210	84	840
PCB-1016_1	6.33	DCB-d5	220.0-152.0	222.0-187.1					
PCB-1016_2	6.96	DCB-d5	220.0-152.0	222.0-187.1					
PCB-1016_3	8.02	TCB-d5	255.8-185.9	258.0-186.0					
PCB-1016_4	8.71	TCB-d5	255.8-185.9	258.0-186.0					
PCB-1016_5	9.60	TCB-d5	291.9-222.0	291.9-220.1					
PCB-1221					s	21	1.4	84	5.6
PCB-1221					ws	21	210	84	840
PCB-1221_1	5.51	DCB-d5	188.0-152.0	N/A					
PCB-1221_2	6.02	DCB-d5	188.0-152.0	N/A					
PCB-1221_3	6.32	DCB-d5	222.0-152.0	222.0-187.1					

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Analyte	Approximate Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	matrix	MDL ug/L	MDL ug/kg	PQL ug/L	PQL ug/kg
PCB-1221_4	6.86	DCB-d5	222.0-152.0	222.0-187.1					
PCB-1221_5	6.96	DCB-d5	222.0-152.0	222.0-187.1					
PCB-1232					s	21	1.4	84	5.6
PCB-1232					ws	21	210	84	840
PCB-1232_1	6.33	DCB-d5	222.0-152.0	222.0-187.1					
PCB-1232_2	6.97	DCB-d5	222.0-152.0	222.0-187.1					
PCB-1232_3	8.02	TCB-d5	255.8-185.9	258.0-186.0					
PCB-1232_4	8.72	TCB-d5	255.8-185.9	258.0-186.0					
PCB-1232_5	9.61	TCB-d5	291.9-222.0	291.9-220.1					
PCB-1242					s	21	1.4	84	5.6
PCB-1242					ws	21	210	84	840
PCB-1242_1	6.32	DCB-d5	222.0-152.0	222.0-187.1					
PCB-1242_2	6.96	DCB-d5	222.0-152.0	222.0-187.1					
PCB-1242_3	8.02	TCB-d5	255.8-185.9	258.0-186.0					
PCB-1242_4	8.50	TCB-d5	255.8-185.9	258.0-186.0					
PCB-1242_5	8.85	TCB-d5	255.8-185.9	258.0-186.0					
PCB-1248					s	21	1.4	84	5.6
PCB-1248					ws	21	210	84	840
PCB-1248_1	8.02	DCB-d5	255.8-185.9	258.0-186.0					
PCB-1248_2	8.51	DCB-d5	255.8-185.9	258.0-186.0					
PCB-1248_3	9.60	TCB-d5	291.9-222.0	291.9-220.1					
PCB-1248_4	10.40	TCB-d5	291.9-222.0	291.9-220.1					
PCB-1248_5	10.48	TCB-d5	291.9-222.0	291.9-220.1					
PCB-1254					s	21	1.4	84	5.6
PCB-1254					ws	21	210	84	840
PCB-1254_1	9.60	TCB-d5	291.9-222.0	291.9-220.1					
PCB-1254_2	10.39	TCB-d5	291.9-222.0	291.9-220.1					
PCB-1254_3	11.72	TCB-d5	325.9-255.9	325.9-253.9					
PCB-1254_4	12.26	TCB-d5	325.9-255.9	325.9-253.9					
PCB-1254_5	13.34	HCB-d3	359.8-289.9	359.8-324.9					
PCB-1260					s	21	1.4	84	5.6
PCB-1260					ws	21	210	84	840
PCB-1260_1	12.24	TCB-d5	359.8-289.9	359.8-324.9					
PCB-1260_2	12.76	TCB-d5	359.8-289.9	359.8-324.9					
PCB-1260_3	13.69	HCB-d3	393.8-323.9	393.8-358.7					
PCB-1260_4	14.06	HCB-d3	393.8-323.9	393.8-358.7					

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Analyte	Approximate Retention Time (min)	Associated internal standard	Quantifier transition	Qualifier transition	matrix	MDL ug/L	MDL ug/kg	PQL ug/L	PQL ug/kg
PCB-1260_5	14.20	HCB-d3	393.8-323.9	393.8-358.7					
DCB-d5	6.68	Internal standard	226.9-157.1	226.9-192.1					
TCB-d5	9.40	Internal standard	296.8-225.0	296.8-262.0					
HCB-d3	14.42	Internal standard	362.7-362.7	362.7-292.9					

The same MDL is applied to all PCB Aroclors.
All target analytes are associated to both surrogates.

TABLE 1D: Internal standard associations, MDLs, PQLs and approximate RTs for Chlorinated pesticides and PCB congeners included in LIMS test T-PCBCL-TQ. **LIMS reporting units are ug/kg**

Analyte	Approximate Retention Time (min)	Associated internal standard	MDL ug/L	MDL ug/kg	PQL ug/L	PQL ug/kg
			extract	sample	extract	sample
Tetrachloro-m-xylene	5.99	HCB-d3				
Decachlorobiphenyl surrogate	15.79	HCB-d3				
Alpha-BHC	6.57	Alpha-BHC-d6	0.50	0.20	2.0	0.80
Hexachlorobenzene	6.70	DCB-d5	1.0	0.40	4.0	1.6
Beta-BHC	6.99	Alpha-BHC-d6	0.80	0.32	3.2	1.3
Gamma-BHC	7.09	Alpha-BHC-d6	0.50	0.20	2.0	0.80
Delta-BHC	7.48	TCB-d5	0.80	0.32	3.2	1.3
Heptachlor	8.33	TCB-d5	0.80	0.32	3.2	1.3
Aldrin	8.97	TCB-d5	1.0	0.40	4.0	1.6
Heptachlor Epoxide	9.75	TCB-d5	1.0	0.40	4.0	1.6
Oxychlordane	9.78	TCB-d5	0.80	0.32	3.2	1.3
Trans-Chlordane	10.23	TCB-d5	1.0	0.40	4.0	1.6
DDE-o,p’	10.37	TCB-d5	0.50	0.20	2.0	0.80
Endosulfan I	10.47	TCB-d5	2.0	0.80	8.0	3.2
Cis-Chlordane	10.54	TCB-d5	1.0	0.40	4.0	1.6
Trans-Nonachlor	10.64	TCB-d5	2.0	0.80	8.0	3.2
DDE-p,p’	11.02	TCB-d5	0.50	0.20	2.0	0.80
Dieldrin	11.01	HCB-d3	2.0	0.80	8.0	3.2
DDD-o,p’	11.19	HCB-d3	0.50	0.20	2.0	0.80
Endrin	11.44	HCB-d3	2.0	0.80	8.0	3.2

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Analyte	Approximate Retention Time (min)	Associated internal standard	MDL ug/L	MDL ug/kg	PQL ug/L	PQL ug/kg
Endosulfan II	11.65	HCB-d3	2.0	0.80	8.0	3.2
DDD-p,p’	11.89	HCB-d3	1.0	0.40	4.0	1.6
Cis-Nonachlor	11.94	HCB-d3	2.0	0.80	8.0	3.2
DDT-o,p’	11.95	DDT-p,p’-d8	1.0	0.40	4.0	1.6
Endrin Aldehyde	12.05	HCB-d3	2.0	0.80	8.0	3.2
Endosulfan Sulfate	12.56	HCB-d3	1.0	0.40	4.0	1.6
DDT-p,p’	12.68	DDT-p,p’-d8	1.0	0.40	4.0	1.6
Endrin Ketone	13.52	HCB-d3	2.0	0.80	8.0	3.2
Methoxychlor	13.88	DDT-p,p’-d8	2.0	0.80	8.0	3.2
Mirex	14.34	HCB-d3	1.0	0.40	4.0	1.6
PCB-8	6.57	DCB-d5	1.0	0.40	4.0	1.6
PCB-18	7.25	DCB-d5	1.0	0.40	4.0	1.6
PCB-28	8.05	TCB-d5	0.80	0.32	3.2	1.3
PCB-52	8.69	TCB-d5	2.0	0.80	8.0	3.2
PCB-44	9.09	TCB-d5	0.50	0.20	2.0	0.80
PCB-66	9.93	TCB-d5	0.50	0.20	2.0	0.80
PCB-101	10.42	TCB-d5	0.50	0.20	2.0	0.80
PCB-77	11.16	HCB-d3	0.50	0.20	2.0	0.80
PCB-118	11.70	HCB-d3	0.50	0.20	2.0	0.80
PCB-153	12.18	HCB-d3	0.50	0.20	2.0	0.80
PCB-105	12.26	HCB-d3	0.50	0.20	2.0	0.80
PCB-138	12.76	HCB-d3	0.50	0.20	2.0	0.80
PCB-126	12.94	HCB-d3	0.50	0.20	2.0	0.80
PCB-187	13.11	HCB-d3	0.80	0.32	3.2	1.3
PCB-128	13.33	HCB-d3	0.80	0.32	3.2	1.3
PCB-180	14.04	HCB-d3	0.80	0.32	3.2	1.3
PCB-169	14.30	HCB-d3	0.50	0.20	2.0	0.80
PCB-170	14.41	HCB-d3	0.80	0.32	3.2	1.3
PCB-195	14.87	HCB-d3	0.80	0.32	3.2	1.3
PCB-206	15.46	HCB-d3	0.80	0.32	3.2	1.3
DCB-d5	6.30	Internal standard				
Alpha-BHC-d6	6.52	Internal standard				
TCB-d5	8.88	Internal standard				
DDT-p,p’-d8	12.62	Internal standard				
HCB-d3	13.78	Internal standard				

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All target analytes are associated to both surrogates.

TABLE 2: GC/MS Operating Conditions: (METHOD CL_MRM_yymmdd, AR-MRM-yymmdd) and Cl_T_MRM-yymmdd

Parameter	Setting
Mass spec:	70 eV. Peak width 0.7s. detector setting-gain. Source temp. 300 C. Collision cell He: 2.25 mL/min, Nitrogen 1.5 mL/min.
Scan Time:	About 3.3 cycles/s. MRM mode dwell times variable, summing up to about 300 ms per time segment. Gain 20 for each transition monitored for most analytes. Gain 10 is used for PCB aroclors and the tissue method. Time filtering “on”.
GC Oven Temperature Program:	50 °C for 1.5 min, to 160 °C at 55 C °/min, hold 0 min, to 240 C at 8 C/min hold 0 min, to 280 °C at 50 C °/min, hold 0 min, to 290 at 100 C °/min hold 3 min (7 min for chlorinated pesticides in soil, AR and tissue methods). This program is the same for full scan (used for RT shifts determination and degradation mix analysis) or MRM.
Injector operating conditions:	Temp: 60 °C for 0.35 min; 900 C °/min to 280 C. hold for 14 min, 900 C °/min to 310 hold until end run. Mode: pulsed splitless; pulse pressure 30 PSI for 1.4 min after pulse pressure: Ramped Flow ON, 2.8154 psi at 60 °C (0.8 mL/min) for NP method or 3.3217 psi at 60 °C (0.9 mL/min) for CL, T_CL and AR methods ; Cryo: ON (nitrogen gas); Cryo use temperature 150 °C
Column 1 configuration	HP-5MS UI, 5m-0.25mm-0.25um; in: front MMI inlet, out aux EPC 4 (EPC 6 in TQ-2)
Column 1 flow CL CL_T and AR methods	0.9 ml/min for 17 min, then at 100 mL/min to -2.5 mL/min for 1.5 min, then at 100 mL/min to -5 mL/min for until end run
Column 2 configuration	HP-5MS UI, 15m-0.25mm-0.25um; in: t aux EPC 4 (EPC 6 in TQ-2); out: vacuum
Column 2 flow CL CL_T and AR methods	1.0 ml/min for 18.53 min, then at 100 mL/min to 2.4 mL/min until end run
MS interface temperature:	300 °C
Injection Type:	Pulsed Splitless (cold). Pulse pressure 30 PSI for 1.4 min; purge to split vent 50 mL/min at 1.5 min. Gas saver OFF.
Injection Volume:	2 µL
Backflash:	Concurrent + end run; see columns flows conditions
Total Run Time CL CL_T and AR methods	21.40 min.

TABLE 2-B: GC/MS Operating Conditions: METHOD NP_MRM-yymmdd

Parameter	Setting
Mass spec:	70 eV. Peak width 0.7s. detector setting-gain. Source temp. 300 C. Collision cell He: 2.25 mL/min, Nitrogen 1.5 mL/min.

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Parameter	Setting
Scan Time:	About 3.3 cycles/s. MRM mode dwell times variable, summing up to about 300 ms per time segment. Gain 20 for each transition monitored for most analytes. Time filtering “on”.
GC Oven Temperature Program:	50 °C for 1.5 min, to 160 °C at 55 C °/min, hold 0 min, to 200 C at 13 C/min hold 0 min, to 280 °C at 55 C °/min, hold 0 min, to 290 at 100 C °/min hold 5.9 min.
Injector operating conditions:	Temp: 60 °C for 0.35 min; 900 C °/min to 280 C. hold for 14 min, 900 C °/min to 310 hold until end run. Mode: pulsed splitless; pulse pressure 30 PSI for 1.4 min after pulse pressure: Ramped Flow ON, 4.4394 psi at 60 °C (1.1 mL/min) cryo: ON (nitrogen gas); Cryo use temperature 150 °C
Column 1 configuration	HP-5MS UI, 5m-0.25mm-0.25um; in: front MMI inlet, out aux EPC 4 (EPC 6 in TQ-2)
Column 1 flow NP method	1.1 ml/min for 9.5 min, then at 100 mL/min to -2.5 mL/min for 1.5 min, then at 100 mL/min to -5 mL/min for until end run
Column 2 configuration	HP-5MS UI, 15m-0.25mm-0.25um; in: t aux EPC 4 (EPC 6 in TQ-2); out: vacuum
Column 2 flow NP method	1.2 ml/min for 11.036 min, then at 100 mL/min to 2.4 mL/min until end run
MS interface temperature:	300 °C
Injection Type:	Pulsed Splitless (cold). Pulse pressure 30 PSI for 1.4 min; purge to split vent 50 mL/min at 1.5 min. Gas saver OFF.
Injection Volume:	2 µL
Backflash:	Concurrent + end run; see columns flows conditions
Total Run Time NP method:	14.03 min.

TABLE 3: GC AUTOSAMPLER OPERATING PARAMETERS FOR GC/MS/MS ANALYSIS

Autosampler Parameter	Setting
Syringe size	10 ul
Injection volume	2 ul
Last Bottle	150
Solvent A washes	3 pre- 15 post (DI Water)
Solvent A volume	8 ul
Solvent B washes	3 pre- 15 post (Acetone)
Solvent B volume	8 ul
Sample washes	1
Sample wash volume	4 ul
Sample pumps	7
Dwell time pre-inj	0
Dwell time post-inj	0

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Solvent wash draw speed	300 ul/min
Solvent wash dispense speed	6000 ul/min
Sample wash draw speed	50 ul/min
Sample wash dispense speed	6000 ul/min
Injection dispense speed	68ul/min
Viscosity delay	7 sec
Sample depth	disabled
Injection type	3-layer Sandwich
L1 airgap	0.0 ul
L2 Volume	0.2 ul MeOH
L2 airgap	0.0 ul
L3 Volume	0.4 ul analyte protectants
L3 airgap	0.0 ul
Sample overlap	Not enabled

TABLE 4A. MRM method acquisition parameters for Nitrogen-Phosphorus pesticides (ref 15.6)

Time Events:

Time Segments:

Method File	C:\MassHunter\GCMS\1\methods\NP_dMRM_210927.M\qqqacqmethod.xml
Tune File	atunes.eihs.tune.xml
Ion Source	EI
Source Temp. (°C)	300
Electron Energy Mode	Use tune setting
Fixed Electron Energy (eV)	
Stop Mode	By Chromatograph Time
Stop Time (min)	1
Solvent Delay (min)	3.5
Use Gain	Yes
EM Saver	
Auto Baseline Subtract	Yes
Advanced Filtering	Yes

Time filter type: off

Row	Time (min)	Peak Width (sec)

Index	Start Time (min)	Scan Type	Electron Energy (eV)	Data Stored	Delta EMV (V)	Gain
1	3.50	dMRM		X		2

Time Events:

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Time Segments:

Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Dichlorvos		185	Unit	93	Wide	4.00	0.50	0.50	115.3	10
Dichlorvos		109	Unit	79	Wide	4.00	0.50	0.50	115.3	5
Methamidophos		141	Unit	95	Wide	4.19	0.30	0.70	68.7	5
Methamidophos		141	Unit	79	Wide	4.19	0.30	0.70	68.7	20
EPTC-d14		203.1	Unit	94.1	Wide	4.33	0.30	0.30	60.6	8
EPTC-d14		142.1	Unit	94.1	Wide	4.33	0.30	0.30	60.6	2
EPTC		189.1	Unit	128.1	Wide	4.36	0.30	0.30	51	5
EPTC		128.08	Unit	86.1	Wide	4.36	0.30	0.30	51	5

Compound Table:

Time Filter Table:

Total MRMs	198
Minimum Concurrent MRMs	2
Maximum Concurrent MRMs	47
Min Dwell (group average)	15
Max Dwell (group average)	214.7
Estimated Cycle Time	574.7126

DMRM Statistics:

Triple Quadrupole Acquisition Method - MS Parameters Report

Compound Table:

Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Butylate		217.1	Unit	156.1	Wide	4.66	0.30	0.30	49.5	5
Butylate		174.1	Unit	146.1	Wide	4.66	0.30	0.30	49.5	10
Mevinphos		192	Unit	127	Wide	4.74	0.30	0.30	51.9	10
Mevinphos		127	Unit	95	Wide	4.74	0.30	0.30	51.9	15
Etridiazole		210.93	Unit	182.94	Wide	4.80	0.30	0.30	61.1	15
Etridiazole		210.93	Unit	139.95	Wide	4.80	0.30	0.30	61.1	15
Molinate		187	Unit	158	Wide	5.19	0.30	0.30	84	9
Molinate	X	187	Unit	126	Wide	5.19	0.30	0.30	84	5
DEET		190.1	Unit	145	Wide	5.43	1.00	1.00	47	24
DEET		190.1	Unit	117	Wide	5.43	1.00	1.00	47	10
Demeton-O		171	Unit	115	Wide	5.58	0.30	0.30	58	10
Demeton-O		171	Unit	97	Wide	5.58	0.30	0.30	58	25
TBP-d27	X	103.1	Unit	83	Wide	5.64	0.30	0.30	48.8	20

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Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
TBP-d27	X	103.1	Unit	63	Wide	5.64	0.30	0.30	48.8	37
Ethoprop		158	Unit	114	Wide	5.71	0.30	0.30	45.1	5
Ethoprop		158	Unit	97	Wide	5.71	0.30	0.30	45.1	15
Naled		184.9	Unit	93	Wide	5.86	0.30	0.30	36	15
Naled		144.9	Unit	109	Wide	5.86	0.30	0.30	36	15
Atrazine Desethyl		187	Unit	110.1	Wide	5.94	0.30	0.50	27.8	21
Atrazine Desethyl		186.9	Unit	172.1	Wide	5.94	0.30	0.50	27.8	5
Atrazine Desethyl		145	Unit	110.1	Wide	5.94	0.30	0.50	27.8	10
Phorate		231	Unit	174.9	Wide	6.04	0.30	0.30	27.6	15
Phorate		231	Unit	128.9	Wide	6.04	0.30	0.30	27.6	15
Monocrotophos		192	Unit	164	Wide	6.06	0.30	0.50	25	5
Monocrotophos		192	Unit	127	Wide	6.06	0.30	0.50	25	10
Demeton-S		171	Unit	115	Wide	6.22	0.30	0.30	23.7	10
Demeton-S		171	Unit	97	Wide	6.22	0.30	0.30	23.7	25
Prometon		225.2	Unit	210.2	Wide	6.31	0.30	0.30	21.2	10
Prometon		225.2	Unit	183.1	Wide	6.31	0.30	0.30	21.2	10
Prometon		210	Unit	112.1	Wide	6.31	0.30	0.30	21.2	10
Simazine--d10		211.3	Unit	179.1	Wide	6.32	0.30	0.30	21.2	3
Simazine--d10		179.2	Unit	144	Wide	6.32	0.30	0.30	21.2	5
Atrazine-d5	X	205.1	Unit	127.1	Wide	6.33	0.30	0.30	20.8	10
Atrazine-d5	X	205.1	Unit	105.1	Wide	6.33	0.30	0.30	20.8	15
Atrazine		200.1	Unit	122.1	Wide	6.35	0.30	0.30	21	10
Atrazine		200.1	Unit	104	Wide	6.35	0.30	0.30	21	20
Simazine		201.1	Unit	173.1	Wide	6.37	0.30	0.30	21.6	15
Simazine		201.1	Unit	138.1	Wide	6.37	0.30	0.30	21.6	15
Simazine		185.6	Unit	90.9	Wide	6.37	0.30	0.30	21.6	9
Terbufos-d10		241.1	Unit	130.9	Wide	6.48	0.30	0.30	22.6	25
Terbufos-d10		163	Unit	98.9	Wide	6.48	0.30	0.30	22.6	13
Terbuthylazine		213.9	Unit	132	Wide	6.52	0.30	0.30	22.7	10
Terbuthylazine		213.9	Unit	104	Wide	6.52	0.30	0.30	22.7	20
Terbufos		231	Unit	174.9	Wide	6.53	0.30	0.30	22.7	10
Terbufos		231	Unit	128.9	Wide	6.53	0.30	0.30	22.7	25
Pronamide		172.9	Unit	145.1	Wide	6.55	0.30	0.30	23.2	15
Pronamide		172.9	Unit	109.1	Wide	6.55	0.30	0.30	23.2	30
Fonofos		246	Unit	137	Wide	6.57	0.30	0.30	23.6	10
Fonofos		246	Unit	109	Wide	6.57	0.30	0.30	23.6	18
Disulfoton		185.9	Unit	108.9	Wide	6.58	0.30	0.30	23.6	7
Disulfoton		185.9	Unit	97	Wide	6.58	0.30	0.30	23.6	17
Diazinon		304.1	Unit	179.1	Wide	6.65	0.30	0.30	24.2	10
Diazinon		179.1	Unit	121.1	Wide	6.65	0.30	0.30	24.2	40
Caffeine-d9		203.1	Unit	115.1	Wide	6.95	0.30	0.30	21.8	7

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Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Caffeine-d9		203.1	Unit	60.1	Wide	6.95	0.30	0.30	21.8	23
Caffeine		194	Unit	137.1	Wide	6.99	0.30	0.30	20.7	7
Caffeine		194	Unit	109.1	Wide	6.99	0.30	0.30	20.7	12
Metribuzin-d3		216.8	Unit	201	Wide	7.06	0.30	0.30	19.4	0
Metribuzin-d3		202	Unit	118	Wide	7.06	0.30	0.30	19.4	5
Propanil		161	Unit	99	Wide	7.08	0.30	0.30	18.3	30
Propanil		161	Unit	90	Wide	7.08	0.30	0.30	18.3	25
Dimethenamid		230	Unit	154	Wide	7.08	0.30	0.30	18.3	9
Dimethenamid		154	Unit	111	Wide	7.08	0.30	0.30	18.3	13
Metribuzin		198	Unit	82	Wide	7.08	0.30	0.30	18.3	15
Metribuzin		198	Unit	55	Wide	7.08	0.30	0.30	18.3	30
Acetochlor		223	Unit	147.1	Wide	7.12	0.30	0.30	17.7	7
Acetochlor		223	Unit	132	Wide	7.12	0.30	0.30	17.7	21
Chlorpyriphos Methyl		286	Unit	270.9	Wide	7.15	0.30	0.30	17	30
Chlorpyriphos Methyl		286	Unit	93	Wide	7.15	0.30	0.30	17	30
Parathion Methyl		262.9	Unit	124.9	Wide	7.15	0.30	0.30	17	15
Parathion Methyl		262.9	Unit	109	Wide	7.15	0.30	0.30	17	10
Alachlor		269	Unit	187.7	Wide	7.21	0.30	0.30	15.8	20
Alachlor		188.1	Unit	160.1	Wide	7.21	0.30	0.30	15.8	10
Alachlor		161.1	Unit	146.1	Wide	7.21	0.30	0.30	15.8	12
Ametryn		227.1	Unit	155.2	Wide	7.23	0.30	0.30	15.2	30
Ametryn		227.1	Unit	58.3	Wide	7.23	0.30	0.30	15.2	30
Fipronil Desulfinyl		387.9	Unit	332.9	Wide	7.23	0.30	0.30	15.2	18
Fipronil Desulfinyl		387.9	Unit	280.9	Wide	7.23	0.30	0.30	15.2	35
Prometryn		241.1	Unit	184.2	Wide	7.26	0.30	0.30	15	30
Prometryn		241.1	Unit	58.2	Wide	7.26	0.30	0.30	15	30
Metalaxyl		249.1	Unit	190.1	Wide	7.27	0.30	0.30	15.2	10
Metalaxyl		234.1	Unit	174.1	Wide	7.27	0.30	0.30	15.2	10
Dithiopyr		354.1	Unit	306	Wide	7.35	0.30	0.30	15.2	5
Dithiopyr		354.1	Unit	286	Wide	7.35	0.30	0.30	15.2	13
Prodiamine		321	Unit	279	Wide	7.39	0.30	0.30	15.3	4
Prodiamine		321	Unit	203	Wide	7.39	0.30	0.30	15.3	13
Bromacil		231	Unit	188	Wide	7.46	0.30	0.50	19.3	7
Bromacil		205	Unit	132	Wide	7.46	0.30	0.50	19.3	30
Malathion		173.1	Unit	117	Wide	7.48	0.30	0.30	15.6	10
Malathion		173.1	Unit	99	Wide	7.48	0.30	0.30	15.6	15
Thiobencarb		257.1	Unit	100	Wide	7.48	0.30	0.30	15.6	5
Thiobencarb		125	Unit	89	Wide	7.48	0.30	0.30	15.6	12
Metolachlor		238	Unit	162	Wide	7.53	0.30	0.30	16.3	10
Metolachlor		162.1	Unit	133.1	Wide	7.53	0.30	0.30	16.3	15
Parathion Ethyl d10		301	Unit	147	Wide	7.54	0.30	0.30	16.3	4

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Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Parathion Ethyl d10		301	Unit	115	Wide	7.54	0.30	0.30	16.3	20
Chlorpyrifos Ethyl		196.9	Unit	168.9	Wide	7.56	0.30	0.30	17.4	15
Chlorpyrifos Ethyl		196.9	Unit	107	Wide	7.56	0.30	0.30	17.4	40
Parathion Ethyl		291	Unit	137	Wide	7.58	0.30	0.30	18.6	10
Parathion Ethyl		291	Unit	109	Wide	7.58	0.30	0.30	18.6	15
Cyanazine		225.1	Unit	198.1	Wide	7.58	0.30	0.30	18.6	10
Cyanazine		225.1	Unit	189.1	Wide	7.58	0.30	0.30	18.6	10
Triadimefon		208.1	Unit	181.1	Wide	7.59	0.30	0.30	19.6	10
Triadimefon		208.1	Unit	111	Wide	7.59	0.30	0.30	19.6	25
Cyprodinil		224	Unit	208.1	Wide	7.78	0.30	0.30	22.9	25
Cyprodinil		224	Unit	118	Wide	7.78	0.30	0.30	22.9	45
Pendimethalin		252.1	Unit	191.1	Wide	7.82	0.30	0.30	23.1	8
Pendimethalin		252.1	Unit	162.1	Wide	7.82	0.30	0.30	23.1	15
Fipronil Sulfide		419.9	Unit	351	Wide	7.84	0.30	0.30	23.3	10
Fipronil Sulfide		350.9	Unit	255	Wide	7.84	0.30	0.30	23.3	15
Fipronil		367	Unit	255	Wide	7.90	0.30	0.30	23.7	15
Fipronil		367	Unit	213	Wide	7.90	0.30	0.30	23.7	20
Stirophos		329	Unit	109	Wide	8.13	0.30	0.30	23.9	25
Stirophos		329	Unit	79	Wide	8.13	0.30	0.30	23.9	35
Fenamiphos		303	Unit	195	Wide	8.19	0.30	0.30	22.4	5
Fenamiphos		154	Unit	139	Wide	8.19	0.30	0.30	22.4	10
Flutolanil		280.9	Unit	173	Wide	8.19	0.30	0.30	21.4	10
Flutolanil		173	Unit	145.1	Wide	8.19	0.30	0.30	21.4	20
Flutolanil		173	Unit	95	Wide	8.19	0.30	0.30	21.4	35
Napropamide		271.1	Unit	128.1	Wide	8.20	0.30	0.30	21.4	5
Napropamide		271.1	Unit	71.1	Wide	8.20	0.30	0.30	21.4	15
Fludioxonil		248	Unit	182	Wide	8.29	0.30	0.30	19.5	15
Fludioxonil		248	Unit	127	Wide	8.29	0.30	0.30	19.5	35
Imazalil		214.9	Unit	173	Wide	8.29	0.30	0.70	19.7	15
Imazalil		173	Unit	145	Wide	8.29	0.30	0.70	19.7	20
Oxadiazon		301.9	Unit	175	Wide	8.29	0.30	0.30	19.5	13
Oxadiazon		174.9	Unit	112	Wide	8.29	0.30	0.30	19.5	15
Oxyfluorfen		252	Unit	196.1	Wide	8.33	0.30	0.30	19.4	25
Oxyfluorfen		252	Unit	146	Wide	8.33	0.30	0.30	19.4	40
Myclobutanil		179	Unit	152	Wide	8.33	0.30	0.30	19.4	6
Myclobutanil		179	Unit	125	Wide	8.33	0.30	0.30	19.4	15
Fipronil Sulfone		382.9	Unit	255	Wide	8.35	0.30	0.30	19.3	20
Fipronil Sulfone		255	Unit	228	Wide	8.35	0.30	0.30	19.3	10
Fluazifop-P-butyl		383	Unit	282.1	Wide	8.42	0.30	0.30	19.5	20
Fluazifop-P-butyl		282	Unit	238.1	Wide	8.42	0.30	0.30	19.5	20
Chlorfenapyr		326	Unit	247	Wide	8.44	0.30	0.30	19.7	15

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Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Chlorfenapyr		247.1	Unit	227.1	Wide	8.44	0.30	0.30	19.7	15
Ethion		231	Unit	174.9	Wide	8.59	0.30	0.30	20	10
Ethion		231	Unit	128.9	Wide	8.59	0.30	0.30	20	25
Carfentrazone Ethyl		340	Unit	312.1	Wide	8.74	0.30	0.30	19.8	10
Carfentrazone Ethyl		330	Unit	310.1	Wide	8.74	0.30	0.30	19.8	10
Carbophenothion		343.9	Unit	158.9	Wide	8.75	0.30	0.30	19.8	13
Carbophenothion		341.9	Unit	157	Wide	8.75	0.30	0.30	19.8	13
Norflurazon		303.3	Unit	173.1	Wide	8.81	0.30	0.30	20	8
Norflurazon		303.3	Unit	145	Wide	8.81	0.30	0.30	20	21
Pyraflufen-ethyl		412.02	Unit	349.02	Wide	8.83	0.30	0.30	20.1	15
Pyraflufen-ethyl		349.02	Unit	307.02	Wide	8.83	0.30	0.30	20.1	15
Hexazinone-d6		177.2	Unit	91.1	Wide	8.90	0.30	0.30	19.9	12
Hexazinone-d6		177.2	Unit	77.1	Wide	8.90	0.30	0.30	19.9	15
Hexazinone		171.1	Unit	85.1	Wide	8.90	0.30	0.30	19.9	15
Hexazinone		128	Unit	83	Wide	8.90	0.30	0.30	19.9	12
Propiconazole		259	Unit	173	Wide	8.91	0.30	0.30	19.9	20
Propiconazole		172.9	Unit	144.9	Wide	8.91	0.30	0.30	19.9	15
Tebuconazole		252	Unit	127	Wide	8.92	0.30	0.30	20.9	25
Tebuconazole		250	Unit	125	Wide	8.92	0.30	0.30	20.9	27
Propargite		173.1	Unit	135.1	Wide	8.93	0.30	0.30	22.5	16
Propargite		173.1	Unit	107.1	Wide	8.93	0.30	0.30	22.5	24
Phenytoin		209	Unit	180	Wide	8.94	1.00	1.00	30.2	15
Phenytoin		180	Unit	76.9	Wide	8.94	1.00	1.00	30.2	35
Iprodione		316	Unit	56	Wide	9.07	0.30	0.30	24.8	25
Iprodione		313.9	Unit	56	Wide	9.07	0.30	0.30	24.8	25
Phosmet		160	Unit	77	Wide	9.15	0.30	0.30	27	25
Phosmet		160	Unit	51	Wide	9.15	0.30	0.30	27	50
Fluxapyroxad		381	Unit	159	Wide	9.17	0.30	0.30	29.2	12
Fluxapyroxad		159	Unit	139	Wide	9.17	0.30	0.30	29.2	10
Sulfentrazone		385.9	Unit	351.1	Wide	9.23	0.30	0.30	31.5	15
Sulfentrazone		385.9	Unit	307.1	Wide	9.23	0.30	0.30	31.5	15
Sulfentrazone		306.9	Unit	145.9	Wide	9.23	0.30	0.30	31.5	15
Pyriproxyfen		136.1	Unit	96	Wide	9.42	0.30	0.30	48.8	10
Pyriproxyfen		136.1	Unit	78	Wide	9.42	0.30	0.30	48.8	20
Azinphos Methyl		160.1	Unit	132.1	Wide	9.61	0.30	0.30	60.8	0
Azinphos Methyl		160.1	Unit	77.1	Wide	9.61	0.30	0.30	60.8	20
Pyridaben		147	Unit	132	Wide	9.88	0.30	0.30	72.9	10
Pyridaben		147	Unit	117	Wide	9.88	0.30	0.30	72.9	20
Coumaphos		361.9	Unit	109	Wide	10.03	0.30	0.30	87.2	15
Coumaphos		361.9	Unit	81	Wide	10.03	0.30	0.30	87.2	35
Fenbuconazole		198	Unit	129	Wide	10.10	0.30	0.30	130.3	10

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Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Fenbuconazole		129	Unit	102	Wide	10.10	0.30	0.30	130.3	15
Flumioxazin		354	Unit	326	Wide	10.87	0.30	0.30	214.7	10
Flumioxazin		354	Unit	312	Wide	10.87	0.30	0.30	214.7	10
Difenoconazole		323	Unit	265	Wide	11.17	0.30	0.30	147.5	15
Difenoconazole		265	Unit	139	Wide	11.17	0.30	0.30	147.5	50
Azoxystrobin-d4		348	Unit	333.2	Wide	11.50	0.30	0.30	94.9	15
Azoxystrobin-d4		348	Unit	172	Wide	11.50	0.30	0.30	94.9	35
Dimethomorph		303	Unit	165	Wide	11.56	0.30	0.30	85.3	10
Dimethomorph		300.9	Unit	165	Wide	11.56	0.30	0.30	85.3	10
Azoxystrobin		388.1	Unit	345.2	Wide	11.63	0.30	0.30	94.9	20
Azoxystrobin		344.1	Unit	329.1	Wide	11.63	0.30	0.30	94.9	20
Loratadine		382.1	Unit	292	Wide	12.04	0.30	0.30	148.8	25
Loratadine		382.1	Unit	245.1	Wide	12.04	0.30	0.30	148.8	20

TABLE 4B. MRM method acquisition parameters for Chlorinated pesticides (soil mix) (ref 15.6)

Method File	C:\MassHunter\GCMS\1\methods\SCL_dMRM_200603.M\qqqacqmethod.xml
Tune File	atunes.eihs.tune.xml
Ion Source	EI
Source Temp. (°C)	300
Electron Energy Mode	Use tune setting
Fixed Electron Energy (eV)	
Stop Mode	By Chromatograph Time
Stop Time (min)	1
Solvent Delay (min)	4
Use Gain	Yes
EM Saver	
Auto Baseline Subtract	Yes
Advanced Filtering	No

Time filter type: off		
Row	**Time (min)**	**Peak Width (sec)**

Index	Start Time (min)	Scan Type	Electron Energy (eV)	Data Stored	Delta EMV (V)	Gain
1	4.00	dMRM		X		2

Time Events:

Time Segments:

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Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Tetrachloro-m-xylene		206.9	Unit	171.9	Wide	6.39	0.30	0.30	75.7	27
Tetrachloro-m-xylene		206.9	Unit	136	Wide	6.39	0.30	0.30	75.7	20
Ethalfluralin		316	Unit	276	Wide	6.62	0.30	0.30	37.8	11
Ethalfluralin		276	Unit	202	Wide	6.62	0.30	0.30	37.8	18
Trifluralin-d14	X	315	Unit	267.1	Wide	6.68	0.30	0.30	29.5	7
Trifluralin-d14	X	266.9	Unit	163.1	Wide	6.68	0.30	0.30	29.5	17
DCB-d5	X	226.9	Unit	192.1	Wide	6.74	0.30	0.30	26.1	12
DCB-d5	X	226.9	Unit	157.1	Wide	6.74	0.30	0.30	26.1	28

Compound Table:

Time Filter Table:

Total MRMs	101
Minimum Concurrent MRMs	2
Maximum Concurrent MRMs	16
Min Dwell (group average)	21.8
Max Dwell (group average)	149.6
Estimated Cycle Time	301.0924

DMRM Statistics:

Triple Quadrupole Acquisition Method - MS Parameters Report

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Compound Table:

Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Trifluralin		306.1	Unit	264	Wide	6.75	0.30	0.30	27.7	5
Trifluralin		306.1	Unit	160	Wide	6.75	0.30	0.30	27.7	30
alpha-BHC-d6	X	223.8	Unit	187	Wide	6.99	0.30	0.30	28.7	8
alpha-BHC-d6	X	223.8	Unit	150	Wide	6.99	0.30	0.30	28.7	23
Alpha-BHC		181	Unit	145	Wide	7.06	0.30	0.30	29.8	15
Alpha-BHC		181	Unit	109	Wide	7.06	0.30	0.30	29.8	30
Hexachlorobenzene		283.7	Unit	248.8	Wide	7.17	0.30	0.30	33.4	23
Hexachlorobenzene		283.7	Unit	213.9	Wide	7.17	0.30	0.30	33.4	35
Beta-BHC		181	Unit	145	Wide	7.50	0.30	0.30	49.4	15
Beta-BHC		181	Unit	109	Wide	7.50	0.30	0.30	49.4	30
Gamma-BHC		181	Unit	145	Wide	7.60	0.30	0.30	55.7	15
Gamma-BHC		181	Unit	109	Wide	7.60	0.30	0.30	55.7	30
Delta-BHC		181	Unit	145	Wide	8.03	0.30	0.30	61.9	15
Delta-BHC		181	Unit	109	Wide	8.03	0.30	0.30	61.9	30

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Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Chlorothalonil		265.9	Unit	230.9	Wide	8.12	0.30	0.30	91.1	20
Chlorothalonil		265.9	Unit	133	Wide	8.12	0.30	0.30	91.1	40
Heptachlor		271.9	Unit	236.8	Wide	8.92	0.30	0.30	61.9	25
Heptachlor		271.9	Unit	234.8	Wide	8.92	0.30	0.30	61.9	14
TCB-d5	X	296.8	Unit	262	Wide	9.50	0.30	0.30	52.4	12
TCB-d5	X	296.8	Unit	225	Wide	9.50	0.30	0.30	52.4	28
MGK-264		164.1	Unit	98.1	Wide	9.60	1.00	0.30	69	15
MGK-264		164.1	Unit	80.1	Wide	9.60	1.00	0.30	69	30
Aldrin		262.9	Unit	192.9	Wide	9.61	0.30	0.30	52.4	40
Aldrin		260.9	Unit	190.9	Wide	9.61	0.30	0.30	52.4	40
Dacthal		300.8	Unit	257.8	Wide	9.86	0.30	0.30	58.7	25
Dacthal		300.8	Unit	222.9	Wide	9.86	0.30	0.30	58.7	30
Heptachlor Epoxide		352.9	Unit	281.9	Wide	10.42	0.30	0.30	81.4	16
Heptachlor Epoxide		352.9	Unit	262.8	Wide	10.42	0.30	0.30	81.4	15
Gamma-Chlordane		372.9	Unit	263.9	Wide	10.91	0.30	0.30	40.5	20
Gamma-Chlordane		271.7	Unit	236.9	Wide	10.91	0.30	0.30	40.5	12
Prallethrin		168.1	Unit	123.1	Wide	10.96	0.40	0.40	42	8
Prallethrin		153.1	Unit	107.1	Wide	10.96	0.40	0.40	42	13
Prallethrin		153.1	Unit	90.9	Wide	10.96	0.40	0.40	42	26
Endosulfan I		240.9	Unit	205.9	Wide	11.16	0.30	0.30	35.4	15
Endosulfan I		206.8	Unit	172	Wide	11.16	0.30	0.30	35.4	13
Alpha-Chlordane		372.9	Unit	263.9	Wide	11.23	0.30	0.30	34.5	20
Alpha-Chlordane		271.7	Unit	236.9	Wide	11.23	0.30	0.30	34.5	12
Trans-Nonachlor		408.7	Unit	372.7	Wide	11.34	0.30	0.30	37.2	10
Trans-Nonachlor		408.7	Unit	299.8	Wide	11.34	0.30	0.30	37.2	19
DDE-p,p'		246	Unit	176.1	Wide	11.70	0.30	0.30	47.8	40
DDE-p,p'		246	Unit	175.1	Wide	11.70	0.30	0.30	47.8	40
Dieldrin		262.9	Unit	192.9	Wide	11.71	0.30	0.30	52.2	40
Dieldrin		260.9	Unit	190.9	Wide	11.71	0.30	0.30	52.2	35
Endrin		262.8	Unit	192.8	Wide	12.17	0.30	0.30	56.8	30
Endrin		262.7	Unit	191.1	Wide	12.17	0.30	0.30	56.8	40
Endosulfan II		241	Unit	206	Wide	12.38	0.30	0.30	49.3	15
Endosulfan II		206.9	Unit	172.1	Wide	12.38	0.30	0.30	49.3	14
DDD-p,p'		235	Unit	199.1	Wide	12.60	0.30	0.30	41.8	20
DDD-p,p'		235	Unit	165.1	Wide	12.60	0.30	0.30	41.8	25
Cis-Nonachlor		408.7	Unit	372.7	Wide	12.67	0.30	0.30	39.7	10
Cis-Nonachlor		408.7	Unit	299.8	Wide	12.67	0.30	0.30	39.7	19
Endrin Aldehyde		344.8	Unit	280.9	Wide	12.79	0.30	0.30	38.2	6
Endrin Aldehyde		344.8	Unit	244.9	Wide	12.79	0.30	0.30	38.2	10
Piperonil Butoxide		176.1	Unit	117.1	Wide	13.16	0.30	0.30	35.1	25
Piperonil Butoxide		176.1	Unit	103.1	Wide	13.16	0.30	0.30	35.1	30

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Compound Name	ISTD ?	Precursor ion	MS1 res	Product ion	MS2 res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Carbophenothion		343.9	Unit	158.9	Wide	13.17	0.30	0.30	35.3	13
Carbophenothion		341.9	Unit	157	Wide	13.17	0.30	0.30	35.3	13
Endosulfan Sulfate		271.7	Unit	236.8	Wide	13.30	0.30	0.30	33	12
Endosulfan Sulfate		269.7	Unit	234.9	Wide	13.30	0.30	0.30	33	12
DDT-D8	X	243.03	Unit	206.14	Wide	13.34	0.30	0.30	42.4	15
DDT-D8	X	243.03	Unit	172.6	Wide	13.34	0.30	0.30	42.4	20
DDT-p,p'		235	Unit	199.1	Wide	13.40	0.30	0.30	72.6	20
DDT-p,p'		235	Unit	165.1	Wide	13.40	0.30	0.30	72.6	30
Endrin Ketone		316.9	Unit	280.9	Wide	14.10	0.30	0.30	61.1	7
Endrin Ketone		316.9	Unit	101.1	Wide	14.10	0.30	0.30	61.1	14
HCB-d3	X	362.7	Unit	362.7	Wide	14.27	0.30	0.30	31.3	5
HCB-d3	X	362.7	Unit	292.9	Wide	14.27	0.30	0.30	31.3	32
Dicofol-d8		142.9	Unit	115.1	Wide	14.29	0.30	0.30	23.6	15
Dicofol-d8		142.9	Unit	78	Wide	14.29	0.30	0.30	23.6	34
Bifenthrin		181.1	Unit	166.1	Wide	14.30	0.30	0.30	23.7	13
Bifenthrin		181.1	Unit	165.1	Wide	14.30	0.30	0.30	23.7	33
Dicofol		253	Unit	141	Wide	14.32	0.30	0.30	21.8	15
Dicofol		251	Unit	139	Wide	14.32	0.30	0.30	21.8	15
Methoxychlor		227.1	Unit	169.1	Wide	14.33	0.30	0.30	23.7	30
Methoxychlor		227.1	Unit	141.1	Wide	14.33	0.30	0.30	23.7	40
Phenothrin		183.1	Unit	168.1	Wide	14.61	0.40	0.40	23.6	15
Phenothrin		183.1	Unit	153.1	Wide	14.61	0.40	0.40	23.6	15
Mirex		271.9	Unit	236.9	Wide	14.78	0.30	0.30	34.9	15
Mirex		271.9	Unit	234.8	Wide	14.78	0.30	0.30	34.9	14
Lambda-Cyhalothrin		208	Unit	181	Wide	14.93	0.40	0.40	42.5	7
Lambda-Cyhalothrin		181.1	Unit	152.1	Wide	14.93	0.40	0.40	42.5	30
Permethrin		183.1	Unit	168.1	Wide	15.44	0.40	0.40	72.3	15
Permethrin		183.1	Unit	153.1	Wide	15.44	0.40	0.40	72.3	15
Beta-Cyfluthrin		226.1	Unit	206.1	Wide	15.87	0.40	0.40	49.3	15
Beta-Cyfluthrin		163	Unit	127.1	Wide	15.87	0.40	0.40	49.3	5
Octachloronaphthalene		354.9	Unit	267	Wide	15.95	0.40	0.40	44.2	15
Octachloronaphthalene		354.9	Unit	251	Wide	15.95	0.40	0.40	44.2	40
Cypermethrin		208.9	Unit	169.2	Wide	16.02	0.40	0.40	49.2	11
Cypermethrin		180.9	Unit	152.1	Wide	16.02	0.40	0.40	49.2	23
Decachlorobiphenyl		497.6	Unit	462.7	Wide	16.35	0.30	0.30	77.5	15
Decachlorobiphenyl		497.6	Unit	427.9	Wide	16.35	0.30	0.30	77.5	20
Deltamethrin		253	Unit	93	Wide	17.37	0.40	0.30	149.6	20
Deltamethrin		181.1	Unit	152.1	Wide	17.37	0.40	0.30	149.6	25

Compound Table:
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TABLE 4C. MRM method acquisition parameters for PCB aroclors (Ref. 15.19)

Triple Quadrupole Acquisition Method - MS Parameters Report

Method File	D:\MassHunter\GCMS\1\methods\AR_dMRM_190115.M,.qqqacqmethod .xml
Tune File	atunes.eiex.tune.xml
Source	EI
Source Temp. (°C)	300
Electron Energy Mode	Use tune setting
Fixed Electron Energy (eV)	
Stop Mode	By Chromatograph Time
Stop Time (min)	1
Solvent Delay (min)	3.70000004768372
Use Gain	Yes
EM Saver	
Auto Baseline Subtract	Yes
Advanced Filtering	No

Time Filter Table:

Time filter type: off

Row Time (min) Peak Width (sec)

Time Segments:

[redacted]	Start Time (min)	Scan Type	Electron Energy (eV)	Data Stored	Delta EMV (V)	Gain
1	4.15	D MRM		X		20

Time Events:

DMRM Statistics:

Total MRMs	28
Minimum Concurrent MRMs	1
Maximum Concurrent MRMs	13
Min Dwell (group average)	22.1
Max Dwell (group average)	80.9
Estimated Cyde Time	286.5936

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Triple Quadrupole Acquisition Method - MS Parameters Report

Compound Table:

Compound Name	ISTD?	Precursor Ion	MSI Res	Product Ion	MS2 Res	RT	Left Delta RT	Right Delta RT	Dwell (ms)	CE (V)
Monochlorobiphenyl-2		153.9	Unit	115.2	Wide	4.20	0.50	3.50	80.9	22
Monochlorobiphenyl		188	Unit	152	Wide	5.30	0.50	2.00	54.3	25
Dichlorobiphenyl		222	Unit	152	Wide	6.20	0.50	6.00	33.1	25
Dichlorobiphenyl-2		222	Unit	187.1	Wide	6.20	0.50	6.00	33.1	9
Dichlorobiphenyl-3		219.8	Unit	149.7	Wide	6.20	0.50	6.00	33.1	26
Tetrachloro-m-xylene		206.9	Unit	171.9	Wide	6.48	0.50	0.50	32.1	27
Tetrachloro-m-xylene		206.9	Unit	136	Wide	6.48	0.50	0.50	32.1	20
DCB-d5	X	226.9	Unit	192.1	Wide	6.81	0.50	0.50	30.5	12
DCB-d5	X	226.9	Unit	157.1	Wide	6.81	0.50	0.50	30.5	28
Trichlorobiphenyl		258	Unit	186	Wide	7.20	0.50	6.00	29.2	25
Trichlorobiphenyl-2		255.8	Unit	185.9	Wide	7.20	0.50	6.00	29.2	21
Tetrachlorobiphenyl		291.9	Unit	222	Wide	8.20	0.50	8.00	27	25
Tetrachlorobiphenyl-2		291.9	Unit	220.1	Wide	8.20	0.50	8.00	27	22
TCB-d5	X	296.8	Unit	262	Wide	9.55	0.50	0.50	27	12
TCB-d5	X	296.8	Unit	225	Wide	9.55	0.50	0.50	27	28
Pentachlorobiphenyl		325.9	Unit	255.9	Wide	9.80	0.50	7.00	25.4	25
Pentachlorobiphenyl-2		325.9	Unit	291	Wide	9.80	0.50	7.00	25.4	10
Pentachlorobiphenyl-3		325.9	Unit	253.9	Wide	9.80	0.50	7.00	25.4	18
Hexachlorobiphenyl		359.8	Unit	289.9	Wide	11.50	0.50	5.50	31.3	25
Hexachlorobiphenyl-2		359.8	Unit	324.9	Wide	11.50	0.50	5.50	31.3	11
Heptachlorobiphenyl		393.8	Unit	323.9	Wide	12.90	0.50	4.00	28.2	25
Heptachlorobiphenyl-2		393.8	Unit	358.7	Wide	12.90	0.50	4.00	28.2	12
Octachlorobiphenyl		427.8	Unit	357.8	Wide	14.00	0.50	3.00	32.9	25
HCB-d3	X	362.7	Unit	362.7	Wide	14.30	0.50	0.50	22.1	5
HCB-d3	X	362.7	Unit	292.9	Wide	14.30	0.50	0.50	22.1	32
Nonachlorobiphenyl		461.7	Unit	391.8	Wide	14.50	0.50	3.00	66.4	25
Decachlorobiphenyl		497.6	Unit	462.7	Wide	16.35	0.50	0.50	27.1	15
Decachlorobiphenyl		497.6	Unit	427.9	Wide	16.35	0.50	0.50	27.1	20

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*Some transitions are not found in any of the quantitation methods. They are only used for pattern recognition.

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TABLE 4D. MRM method acquisition parameters for Chlorinated pesticides (tissue mix)

Analyte	Time segment/	Quant	Collision energy (V)	Qual	Collision energy (V)
	TS start time	Transition	quant	Transition	qual
Tetrachloro-m-xylene	TS1/6.00	206.9 - 136	20	206.9 - 171.9	27
PCB-8	TS2/6.50	222 - 152	25	223.9 - 152	25
Alpha-BHC	TS2/6.50	181 - 145	15	181 - 109	30
Hexachlorobenzene	TS2/6.50	283.7 - 213.9	23	283.7 - 248.8	35
DCB-d5	TS2/6.50	226.9-157.1	28	226.9-192.1	12
Alpha-BHC-d6	TS2/6.50	223.8-187.0	8	223.8-150.0	23
Gamma-BHC	TS3/7.26	181 - 145	15	181 - 109	30
Beta-BHC	TS3/7.26	181 - 145	15	181 - 109	30
PCB-18	TS3/7.26	255.8 - 186	25	258 - 186	25
Delta-BHC	TS3/7.26	181 - 145	15	181 - 109	30
PCB-28	TS4/8.25	255.8 - 186	25	258 - 186	25
Heptachlor	TS4/8.25	271.9 - 236.8	25	271.9 - 234.8	14
PCB-52	TS5/9.00	291.9 - 222	25	219.8 - 149.7	26
TCB-d5	TS5/9.00	296.8-225.0	28	296.8-262	12
Aldrin	TS5/9.00	260.9 - 190.9	40	262.9 - 192.9	40
PCB-44	TS5/9.00	291.9 - 222	25	219.8 - 149.7	26
Heptachlor Epoxide	TS6/10.00	352.9 - 262.8	15	352.9 - 281.9	16
Oxychlordane	TS6/10.00	387.0 – 263.0	14	187.0 – 151.0	4
PCB-66	TS6/10.00	291.9 - 222	25	219.8 - 149.7	26
Trans-Chlordane	TS7/10.65	271.7-236.9	20	372.9-263.9	12
DDE-o,p'	TS7/10.65	246 - 176.1	40	246 - 175.1	40
PCB-101	TS7/10.65	325.9 - 255.9	25	325.9 - 253.9	18
Endosulfan I	TS7/10.65	240.9 - 205.9	15	206.8 - 172	13
Cis-Chlordane	TS7/10.65	271.7-236.9	20	372.9-263.9	12
Trans-Nonachlor	TS7/10.65	408.7 - 299.8	19	408.7 - 372.7	10
Dieldrin	TS8/11.35	262.9 - 192.9	35	260.9 - 190.9	40
DDE-p,p'	TS8/11.35	246 - 176.1	40	246 - 175.1	40
PCB-77	TS8/11.35	291.9 - 222	25	219.8 - 149.7	26
DDD-o,p'	TS8/11.35	235 - 165.1	25	235 - 199.1	20
Endrin	TS9/11.87	262.8 - 192.8	30	262.7 - 191.1	40
Endosulfan II	TS10/12.07	241.0-206.0	14	–206.9-172.1	10
PCB-118	TS10/12.07	325.9 - 255.9	25	325.9 - 253.9	18
DDD-p,p'	TS10/12.07	235 - 165.1	25	235 - 199.1	20
Cis-Nonachlor	TS11/12.33	408.7 - 299.8	10	408.7 - 372.7	19
DDT-o,p'	TS11/12.33	235 - 165.1	25	235 - 199.1	20
Endrin Aldehyde	TS11/12.33	344.8 - 280.9	6	344.8 - 244.9	10
PCB-153	TS11/12.33	359.8 - 289.9	25	359.8 - 324.9	11
PCB-105	TS11/12.33	325.9 - 255.9	25	325.9 - 253.9	18
Endosulfan Sulfate	TS12/12.98	271.7 - 236.8	12	269.7-234.9	12
DDT-p,p'	TS12/12.98	235 - 165.1	30	235 - 199.1	20
DDT-p,p'-d8	TS12/12.98	243-206.1	15	243-172.6	20
PCB-138	TS13/13.37	359.8 - 289.9	25	359.8 - 324.9	11
PCB-126	TS13/13.37	325.9 - 255.9	25	325.9 - 253.9	18

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Analyte	Time segment/	Quant	Collision energy (V)	Qual	Collision energy (V)
PCB-187	TS13/13.37	393.8 - 323.9	25	393.8 - 358.7	12
PCB-128	TS14/13.74	359.8 - 289.9	25	359.8 - 324.9	11
Endrin Ketone	TS14/13.74	316.9 - 280.9	7	316.9 - 101.1	14
Methoxychlor	TS15/14.06	227.1 - 169.1	30	227.1 - 141.1	40
HCB-d3	TS15/14.06	362.7-362.7	5	362.7-292.9	32
PCB-180	TS15/14.06	393.8 - 323.9	25	393.8 - 358.7	12
PCB-169	TS16/14.51	359.8-289.9	25	359.8-324.9	11
Mirex	TS16/14.51	271.9 - 236.9	15	271.9 - 234.8	14
PCB-170	TS16/14.51	393.8 - 323.9	25	393.8 - 358.7	12
PCB-195	TS17/14.98	429.6 - 394.8	15	392.7 - 357.9	15
PCB-206	TS18/15.55	463.6 - 428.8	15	463.6 - 393.9	34
Decachlorobiphenyl	TS18/15.55	497.6 - 427.9	20	497.6 - 462.7	15

Table 5A: Analyte concentrations for calibration standards and ICV for Nitrogen Phosphorus pesticides (ug/L). The expected spike concentrations in LFBs/MSs are 80% of L-5 whereas in the CCV and ICV are equal to L5

ANALYTE	L8	L7	L6	L5	L4	L3	L2	L1	ICV
NPTQ MIX	ppb	ppb	ppb	ppb	ppb	ppb	ppb	ppb	ppb
Acetochlor	200	100	40	20	10	4	2	1	20
Alachlor	200	100	40	20	10	4	2	1	60
Ametryn	200	100	40	20	10	4	2	1	20
Atrazine	200	100	40	20	10	4	2	1	20
Atrazine Desethyl	800	400	160	80	40	16	8	4	80
Azinphos Methyl	800	400	160	80	40	16	8	4	80
Azoxystrobin	400	200	80	40	20	8	4	2	20
Bromacil	400	200	80	40	20	8	4	2	40
Butylate	200	100	40	20	10	4	2	1	20
Caffeine	2000	1000	400	200	100	40	20	10	200
Carbophenothion	400	200	80	40	20	8	4	2	40
Carfentrazone Ethyl	100	50	20	10	5	2	1	0.5	20
Chlorfenapyr	200	100	40	20	10	4	2	1	20
Chlorpyrifos Ethyl	200	100	40	20	10	4	2	1	20
Chlorpyrifos Methyl	100	50	20	10	5	2	1	0.5	10
Coumaphos	400	200	80	40	20	8	4	2	40
Cyanazine	800	400	160	80	40	16	8	4	20
Cyprodinil	100	50	20	10	5	2	1	0.5	10
DEET	800	400	160	80	40	16	8	4	20
Demeton	1600	800	320	160	80	32	16	8	70
Diazinon	100	50	20	10	5	2	1	0.5	20
Difenoconazole	200	100	40	20	10	4	2	1	20
Dimethenamid	100	50	20	10	5	2	1	0.5	10
Dimethomorph	200	100	40	20	10	4	2	1	20
Disulfoton	200	100	40	20	10	4	2	1	10

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ANALYTE	L8	L7	L6	L5	L4	L3	L2	L1	ICV
Dithiopyr	200	100	40	20	10	4	2	1	20
EPTC	400	200	80	40	20	8	4	2	40
Ethion	200	100	40	20	10	4	2	1	20
Ethoprop	100	50	20	10	5	2	1	0.5	10
Etridiazole	100	50	20	10	5	2	1	0.5	10
Fenamiphos	200	100	40	20	10	4	2	1	20
Fenbuconazole	200	100	40	20	10	4	2	1	20
Fipronil	200	100	40	20	10	4	2	1	20
Fipronil Desulfinyl	100	50	20	10	5	2	1	0.5	20
Fipronil Sulfide	100	50	20	10	5	2	1	0.5	10
Fipronil Sulfone	100	50	20	10	5	2	1	0.5	10
Fluazifop-P-butyl	100	50	20	10	5	2	1	0.5	20
Fludioxonil	100	50	20	10	5	2	1	0.5	20
Flumioxazin	800	400	160	80	40	16	8	4	60
Flutolanil	100	50	20	10	5	2	1	0.5	20
Fluxapyroxad	100	50	20	10	5	2	1	0.5	20
Fonofos	100	50	20	10	5	2	1	0.5	5
Hexazinone	400	200	80	40	20	8	4	2	60
Imazalil	400	200	80	40	20	8	4	2	20
Iprodione	200	100	40	20	10	4	2	1	20
Loratadine	200	100	40	20	10	4	2	1	20
Malathion	200	100	40	20	10	4	2	1	20
Metalaxyl	200	100	40	20	10	4	2	1	80
Metolachlor	400	200	80	40	20	8	4	2	60
Metribuzin	400	200	80	40	20	8	4	2	40
Mevinphos	200	100	40	20	10	4	2	1	20
Molinate	200	100	40	20	10	4	2	1	20
Myclobutanil	200	100	40	20	10	4	2	1	20
Naled	400	200	80	40	20	8	4	2	40
Napropamide	800	400	160	80	40	16	8	4	80
Norflurazon	400	200	80	40	20	8	4	2	60
Oxadiazon	100	50	20	10	5	2	1	0.5	20
Oxyfluorfen	100	50	20	10	5	2	1	0.5	20
Parathion Ethyl	100	50	20	10	5	2	1	0.5	10
Parathion Methyl	200	100	40	20	10	4	2	1	20
Pendimethalin	400	200	80	40	20	8	4	2	40
Phenytoin	800	400	160	80	40	16	8	4	80
Phorate	100	50	20	10	5	2	1	0.5	10
Phosmet	800	400	160	80	40	16	8	4	80
Prodiamine	100	50	20	10	5	2	1	0.5	20
Prometon	400	200	80	40	20	8	4	2	40
Prometryn	100	50	20	10	5	2	1	0.5	20
Pronamide	100	50	20	10	5	2	1	0.5	10
Propanil	100	50	20	10	5	2	1	0.5	10
Propargite	400	200	80	40	20	8	4	2	40

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ANALYTE	L8	L7	L6	L5	L4	L3	L2	L1	ICV
Propiconazole	200	100	40	20	10	4	2	1	20
Pyraflufen Ethyl	100	50	20	10	5	2	1	0.5	10
Pyridaben	400	200	80	40	20	8	4	2	40
Pyriproxyfen	100	50	20	10	5	2	1	0.5	20
Simazine	200	100	40	20	10	4	2	1	20
Stirophos	200	100	40	20	10	4	2	1	20
Sulfentrazone	400	200	80	40	20	8	4	2	40
Tebuconazole	400	200	80	40	20	8	4	2	60
Terbufos	100	50	20	10	5	2	1	0.5	10
Terbuthylazine	200	100	40	20	10	4	2	1	20
Thiobencarb	400	200	80	40	20	8	4	2	40
Tridimefon	100	50	20	10	5	2	1	0.5	10
Simazine-d10	200	100	40	20	10	4	2	1	20
Terbufos-d10	200	100	40	20	10	4	2	1	20

Methamidophos, Monocrotophos are not currently analyzed in water.

Table 5B: Analyte concentrations in calibration standards and ICV for Chlorinated pesticides (ug/L) (Test ID S-PSCL-TQ). These standards are also used to run abbreviated version of the T-PCBCL-TQ test. (pesticides only, without PCB congeners and DDT-o,p', DDD-o,p' and DDE-o,p')

	L9	L8	L7	L6/ccv	L5	L4	L3	L2	L6 ICV
PEST-CL	ppb	ppb	ppb	ppb	ppb	ppb	ppb	ppb	ppb
Aldrin	400	200	100	40	20	12	4	2	20
Alpha-BHC	200	100	50	20	10	6	2	1	20
Alpha-Chlordane	200	100	50	20	10	6	2	1	20
Beta-BHC	200	100	50	20	10	6	2	1	20
Beta-Cyfluthrin	800	400	200	80	40	24	8	4	100
Bifenthrin	200	100	50	20	10	6	2	1	20
Carbophenothion	800	400	200	80	40	24	8	4	20
Chlorothalonil	800	400	200	80	40	24	8	4	20
Cis-Nonachlor	200	100	50	20	10	6	2	1	20
Cypermethrin	800	400	200	80	40	24	8	4	100
Dacthal	200	100	50	20	10	6	2	1	20
DDD-p,p'	200	100	50	20	10	6	2	1	20
DDE-p,p'	200	100	50	20	10	6	2	1	20
DDT-p,p'	400	200	100	40	20	12	4	2	20
Delta-BHC	800	400	200	80	40	24	8	4	20
Deltamethrin	800	400	200	80	40	24	8	4	100
Dicofol	800	400	200	80	40	24	8	4	100
Dieldrin	800	400	200	80	40	24	8	4	20
Endosulfan I	800	400	200	80	40	24	8	4	20
Endosulfan II	800	400	200	80	40	24	8	4	20
Endosulfan Sulfate	400	200	100	40	20	12	4	2	20

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	L9	L8	L7	L6/ccv	L5	L4	L3	L2	L6 ICV
PEST-CL	ppb	ppb	ppb	ppb	ppb	ppb	ppb	ppb	ppb
Endrin	800	400	200	80	40	24	8	4	20
Endrin Aldehyde	800	400	200	80	40	24	8	4	20
Endrin Ketone	800	400	200	80	40	24	8	4	20
Ethalfluralin	200	100	50	20	10	6	2	1	20
Gamma-BHC	200	100	50	20	10	6	2	1	20
Gamma-Chlordane	200	100	50	20	10	6	2	1	20
Heptachlor	200	100	50	20	10	6	2	1	20
Heptachlor Epoxide	200	100	50	20	10	6	2	1	20
Hexachlorobenzene	800	400	200	80	40	24	8	4	20
Lambda-Cyhallothrin	800	400	200	80	40	24	8	4	100
Methoxychlor	200	100	50	20	10	6	2	1	20
Mirex	400	200	100	40	20	12	4	2	20
Oxychlordane	200	100	50	20	10	6	2	1	20
Permethrin	800	400	200	80	40	24	8	4	100
Phenothrin	800	400	200	80	40	24	8	4	100
Prallethrin	800	400	200	80	40	24	8	4	100
Trans-Nonachlor	200	100	50	20	10	6	2	1	20
Trifluralin	400	200	100	40	20	12	4	2	20
Tetrachloro-m-xylene	200	100	50	20	10	6	2	1	20
DCB	200	100	50	20	10	6	2	1	20

L-1 calibration standard is used only for water samples by W-PCL-TQ-R

Table 5C. Analyte concentrations in calibration standards and ICV for PCB Aroclors (ug/L; test ID S-PCB-TQ). The expected spike concentrations in LFBs.MSs are equal to 160 ug/L. L-1 standards are not used for soil samples.

AROCLORS	L-7	L-6	L-5	L-4	L-3	L-2	ICV L-4
Tetrachloro-m-xylene	100	75	50	25	10	5	25
PCB-1016	1000	750	500	250	100	50	250
PCB-1221	1000	750	500	250	100	50	250
PCB-1232	1000	750	500	250	100	50	350
PCB-1242	1000	750	500	250	100	50	250
PCB-1248	1000	750	500	250	100	50	150
PCB-1254	1000	750	500	250	100	50	250
PCB-1260	1000	750	500	250	100	50	250
Decachlorobiphenyl	100	75	50	25	10	5	50

L-1 calibration standard is used only for water samples by W-PCB-TQ-R

Table 5D: Analyte concentrations in calibration standards and ICV for Chlorinated pesticides in tissue (ug/L). Test ID T-PCBCL-TQ. The expected spike concentrations in LFBs/MSs are equal to L5. CCV concentrations are equal to L5. For abbreviated version of the test S-PSCL-TQ standards are used. PCB congeners may be mixed with DDE-o,p', DDD-o,p' and DDT-o,p' and run along with S-PSCL-TQ standards to cover the entire analyte list of T-PCBCL-TQ.

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Analyte	spike	L8	L7	L6	L5	L4	L3	L2	L1	ICV
PCBCL_TQ	T-CL-TQ									ICV
Aldrin	100	200	100	50	20	10	4	2	1	20
Alpha-BHC	100	200	100	50	20	10	4	2	1	20
Cis/Alpha-Chlordane	100	200	100	50	20	10	4	2	1	20
Beta-BHC	100	200	100	50	20	10	4	2	1	20
DDD-p,p'	100	200	100	50	20	10	4	2	1	20
DDE-p,p'	100	200	100	50	20	10	4	2	1	20
Delta-BHC	100	200	100	50	20	10	4	2	1	20
Dieldrin	100	200	100	50	20	10	4	2	1	20
Endosulfan I	100	200	100	50	20	10	4	2	1	20
Endosulfan II	100	200	100	50	20	10	4	2	1	20
Endosulfan Sulfate	100	200	100	50	20	10	4	2	1	20
Endrin Aldehyde	100	200	100	50	20	10	4	2	1	20
Endrin Ketone	100	200	100	50	20	10	4	2	1	20
Gamma-BHC	100	200	100	50	20	10	4	2	1	20
Trans/Gamma-Chlordane	100	200	100	50	20	10	4	2	1	20
Heptachlor	100	200	100	50	20	10	4	2	1	20
Heptachlor Epoxide	100	200	100	50	20	10	4	2	1	20
Methoxychlor	100	200	100	50	20	10	4	2	1	20
Hexachlorobenzene	100	200	100	50	20	10	4	2	1	20
Cis-Nonachlor	100	200	100	50	20	10	4	2	1	20
Trans-Nonachlor	100	200	100	50	20	10	4	2	1	20
DDE-o,p'	100	200	100	50	20	10	4	2	1	20
DDD-o,p'	100	200	100	50	20	10	4	2	1	20
DDT-p,p'	100	200	100	50	20	10	4	2	1	40
DDT-o,p'	100	200	100	50	20	10	4	2	1	20
Endrin	100	200	100	50	20	10	4	2	1	40
Mirex	100	200	100	50	20	10	4	2	1	20
TMX-surrogate	200	200	100	50	20	10	4	2	1	20
DCB-surrogate	200	400	200	100	40	20	8	4	2	40
PCB-8	100	200	100	50	20	10	4	2	1	20
PCB-18	100	200	100	50	20	10	4	2	1	20
PCB-28	100	200	100	50	20	10	4	2	1	20
PCB-52	100	200	100	50	20	10	4	2	1	20
PCB-44	100	200	100	50	20	10	4	2	1	20
PCB-66	100	200	100	50	20	10	4	2	1	20
PCB-101	100	200	100	50	20	10	4	2	1	20
PCB-118	100	200	100	50	20	10	4	2	1	20

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Analyte	spike	L8	L7	L6	L5	L4	L3	L2	L1	ICV
PCB-153	100	200	100	50	20	10	4	2	1	20
PCB-105	100	200	100	50	20	10	4	2	1	20
PCB-138	100	200	100	50	20	10	4	2	1	20
PCB-187	100	200	100	50	20	10	4	2	1	20
PCB-128	100	200	100	50	20	10	4	2	1	20
PCB-180	100	200	100	50	20	10	4	2	1	20
PCB-169	100	200	100	50	20	10	4	2	1	20
PCB-170	100	200	100	50	20	10	4	2	1	20
PCB-195	100	200	100	50	20	10	4	2	1	20
PCB-206	100	200	100	50	20	10	4	2	1	20
PCB-209	100	200	100	50	20	10	4	2	1	20
PCB-77	100	200	100	50	20	10	4	2	1	20
PCB-126	100	200	100	50	20	10	4	2	1	20

PCB-209 included in DCB total

TABLE 6: QC MEASUREMENTS AND ACCEPTANCE CRITERIA

QC MEASUREMENT	ACCEPTANCE CRITERION	CORRECTIVE ACTION
LFB, Matrix Spike precision	≤ 30% except for W-PSNP-TQ	Reanalyze/Re-extract/Flag
LFB/MS recoveries/precision: W-PSNP-TQ	Separate statistical limits for LFBs and MSs; as per QCM limits tables, 50-150% for MS for newly added analytes, with some exceptions as per QCM tables	Reanalyze/Re-extract/Flag
LFB/MS recoveries: S-PSNP-TQ, WS-PSNP-TQ	Separate statistical limits for LFBs and MSs;- Statistical limits for LFB as per QCM tables 50-150% MS for Carbophenothion, Pronamide, Propiconazole, Sulfentrazone; Dimethenamid, Dithiopyr, Fipronil Desulfinyl, Oxadiazon, Flumioxazin, and Prodiamine. 30-120% for Naled and Tebuconazole.	Reanalyze/Re-extract/Flag
LFB/MS recoveries: S-PSCL-TQ, WS-PSCL-TQ	Separate statistical limits for LFBs and MSs as per QC limits tables, as per QC limits tables.	Reanalyze/Re-extract/Flag
LFB/MS recoveries/precision: S-PCB-TQ, WS-PCB-TQ	Separate statistical limits for LFBs and MSs for 1016&1260, as per QCM limits tables 60-130% for other aroclors except 50-130% for PCB-1221, <30% precision	Reanalyze/Re-extract/Flag
LFB/MS recoveries/precision: T-PCBCL-TQ	60-140%, precision<30%	Reanalyze/Re-extract/Flag
Surrogates: W-PSNP-TQ	Simazine-d10 71-140% Terbufos-d10 62-131% Caffeine -d9 20-200% istd/surrogate for isotope dilution).	Reanalyze/Re-extract/Flag

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QC MEASUREMENT	ACCEPTANCE CRITERION	CORRECTIVE ACTION
Surrogates: S-PSNP-TQ, WS-PSNP-TQ	Simazine-d10 48-150% Terbufos-d10 21-153%	Reanalyze/Re-extract/Flag
Surrogates: S-PSCL-TQ, S-PCB-TQ, WS-PSCL-TQ, WS-PCB-TQ	Tetrachloro-m-xylene 43-102% Decachlorobiphenyl 53-135%	Reanalyze/Re-extract/Flag
Surrogates: T-PCBCL-TQ	Tetrachloro-m-xylene 41-95% Decachlorobiphenyl 47-124%	Reanalyze/Re-extract/Flag
ICV	± 30%	Reanalyze/Flag
CCV	± 20%	Re-run and recalibrate/Flag
Linearity criterion	20% RSD, 0.99 R^2	Use appropriate cal fit / Re-run/ Recalibrate
Internal Std. recovery	50-200% Except for (soils only) Hexazinone-d6 25-200% Parathion Ethyl-d10 50-250% 20-200% for caffeine d9 (istd/sur for isotope dilution).	Reanalyze/recalibrate/flag
% cal drift	± 30% of expected value	Change fit/ recalibrate/flag
Instrument performance check	< 20% DDT degradation, tailing factor not more 2.0 for pentachlorophenol.	Perform instrument maintenance, rerun the performance check sample.
Method Blank	<MDL	Rerun/re-extract; qualify samples with “V” if up to 10X the value in method blank.

Statistical recovery limits for LFB/MS and surrogates recoveries are typically based on QC Manager statistics for the last two to five calendar years (if available). The limits are recalculated at least annually.The results of statistical calculations are saved at FLDEP1\DEAR\LABS\LAB5\CHEMISTRY\ORGANIC\QC LIMITS STATS. The statistical recovery limits are then uploaded into QC Manager limits tables. The initial QC limits are replaced with statistical ones whenever enough data points are accumulated. For more details refer to ref 15.8 chapter 5.3 .\

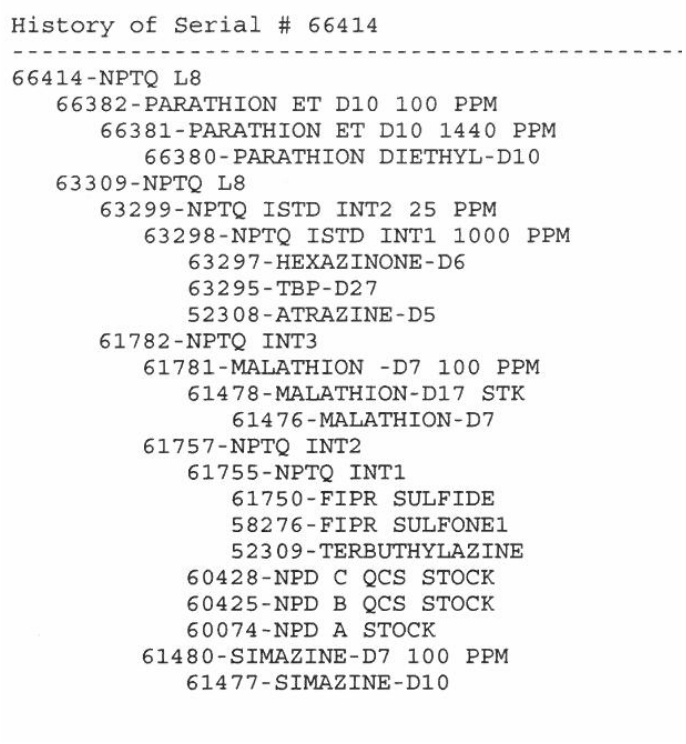
17. APPENDICES

APPENDIX 1

Standard Preparation Procedure

Stock solutions usually come in 1mL glass vials. Take the vials out of the freezer at least 30min before preparation. Open vials and transfer the entire solution into 1mL GC vials (using Pasteur pipettes). Record the transfer date and keep the vial label.
The Intermediate Standard is prepared by diluting the Stock solution. The Working Level Standards are prepared by diluting the Intermediate Standard.
All standard preparations are recorded in the Standard/Reagent Preparation Tracker. In order to prepare fresh standards go to LIMS-Technical-Standard/Reagent Preparation Tracker. Select GC from the pull down list. Hit “Reports” and then “History”. When prompted enter the standard tracking number for the standard you are going to replace. Examine the “History Tree”. An example of a “History Tree” is shown below:

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```
History of Serial # 66414
-------------------------------------------
66414-NPTQ L8
   66382-PARATHION ET D10 100 PPM
      66381-PARATHION ET D10 1440 PPM
         66380-PARATHION DIETHYL-D10
   63309-NPTQ L8
      63299-NPTQ ISTD INT2 25 PPM
         63298-NPTQ ISTD INT1 1000 PPM
            63297-HEXAZINONE-D6
            63295-TBP-D27
            52308-ATRAZINE-D5
         61782-NPTQ INT3
            61781-MALATHION -D7 100 PPM
               61478-MALATHION-D17 STK
                  61476-MALATHION-D7
            61757-NPTQ INT2
               61755-NPTQ INT1
                  61750-FIPR SULFIDE
                  58276-FIPR SULFONE1
                  52309-TERBUTHYLAZINE
               60428-NPD C QCS STOCK
               60425-NPD B QCS STOCK
               60074-NPD A STOCK
            61480-SIMAZINE-D7 100 PPM
               61477-SIMAZINE-D10
```

In order to get exact information on how the standard was prepared look at “history data sheets” that will show exact information on standards preparations.

Additionally, standards preparations are tabulated in excel files “STANDARDS-PREP-yyyy-mm-dd” located at \\FLDEP1\DEAR\LABS\LAB5\Chemistry\organic\GC-MDL-STD-SPK.

Before preparing new standards consult with the GC group supervisor whether any changes to standards preparation procedures should be made. Those may include different prepared volumes, concentrations, new, additional concentration levels, etc.
All freshly prepared standards need to be entered in the Standard Preparation Tracker.

APPENDIX 2

ANALYTE PROTECTANTS

Follow the instructions in appendix 1 to re-prepare analytes protectants solutions.

Notes: Neat D-sorbitol is hydroscopic and should be stored in a desiccator. D-Sorbitol and, especially, gulonolactone are difficult to dissolve in MeOH. To achieve complete dissolution of these components, 1 – 3 hours of hot sonication and repeated vigorous shaking (vortexing) may be needed. To avoid extensive sonication, required quantities of analyte protectants may be initially dissolved in 5 mL of water. The resulting solution may then be brought up to the final volume of 100 mL by adding methanol The resulting solution is saturated with gulonolactone and therefore should be kept at room temperature to avoid excessive precipitation. Some precipitation, however, appears to be unavoidable.

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APPENDIX 3

Tune check criteria

Triple Quadrupole GC/MS System Verification - Tune

Instrument Name	GC_TQ-2 / US12166802	**MS Model**	7000C
Tune Date & Time	4/24/2015 9:50:03 AM	**Source**	EI Extractor
Tune File	D:\MassHunter\GCMS\1\7000\atunes.eiex.tune.xml		

Instrument Actuals

Ionization mode	EI+	Rough Vacuum	1.36E+2 mTorr
Source Temperature	300 °C	High Vacuum	7.73E-5 Torr
Quad. 1 Temperature	150 °C	Turbo Speed	100.0 %
Quad. 2 Temperature	150 °C	Turbo Power	37.304 W
Emission Current	35.0 µA		

MS1 Checktune Results	Value	Limit	Result
Low mass assignment (target 69.00, actual 69.00)	0.00	<= 0.20	OK
Mid mass assignment (target 264.00, actual 264.00)	0.00	<= 0.20	OK
High mass assignment (target 502.00, actual 502.00)	0.00	<= 0.20	OK
Low mass isotope position (target 70.00, actual 70.10)	0.10	<= 0.20	OK
Mid mass isotope position (target 265.00, actual 265.00)	0.00	<= 0.20	OK
High mass isotope position (target 503.00, actual 503.02)	0.02	<= 0.20	OK
Low mass isotope ratio	1.06%	>= 0.5% and <= 1.6%	OK
Mid mass isotope ratio	5.68%	>= 4.2% and <= 6.9%	OK
High mass isotope ratio	9.70%	>= 7.9% and <= 12.3%	OK
Ratio of mid mass to low mass	31.75%	>= 5.0%	OK
Ratio of high mass to low mass	5.18%	>= 0.8%	OK
Low mass precursor ratio	0.13%	<= 3.00%	OK
Mid mass precursor ratio	0.05%	<= 6.00%	OK
High mass precursor ratio	0.03%	<= 12.00%	OK

MS2 Checktune Results			
Low mass assignment (target 69.00, actual 69.00)	0.00	<= 0.20	OK
Mid mass assignment (target 264.00, actual 264.00)	0.00	<= 0.20	OK
High mass assignment (target 502.00, actual 502.00)	0.00	<= 0.20	OK
Low mass isotope position (target 70.00, actual 70.00)	0.00	<= 0.20	OK
Mid mass isotope position (target 265.00, actual 265.10)	0.10	<= 0.20	OK
High mass isotope position (target 503.00, actual 503.05)	0.05	<= 0.20	OK
Low mass isotope ratio	1.12%	>= 0.5% and <= 1.6%	OK
Mid mass isotope ratio	5.58%	>= 4.2% and <= 6.9%	OK
High mass isotope ratio	9.23%	>= 7.9% and <= 12.3%	OK
Low mass precursor ratio	0.45%	<= 3.00%	OK
Mid mass precursor ratio	0.00%	<= 6.00%	OK
High mass precursor ratio	0.05%	<= 12.00%	OK

Detector			
EMV	1687	<= 2900	OK
Maximum gain factor	681	>= 100	OK

Air and Water Check	Abundance	Relative Abundance	Limit	Result
PFTBA (69.00)	14988265			
Water	72765	0.49%	<= 20.00%	OK
Oxygen	132571	0.88%	<= 2.50%	OK
Nitrogen	494093	3.30%	<= 10.00%	OK

* Nitrogen values are calculated from oxygen abundance

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APPENDIX 4

PCB Aroclors patterns and analytical peaks

Sample EIC MRM chromatograms mean Extracted ion chromatograms for all ions used in Aroclor quantitation.

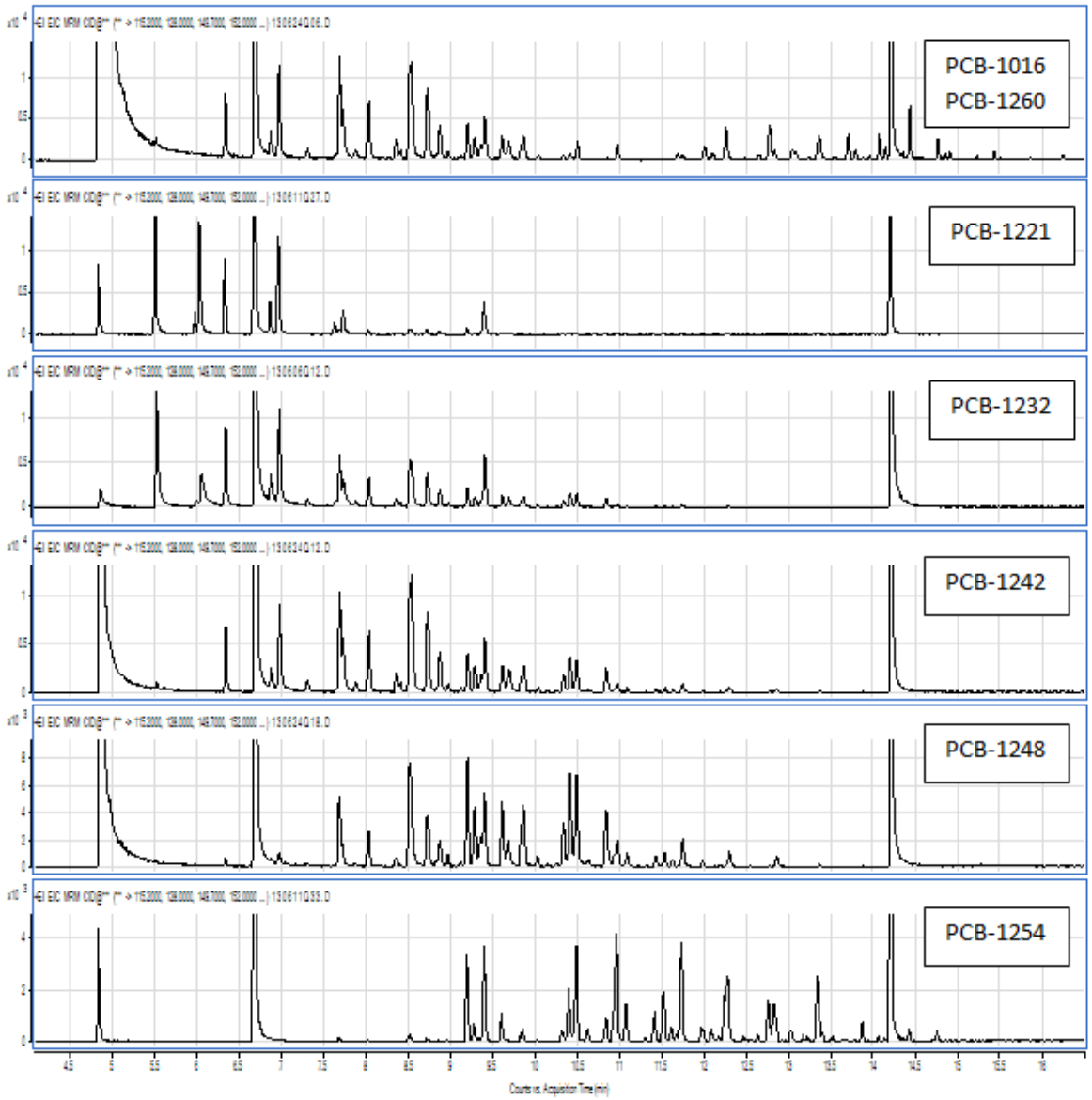


Figure 1 Sample EIC MRM chromatograms for PCB-1016, 1260, 1221 , 1232, 1242, 1248, and 1254 L3: comparison of peak patterns

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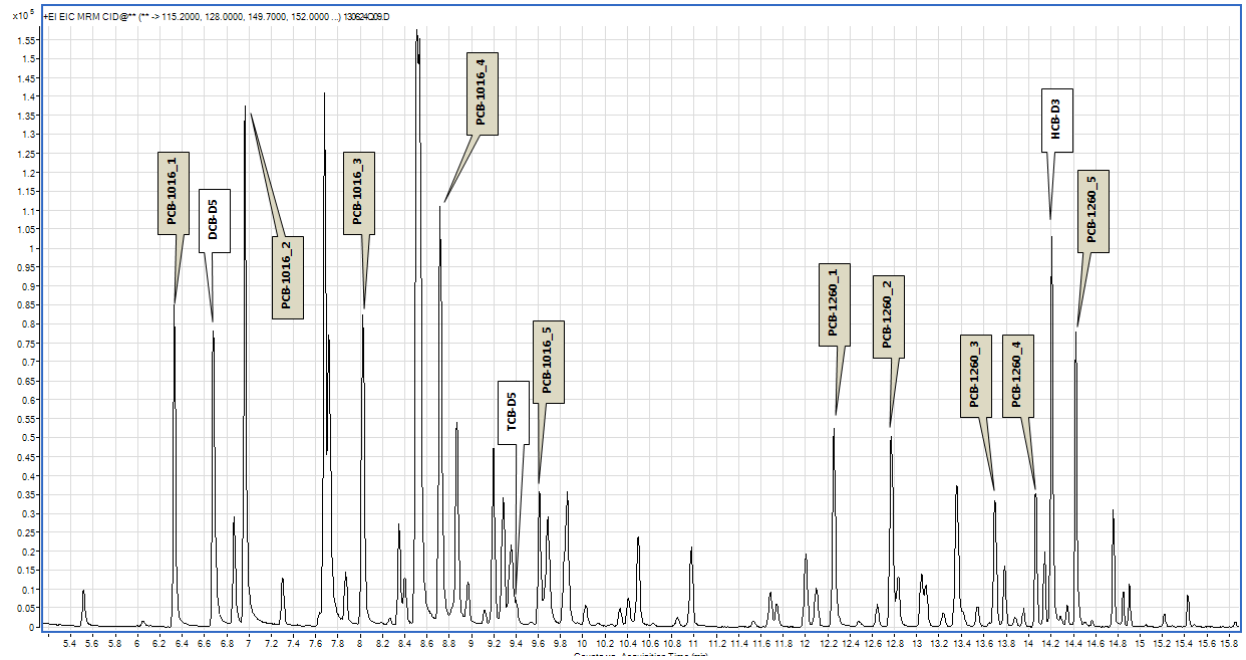


Figure 2 A sample EIC MRM chromatogram for PCB-1016 and PCB 1260 L6: Internal standards and peaks used for quantitation

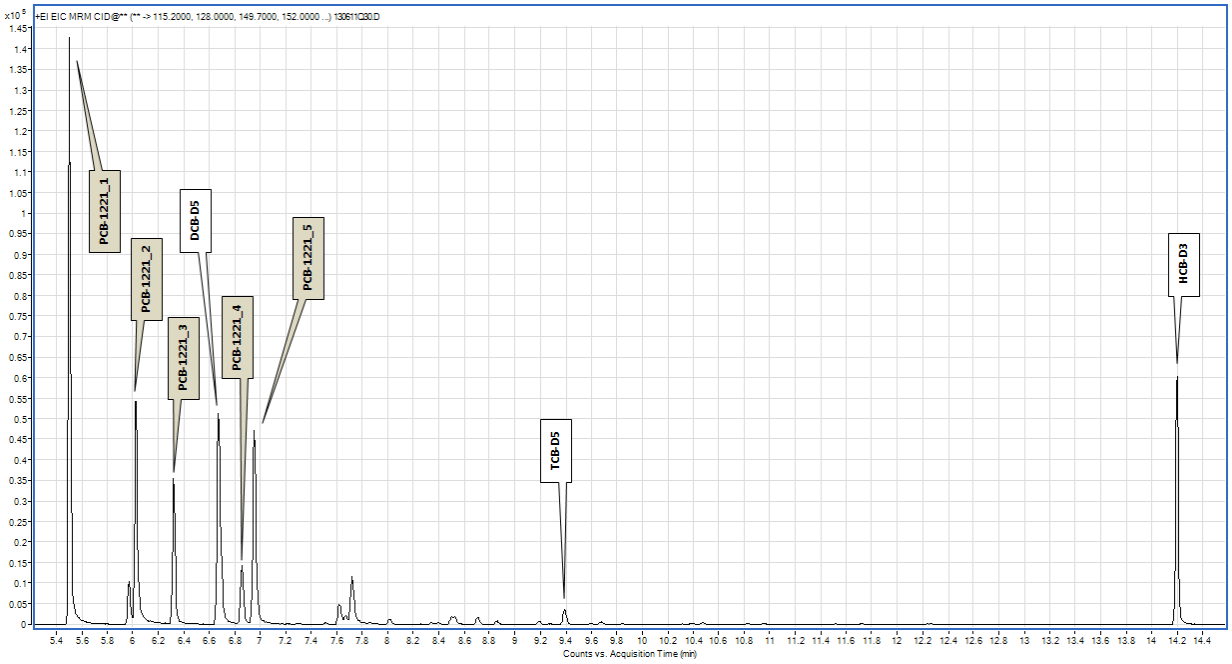


Figure 3 A sample EIC MRM chromatogram for PCB-232 L6: Internal standards and peaks used for quantitation

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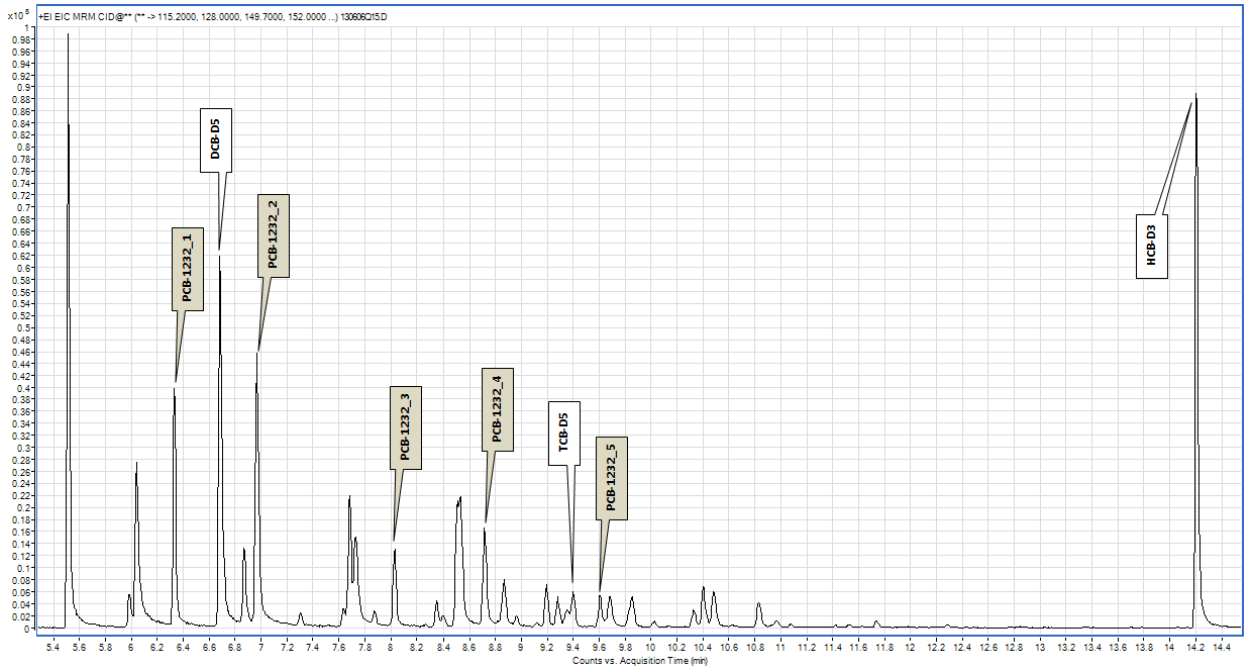


Figure 4 A sample EIC MRM chromatogram for PCB-1232 L6: Internal standards and peaks used for quantitation

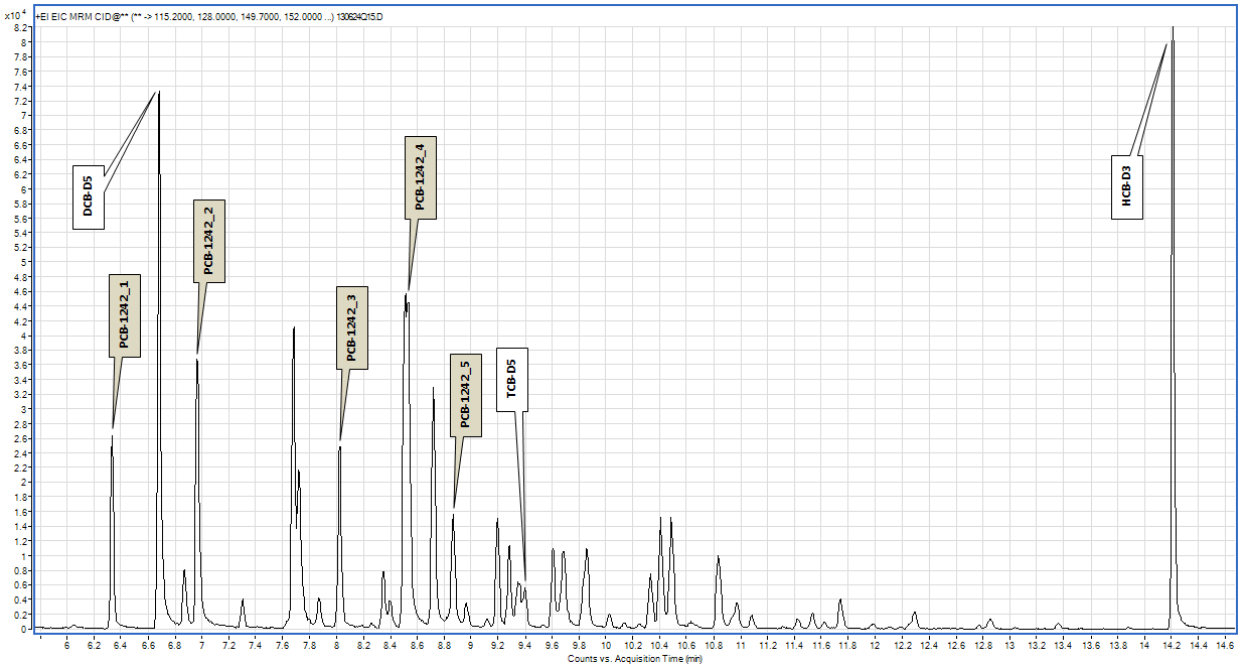


Figure 5 A sample EIC MRM chromatogram for PCB-1242 L6: Internal standards and peaks used for quantitation

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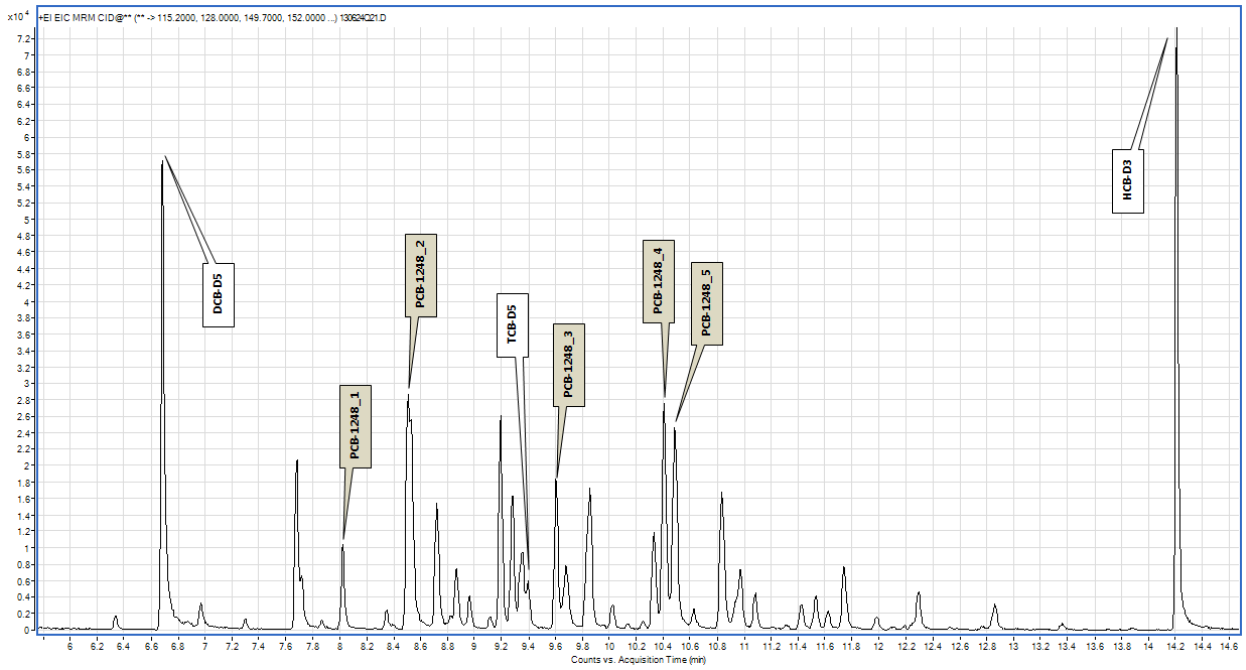


Figure 6 A sample EIC MRM chromatogram for PCB-1248 L6: Internal standards and peaks used for quantitation

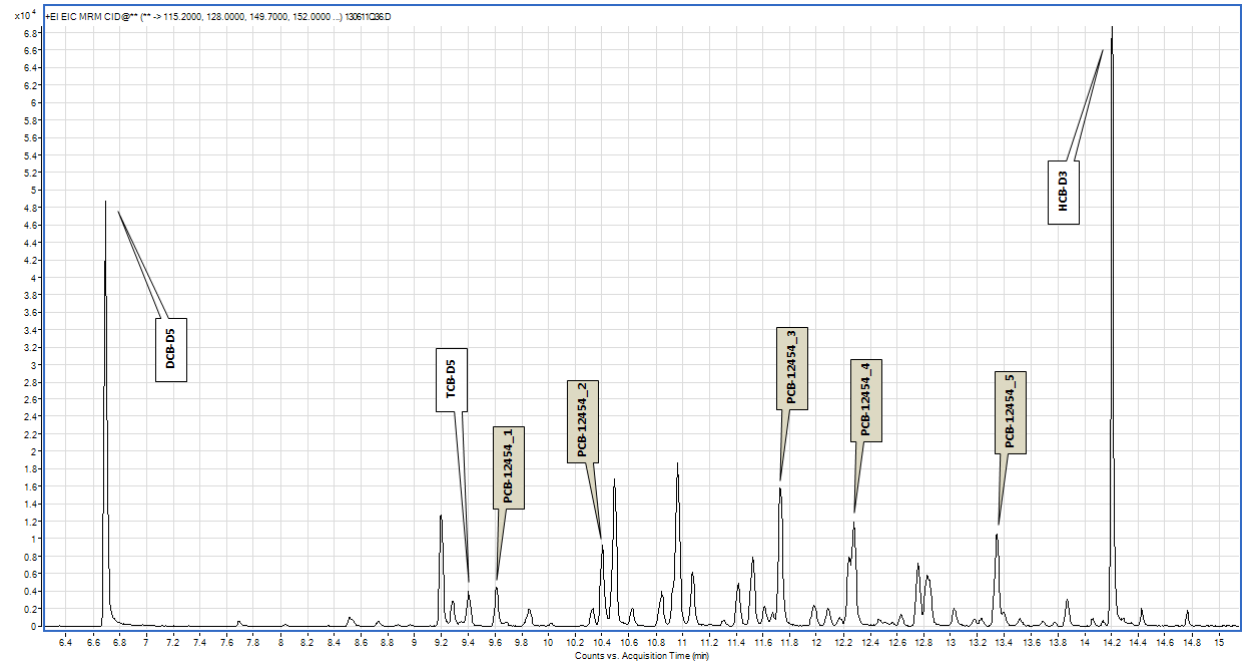


Figure 7 A sample EIC MRM chromatogram for PCB-1254 L6: Internal standards and peaks used for quantitation

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APPENDIX 5

PCB Aroclors pattern analysis in MassHunter Qualitative Analysis software

In order to accomplish PCB aroclors patterns identification, sample chromatograms are compared to the chromatograms of standards of all analyzed aroclors. In most cases this can be achieved by preparing combined extracted ion chromatograms (EIC MRM) for all MRM transitions used in aroclor quantitation. These MRM transitions are listed in the Table 4C-2 and do not include transitions for surrogates and internal standards. Sample chromatograms of this type for all analyzed aroclors can be found in Appendix 4. A Masshunter Qual method *PCB_screening_no_ISTDs.m* containing definition for these chromatograms is available for quick analysis. In complicated cases, EICs for other individual MRM transitions can also be used.

Samples containing PCB-1016 or PCB-1242, especially if weathered or at low concentration, may be challenging to identify due to similarity of corresponding aroclor patterns (Figure 1). For such cases an EIC for a single MRM transition 325.9 – 255.9 (Qual method PCB_screening_no_ISTDs_1060vs1242.m) can be used. This transition allows to focus on small peaks that are present at the later part of the PCB-1242 pattern, but are largely absent in the PCB-1016 (Figure 2).

In some cases, such as when a sample is severly weathered or may have more than one aroclor present, a definitive pattern identification may not be possible. The sample then can be quantified as the closest matching aroclor and the results reported with an appropriate comment and a qualifier (?).

APPENDIX 6

Transferring acquisition methods between TQ-1, TQ-2 and TQ-3

There are two hardware configuration variations between the three instruments that need to be reflected in acquisition methods. First, in TQ-1 and TQ-3 the pressure at the union of the front and back columns is controlled by EPC 4, while in TQ-2 this is done by EPC-6. Second, the back inlet in the TQ-1 is covered and has pressure of 1 psi, while the back inlet in TQ-2 and TQ-3 is uncovered and has pressure 0 psi. addition, Therefore the following steps can help to convert an acquisition method from one instrument to another.

1. Transfer and rename method.

2. Load method in the acquisition software and open GC method window.

3. Configuration –> Columns:

   First column should have the correct EPC (EPC 4 for TQ-1 / TQ-3 and EPC 6 for TQ-2) as the Outlet and the second column should have the same EPC as inlet.

4. Configuration –> Modules:

   Select He gas for the correct EPC (EPC 4 for TQ-1 / TQ-3 and EPC 6 for TQ-2) and set the other EPCs to N_2.

5. Columns: check or uncheck Control Mode as follows:

   a. Column 2 – On

   b. Back inlet – Off

   c. Aux EPC-6 – Off for TQ-1 / TQ-3 or Aux EPC-4 – Off for TQ-2

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d. He Backflash EPC (for TQ-3) should stay Off

6. Inlets: Back Inlet Pressure box should be checked for TQ-1; for TQ-2 / TQ-3 the pressure should be 0 and Pressure box unchecked.

7. If needed, adjust injection volume by going to ALS > Front Injector and typing in the desired volume.*

8. Apply the method and exit GC method window.

9. Open MS method window.

e. The autotune file *atunes.eihs.tune.xml* for all three instruments.

10. Check the GC keypad to get rid of all blinking "Off"s, if needed, and make sure that:

a. For TQ-3 Aux EPC > Collision gas cell > Back Flash Pressure should be Off

b. EPC in use should be On (EPC 4 for TQ-1 /TQ-3 and EPC 6 for TQ-2)

c. EPC not in use should be Off (EPC 6 for TQ-1 / TQ-3 and EPC 4 for TQ-2)

d. Back Inlet Temperature should be Off

e. Back Inlet Pressure is 1 psi for TQ-1 and Off for TQ-2 /TQ-3

11. Save the method.

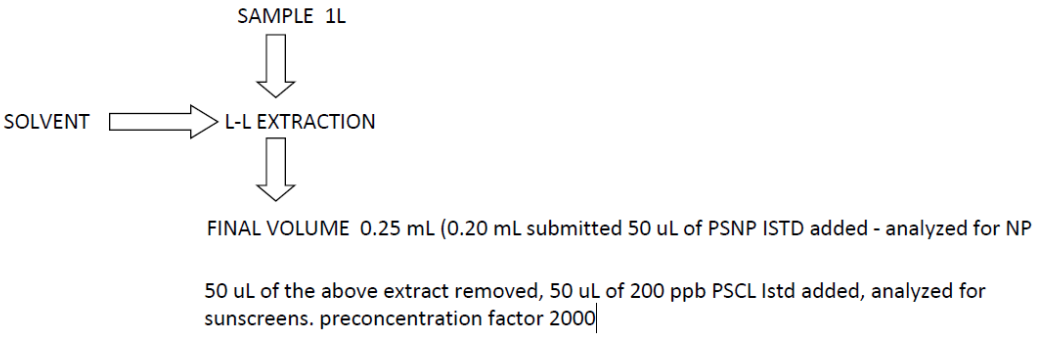
12. Try to run the method. If it does not work, repeat steps 8 and 9 as needed until the method can be used.

APPENDIX 7: Sample Preparation Flowcharts

Water samples GC/MS or GC/MS/MS PREP ID: EPA 3510C

Sunscreens and NP pesticides in water

W-PSNP-TQ, W-TR-SQ-R

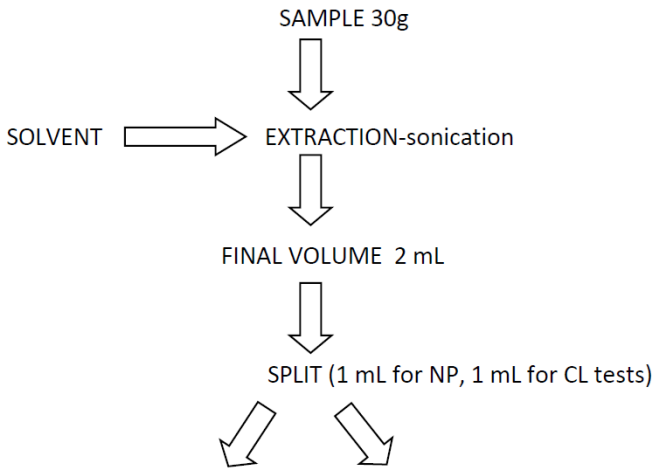


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Soil TQ/NCI PREP ID: **3550C (TQ)**

Chlorinated pesticides, PCBs/NP pesticides in soil

S-PSCL-TQ, S-PCB-TQ/ S-CT-CI/S-PSNP-TQ



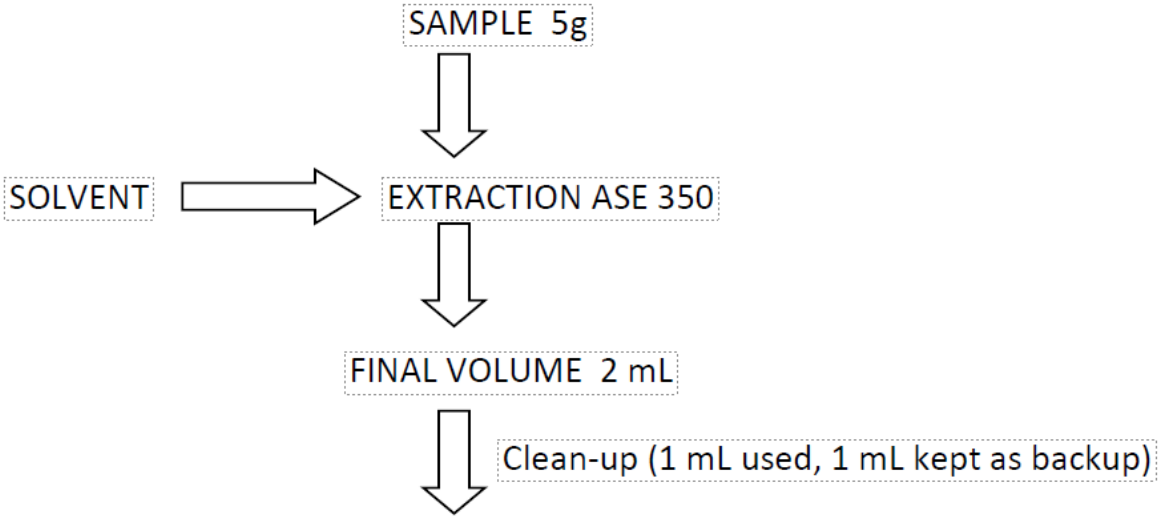
Aliquot 1	Aliquot 2
S-PSNP-TQ	S-PSCL-TQ, S-PCB –TQ, S-CT-CI
1 mL vialed for GPC, 0.8 mL injected on GPC (3% MeOH in CH2Cl2) 0.6 mL submitted. 160 uL NPTQ ISTD added + 40 uL Iso-octane	1 mL vialed for GPC, 0.8 mL injected on GPC, then followed by Florisil cleanup , submitted volume 0.7 mL + 80uL of 1000 ppb PSCL ISTD + 20 uL of iso-octane Alternatively, for PCBs and some chlorinated pesticides, 1 mL cleaned with sulfuric acid/TBA 0.9 mL submitted + 100 uL of 1000 ppb PSCL ISTD

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Tissue TQ/NCI PREP ID: SOP GC-004 (TQ)

Chlorinated pesticides, PCBs in fish tissue

T-PCBCL-TQ/T-CT-CI



1 mL vialed for GPC, 0.8 mL injected on GPC, then

followed by Florisil cleanup

submitted volume 0.7 mL + 80uL of 10000 ppb PSCL ISTD and and 20 ul of iso-octane

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Appendix 8: GC group custom report templates

GC group custom report templates for Agilent MassHunter

Agilent MassHunter Quant and Qual software reporting is accomplished through use of templates. Templates contain information on what data is drawn from a Quant batch or a Qual analysis results and how it is arranged and formatted on a page. Reports are generated in Microsoft Excel. MassHunter software comes with a selection of standard templates that are located under Computer\Data (D:)\MassHunter\Report Templates. MassHunter templates are customizable. They can be viewed and modified in MS Excel. Agilent MassHunter Workstation Software Reporting Familiarization Guide can be found in the MassHunter software distribution package. GC Group custom report templates are stored at \\FLDEP1\DEAR\LABS\LAB5\Chemistry\Organic\GCGROUP\MS-QQQ_backup_files\Templates and also in each instrument computer that uses them (typically in a custom folder within Computer\Data (D:)\MassHunter\Report Templates). Some of the GC group reports also require additional post-processing. Post-processing is automated by means of custom VBA macros added to Excel. Macros are stored in \\FLDEP1\DEAR\LABS\LAB5\Chemistry\Organic\GCGROUP\MS-QQQ_backup_files\GC_group_custom_macros.xlam.

Introduction to Reference Tables and VLOOKUP function

Reference tables. In order to calculate ICV, CCV, and Spike recoveries and to assign the pass/fail status to the results, MassHunter report templates require some information that is currently not available in Quant methods and cannot be automatically drawn from a Quant batch into a report. For example, expected ICV/CCV concentrations and QC control limits are currently not included with the MassHunter Quant methods and have to be made available to the report templates by alternative means. This is accomplished by adding a reference table to the corresponding report template (Figures 1 & 2). For ICV and CCV templates, the reference table should contain names of all analytes used in analysis and their expected concentrations. In addition, the Spike report template reference table also lists control limits. Many templates also use a reference table for instrument serial numbers associated with instrument names. It is recommended to place a reference table in a separate sheet within a template.

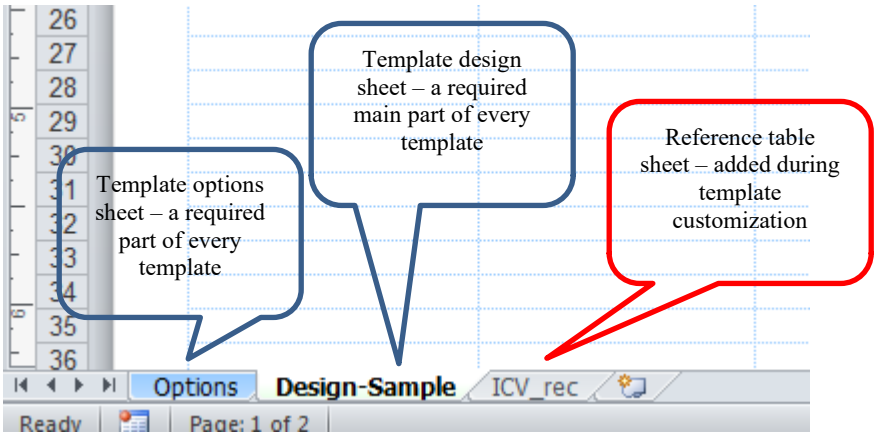
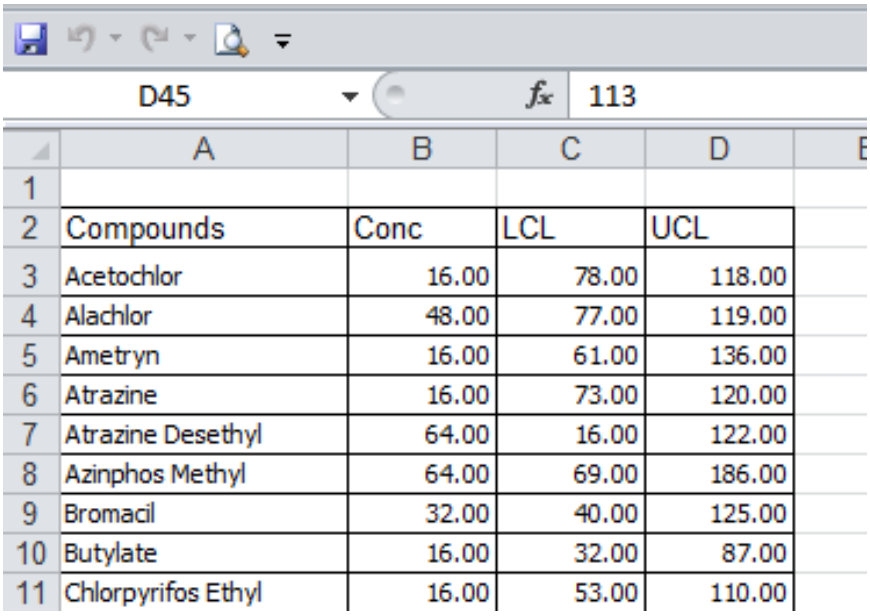


Figure 8. An example of sheets in a massHunter report template using a reference table and VLOOKUP function.

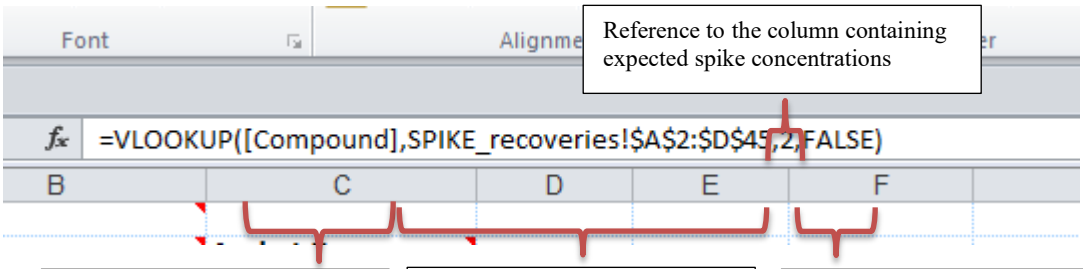
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D45 | fx | 113

	A	B	C	D
1				
2	Compounds	Conc	LCL	UCL
3	Acetochlor	16.00	78.00	118.00
4	Alachlor	48.00	77.00	119.00
5	Ametryn	16.00	61.00	136.00
6	Atrazine	16.00	73.00	120.00
7	Atrazine Desethyl	64.00	16.00	122.00
8	Azinphos Methyl	64.00	69.00	186.00
9	Bromacil	32.00	40.00	125.00
10	Butylate	16.00	32.00	87.00
11	Chlorpyrifos Ethyl	16.00	53.00	110.00

VLOOKUP function. Report templates use VLOOKUP Excel function to locate information in the reference tables. VLOOKUP function is an Excel function that finds specified information in the leftmost column of a table and returns a value found in the selected column of the same row of the table. For example, it can find analyte name "Butylate" in the table above and return its expected concentration. Formal representation of the VLOOKUP function is =VLOOKUP(lookup_value, table_array, col_index_num, range_lookup). For example, VLOOKUP function used for finding expected spike concentration in the Spike template reads as follows (Figure 3):



Figu

More information on use of VLOOKUP in MassHunter templates can be found in the Agilent MassHunter Workstation Software Reporting Guide.

How to change expected concentrations or control limits for existing analytes in ICV, CCV, or Spike report templates

1. To edit a template, right click on the file name and select Open. Note: if you attempt to open the file by double-clicking, a copy of the original report will open as a spread sheet instead of a template (*.xlsx instead of *.xltx).
2. In the opened template, click on the sheet that contain the reference table. Simply type in desired corrections into the table cells. **Important**: do not change analyte names (they should match exactly the names in the Quant method) and do not change number or location of rows and columns in the table (VLOOKUP looks for a specific cell range and specific columns in it).

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3. When done, save the template and test it. If something did not work, a copy of the original template can be found in the backup folder at \\FLDEP1\DEAR\LABS\LAB5\Chemistry\Organic\GCGROUP\MS-QQQ_backup_files\Templates
4. Once the modifications are tested and found satisfactory, replace the old template with the new one on each computer that uses it and in the backup folder.

How to add new analytes to ICV, CCV, or Spike reports

1. To edit a template, right click on the template file name and select Open. Note: if you attempt to open the file by double-clicking, a copy of the original report will open as a spread sheet instead of a template (*.xlsx instead of *.xltx).
2. In the opened template, click on the sheet that contains the reference table.
3. Click on the bottom right corner of the table and note the address of the cell (see Figure 4 for an example).
4. Select a row **within** the table by right-clicking on the corresponding row number on the left border of the spread sheet. Select Insert in the menu that appears. An empty row should appear above the row originally selected.
5. Type in information for the new analyte. Take care to use correct spelling for the analyte name and type in concentration and control limits into correct columns. **Important**: do not modify number or location of the columns in the table.
6. Insert and fill out more analyte rows if necessary.

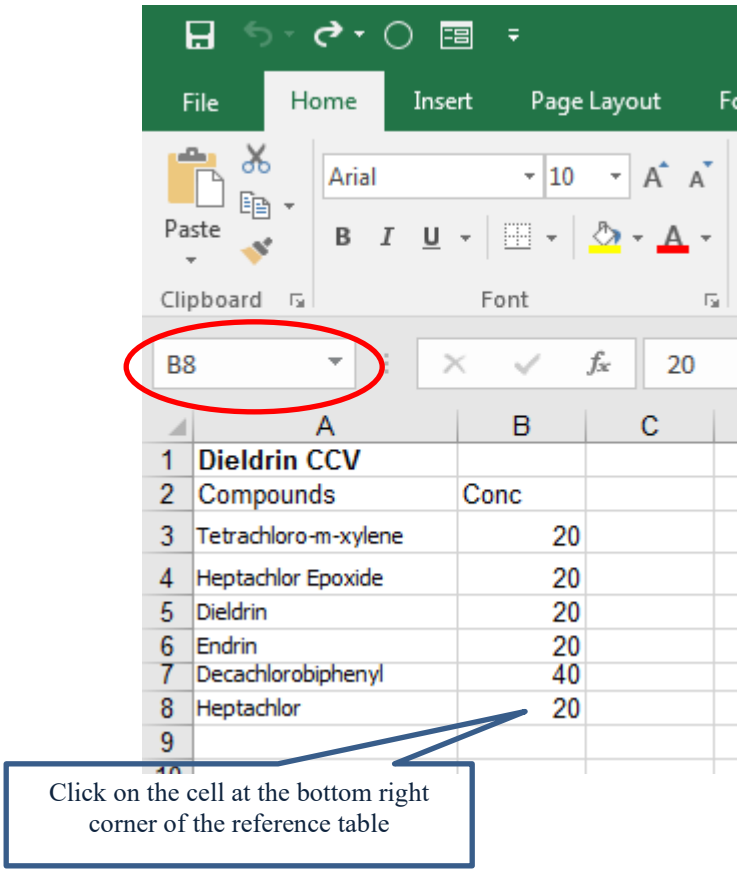


Figure 11. Checking the range of the reference table: the range of cells occupied by the data in the table can be defined as the addresses of its top left and bottom right corner. In this case they are A3 (cell with the "Tetrachloro-m-xylene") and B8.

7. As before, click on the bottom right corner of the table and note the address of the cell. It should have the same column as before, but a higher row number according to how many rows were inserted. E.g. after inserting two rows B8 will become B10.
8. Save changes.
9. Click on the Design-Sample sheet tab. Locate table named Results. Among the table headers, find Exp Conc header in the Results table and click on the cell directly below. This cell should contain the VLOOKUP formula for finding expected concentration (Figure 5). Check that the range of cells VLOOKUP uses matches the new range occupied by the reference table. For example, the function may read "=VLOOKUP([Compound, CCV_rec!$A$3:$B$8,2,FALSE)." Here the cells range reference is "CCV_rec!$A$3:$B$8", where $A$3 is the address of the top left corner of the table, and $B$8 is the address of the bottom right corner. (The dollar signs are added here to indicate that the location of the table is constant.) If the new analyte rows were inserted correctly, the VLOOKUP formula should have automatically changed to reflect the expanded range of the table. For example, after inserting two new rows in the table, the reference range

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"CCV_rec!$A$3:$B$8" should change to "CCV_rec!$A$3:$B$10". Please note, that only the bottom right corner address should change.

10. If the analyte rows were added instead of inserted, the VLOOKUP formula would not change automatically and has to be corrected manually. To do so, click into the formula in the correct location and type in the correction. Be extremely careful not to change anything else in the formula: the extent of the correction should be replacement of one number with another (e.g. replace "8" with "10"). Do not remove dollar signs or add spaces. After the correction is complete, hit Enter to exit the formula editor and save the file.

11. Spike report templates use reference table not only for expected concentration data, but also for high and low recovery limits. For these templates, step 9 should be executed three times: for Exp Conc column, for "Limit low" and "Limit high" columns.

12. Test the template by generating a new report. If something did not work, check that the reference table is correct (especially analyte name spellings) or edit the VLOOKUP formula in its entirety (instructions on use of VLOOKUP function can be found in the MassHunter Workstation Software Reporting Guide). Note: it is possible to test the template from within the Excel, without using the MassHunter Quant. This is explained in the Reporting Guide.

13. Once the modifications are tested and found satisfactory, replace the old template with the new one on each computer that uses it and in the \\FLDEP1\DEAR\LABS\LAB5\Chemistry\Organic\GCGROUP\MS-QQQ_backup_files\Templates.

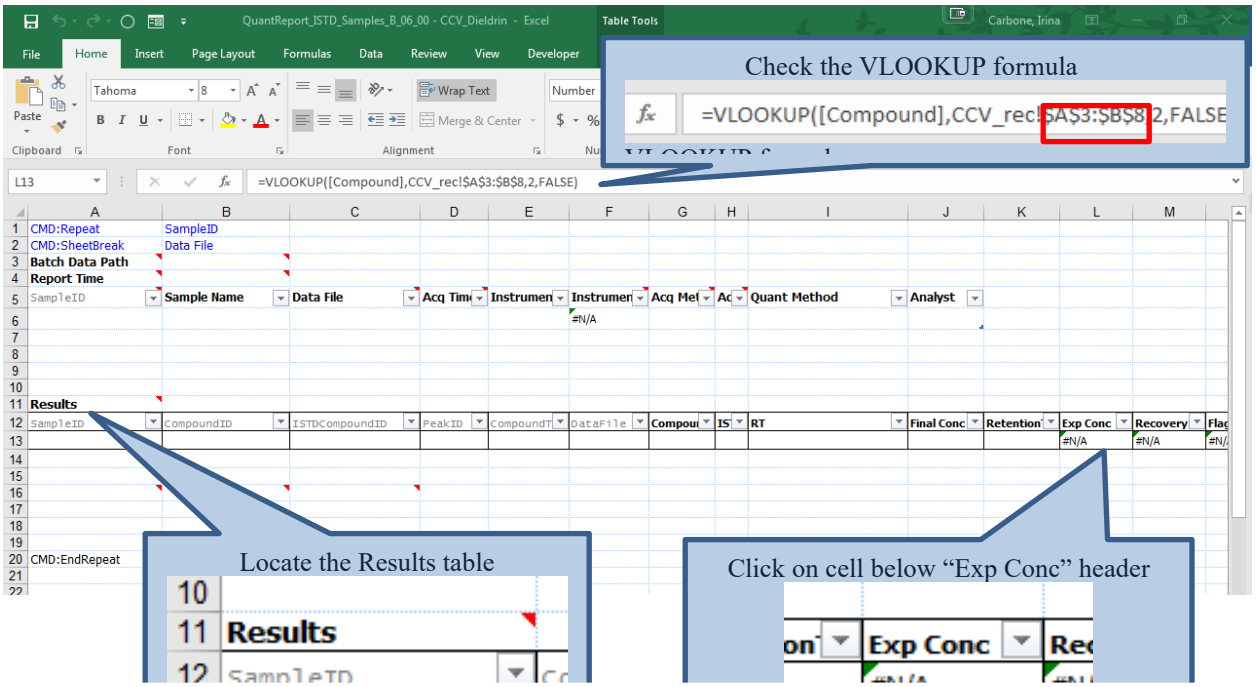


Figure 5. Viewing VLOOKUP formula for expected concentration in the Design-Sample sheet of a template

Displaying instruments serial numbers in the reports

Just like CCV/ICV/Spike expected concentrations or control limits, Instruments serial numbers are not stored in the Quant methods and have to be added to the templates by alternative means. A number of templates have an additional reference table with instrument names and their corresponding serial numbers. Instrument name is stored in the MassHunter configuration module and is available to MassHunter Quant. (To view the instrument name within Quant software, simply add an instrument name column to the results table). A template can read the instrument name from the Quant software and then use VLOOKUP function

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to get the corresponding serial number for its reference table. Serial number reference tables can be modified in the same way as the reference tables for CCV/ICV and spikes.

MassHunter reports postprocessing with macros

Several of the currently used reports require additional editing after they are generated from MassHunter templates. These are Calibration levels report, LFB and MS reports, and Decomposition Check report. Additionally, there is a printout macro for printing multi-sheet reports. All macros are written in the file named GC_group_custom_macros.xlam. A copy of this file is stored at \\FLDEP1\DEAR\LABS\LAB5\Chemistry\Organic\GCGROUP\MS-QQQ_backup_files. Each instrument computer also has a copy. The location of the copy on instrument computers is dependent on the Window version installed. For Window 7 this location is Computer\PROGRAMS (C:)\Users\lab_gcuser\AppData\Roaming\Microsoft\AddIns\. When an *.xlam file is in this directory, Excel can read and use macros stored in it. Note: excel should be configured for macros use (Trust Center Settings > Macro Settings > enable all macros; GC_group macros are not digitally signed). To add/remove a macro in the excel ribbon, open a blank Excel file, right-click on the ribbon, select Customize the Ribbon, and choose among Macros available to add it to the desired Tab/Group.

Instructions for installing macros on a new computer;

1. **Check that developer tab and macros are enabled.**
   a. Open a blank Excel file and click File then options then customize ribbon
   b. On the right check the Developer box
   c. Click trust center then trust center settings then macro settings
   d. Select enable VBA macros then click OK
   e. Close Excel file

2. **Check that macro file GC_group_custom_macros.xlam is in the AddIns folder.**
   a. Open the remote folder gcgroup then MS-QQQ_backup_files folder
   b. The GC_group_custom_macros.xlam file is in the MS-QQQ_backup_files folder
   c. Place the .xlam file in the C:\Users\lab_user\AppData\Roaming\Microsoft\AddIns\
   d. Check the hidden file box under View tab, if the file is not visible

3. **Check that file GC_group_custom_macros is active.**
   a. Open a blank Excel file and click the developer tab and then select excel add-ins in the ribbon
   b. Check the file box and click OK

4. **Check that GC Group tab is active and has macros.**
   a. Right click the ribbon and select customize the ribbon
   b. In the right column select New Tab and rename it as GC Group
   c. Rename the New Group as GC Group and select blue right-hand arrow as an icon
   d. Add the following macros from the left side: Calibration_levels_used, Universal_SheetsPrintOut and Suitability_report_scan
   e. Click OK and close Excel file

5. **Check that new link is added in the ribbon and has correct destination.**
   a. Open the remote folder gcgroup and find MS-QQQ_backup_files
   b. Open LIMS Upload file and select Visual Basic under the Developer tab in the ribbon
   c. Right click on Modules and select Insert then Module
   d. Copy and paste the script from an existing module to a new one
   e. Rename the Module as TQ-4 under Name in the Properties tab
   f. Check strFilePath = "Y:\UPLOAD_GC_TQ-4\" for instrument TQ-4
   g. Check that strFileName and MsgBox end with Q4
   h. Save and close the LIMS Upload file

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6. **Check that link is active.**
   a. Open a blank Excel file and select the GC Group tab in the ribbon. If the macros won't show up in "b" below then do this directly from the "LIMS upload" file on GCgroup location.
   b. Select Macros in the left column then add TQ_4.NotePad to GC Group in the right column and click OK
   c. Click the link in the ribbon for instrument TQ-4
   d. A pop-up with date will appear, then click OK
   e. Check Y:\UPLOAD_GC_TQ-4\ for the latest file
   f. Do not save the Excel file then close it.

9) ADDING NEW ANALYTES TO MASSHUNTER QUANT

1) **MRM compound setup**

   a) right click on the first compound line – add new compound.

   b) TS not too important since we are using dynamic MRM

   c) scan—MRM

   d) type: ISTD, surrogate or target

   e) enter precursor and product ions for what you think will the quantifier. This can be rectified later if wrong transition is selected here.

   f) enter RT, order by retention time from lowest to highest!

   g) ion polarity should be positive (except for NCI?)

2) **Retention time setup** – enter (typically) 0.30 min for both left and right RT delta. RT delta units must be minutes!

3) **Istd setup**. Select type. If type ISTD, leave none in ISTD compound name column, check the box under ISTD flag and put 100 under istd conc (unless different than 100 in special cases)

   If type surrogate or target select associate ISTD in the ISTD compound name column, and type 100 under ISTD conc.

4) **Concentration setup**

   a) Change unit to ug\L

   b) For calibration levels, copy calibration levels from another compound with the same concentrations. You can skip this Step for istds.

5) **Qualifier setup**.

   a) Under uncertainty it should be "absolute" if qualifier is smaller (less than 100%) than quantifier. Change to "relative" if qualifier is higher than 100%.

   b) right click-add qualifier

   c) choose precursor and product ion

   d) enter a number (any number) under Rel Resp

   e) change uncertainty to 30

6) C**alibration curve setup** does not need to be edited. Whatever is selected there will work at first and can be modified later. However, weighing can never be set to none!

7) G**o to outlier setup tasks**

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a) **under retention time** enter RT window 0.060 (typically), and RT units – minutes.

b) enter MDL under "**Limit of Detection**'.

c) under **ISTD response percent deviation** enter -50.0 and 100

d) under "**accuracy**" enter 30.0

e) under "**surrogate percent recovery**" enter (if surrogate) min limit, max limit and surrogate conc

SPECIAL PEAKS

8) "**Sum all** peaks" (applicable to many pyrethroids)

A) Go to advanced tasks – integration parameters setup and select Universal integrator.

B) Enter area sum on and area sum off times (this is the integration window!. Click apply, but never apply to all!

9) Summary peaks

Go to MRM compound set up and add columns (after selecting quantifier) *cmpd group* and *Compound math*.

Enter the actual peaks (like Naled -1 and Naled-2) and follow the entire procedure above. Create the summary peak (example Naled) with RT somewhere between the component peaks, for convenience.

Call the component peaks and the summary peak with the same name (capital letter that is not already used for something else; like A, B or C). Under compound math enter response sum for the summary peak only. Remember to enter the MDL for the summary peak as well

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Appendix of Significant Changes

07/18/2013 Major expansion of the SOP due to the addition of the chlorinated pesticides and PCBs in soil tests. Changes throughout the entire SOP, including tables and standard preparation procedures.

11/25/2013 Tune procedure section was modified to explain modification to EPA 8270D DFTPP tune'
CCV criterion was changed to +- 20% to follow exactly the EPA method requirement.
Statistical formula to calculate surrogate recoveries was corrected.
Chapter 9.6.10 was added describing quantitation of positives in detail
Addition of waste tests (tables 1B and 1 C)
Addition of Fipronil metabolites Sulfide and Sulfone to test W-PSNP-TQ
Addition of analysis of chlorinated pesticides and PCB congeners in Tissue T-PCBCL-TQ

01/22/2014 Updated acceptance criteria in Table 6.
Updated MDLs for Mirex
Updated standards concentrations
Changed the degradation/tailing factor check to the MRM mode.

03/03/2014 Addition of analysis of Dieldrin in water (test ID: W-PSCL-TQ)

04/28/2014 Description of DDT decomposition /pentachlorophenol tailing factor check updated.
The injection technique changed to three-layer sandwich.

04/28/2015 Instruments upgraded to 7000C; Updated QC limits and methods tables
Updated concentrations tables and tune check report (appendix 5)

08/06/2015 Added appendix 7; "Transferring acquisition methods between TQ-1 and TQ -2"Updated QC recovery limits
5-Nitroquinoline surrogate for test W-PSNP-TQ replaced with Simazine-d10 and Malathion-d7.
New analytes added to test W-PSNP-TQ and the entire list revalidated (new GC method).

10/05/2015 Two new analytes added to test W-PSNP-TQ (Parathion Ethyl and Parathion Methyl) and a new internal standard
New MDLs for Pendimethalin and Norflurazon
Standard preparation chapter was re-written. Standard preparations were referenced to the standard preparations tracker.

02/02/2016 Updated QC recovery limits based on the recent statistics.
Changed calibration drift acceptance criterium to 70-130% based on EPA 8270D.
Updated concentrations in calibration levels for test W-PSNP-TQ (Table 5A).

04/11/2016 Requirement listed in 9.3.3.1 removed (FDEP response to CERP audit item 4d)
Diatomaceous earth blank added (tissues only) in 9.4.2. (FDEP response to CERP audit item 4e).
Including origin in calibration curves prohibited. Ignoring origin recommended as first choice. Paragraph 9.2.1 (FDEP response to CERP audit item 4l).
Section 9.6.7 Clarification of recovery limits calculations for LFBs and Matrix spikes (FDEP response to CERP audit, section 6b)
Addition of W-DIELDRIN test throughout the SOP.

9/15/2016 Chapter 8.1 rewritten for clarity as per CERP audit recommendation.
QC recovery limits table updated (Table 6.) Preparation flowcharts added as appendix 6.

01/17/2017 Updated QC control limits,
Appendix 5 added (PCB aroclors analysis)

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	Appendix 5 updated to include GC-TQ-3 (Agilent 7010 GC/MS/MS) and renamed as Appendix 6; Appendix 6 renamed as appendix 7 Updated standard concentration tables Added PCB-169 analysis to tissue tests.
05/19/2017	Updated concentrations for analyte protectants Updated QC control limits Added analysis of NP pesticides in soil (S-PSNP-TQ, WS-PSNP-TQ); updates to tables 1a and 4A.
01/29/2018	Removed W-PSCL-TQ test. Added chapter about the use of PCB-1268 to determine the presence of Decachlorobiphenyl surrogate in the sample. Updated MDLs and QC limits. Appendix 8: custom report templates added. Appendix 6 updated. Added Terbufos-d10 surrogate for W-PSNP-TQ. Added new internal standards to chlorinated pesticides analysis.
09/25/2018	Brief discussion of analyzing mixes of PCB-aroclors is added. Terbufos -d10 replaces Malathion-d7 as a surrogate for S-PSNP-TQ. Added 6-new analytes to table "1A-Water", Table 4A and Table 6. Updated table 4B. Removal of calibration points discussed (chapter 9.2.1).
12/14/2018	Added Aldrin to W-Dieldrin test. Removed some unnecessary transitions from S-PSCL-TQ test. Added internal standard EPTC-d14 for NP tests (water and soil).
02/19/2019	Updated QC recovery limits, MDLs and standards concentrations. Updated acquisition methods to dMRM. Updated initial calibration requirements. Added five new analytes (Ethalfluralin, Hexachlorobenzene, trans-Nonachlor, Cis-Nonachlor, Bifenthrin) to S-PSCL-TQ and WS-PSCL-TQ.
04/26/2019	Updated to EPA 8270E. Some QC limits updated.
01/14/2020	Addition of new analytes to W-PSNP-TQ test. Changes to QC control limits table. Updated some other MDLs due to annual recalculations. Updated MDL determination chapter.
02/25/2020	Addition of Naled to W-PSNP-TQ test. Updates and correction to tables 4A-1, 5A and 6.
03/19/2020	Addition of 12 new analytes to S-PSNP-TQ and revalidation of Bromacil for the same test. Updates to table 1A-soil/waste. Updates to table 6. Added appendix 9 "Adding new analytes to Masshunter quant".
06/29/2020	Added chapter 9.1.2.9 describing RT adjustment procedure for dMRM acquisition method. Updated data archival for the use of automated backups. Elaborated in more detail the analysis of surrogates, matrix spikes and LFBs. .Added six new analytes to S-PSCL-TQ test and all corresponding tables and methods in the tables section.
09/16/2020	Addition of Kepone to the W-DIELDRIN test. Updated standard concentration to reflect recent changes.
10/19/2020	Addition of 12 new analytes to test W-PSNP-TQ.
01/11/2021	Addition of caffeine by isotope dilution to W-PSNP-TQ test. Updated preparation flowcharts. Updated and consolidated tables. Coefficient of correlation R^2 minimum requirement >0.99. Updated control limits for 2021. Updated MDLs due to annual recalculations.
03/15/2021	Minor editorial changes as per CERP audit of 02/26/2021. Added performance check and method blank to table 6. Added graphical depiction of tailing factor determination in chapter 9.3.1. Ref 15.1 corrected. Section 13.1 typographical error corrected. Section 13.5 – PQL acceptance criteria added.
9/24/2021	Addition of oxychlordane to T-PCBCL-TQ test. Updates to S-PSCL-TQ, S-PCB-TQ and T-PCBCL-TQ standards. Removal of W-DIELDRIN test. "Modifications to 8270E" paragraph added.
11/15/2021	Addition of 16 new NP analytes to W-PSNP-TQ test. Updates to tables 1A, 4A and 5A. Updates to preparation flow charts. Field blanks re-extraction rules added.

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01/14/2022 Updated recovery limits. Updated MDLs due to annual recalculations. Added instructions for installing maqcros on a new computer.

05/10/2022 Updated calibration standards for S-PSCL-TQ. Updated recovery limits table 6. Updated chapter 9.6.6.2. Added chapter 2.2 describing Agilent Masshunter Optimizer software. Additional references added. Updated calibration levels for NP pesticides. Surrogate associations clarified.

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