FORENSIC TOXICOLOGY LABORATORY
OFFICE OF CHIEF MEDICAL EXAMINER
CITY OF NEW YORK

IBUPROFEN, NAPROXEN AND WARFARIN by HIGH PERFORMANCE LIQUID CHROMATOGRAPHY

PRINCIPLE

Ibuprofen and naproxen are nonsteroidal anti-inflammatory drugs (NSAID), commonly prescribed as analgesics. Warfarin is an anticoagulant prescribed for patients suffering from coronary artery diseases. Since the prescribed dose is dependent upon the clotting time of the patient, there are occasions in which this would be contraindicated. A patient's medical history is therefore an important factor when scheduling such cases.

This procedure is used for quantitative analysis of ibuprofen (Motrin®), naproxen (Naprosyn®) and warfarin (Coumadin®). The three drugs are identified based on their retention time following separation by high performance liquid chromatography (HPLC) and by the ultra-violet (UV) spectra of the eluting peaks using a diode array detector.

Ibuprofen, naproxen and warfarin are lipophilic in an organic medium and are easily extracted into ethyl acetate. The organic solvent is dried, reconstituted in a mobile phase and injected on an HPLC.

SAFETY

The handling of all reagents, samples and equipment is performed within the guidelines which are detailed in the safety manual.

REAGENTS AND MATERIALS

All reagents are HPLC grade or better.

1. **Deionized water**
2. **Ethyl Acetate**. Fisher Scientific Optima or equivalent. HPLC grade or better.
3. **Sodium Hydroxide Solution, 50% w/w**. Fisher Scientific Optima or equivalent.
4. **Acetonitrile**. Fisher Scientific Optima or equivalent. HPLC grade or better.
5. **Methanol**. Fisher Scientific or equivalent. HPLC grade or better.
6. **85% Phosphoric acid**. Fisher Scientific or equivalent.
7. **Heptane**. Fisher Scientific or equivalent. HPLC grade or better.
8. **Anhydrous Sodium Sulfate**. Fisher Scientific or equivalent.
9. **Flurbiprofen**. (Internal standard). FW 244.3 $C_{15}H_{13}FO_2$. Sigma Chemical Company or equivalent.

10. **Ibuprofen**. FW 206.3 $C_{13}H_{18}O_2$. Sigma Chemical Company or equivalent.
11. **Naproxen**. (free base) FW 217.2 $C_{14}H_{14}O_3$. Sigma Chemical Company or equivalent.
12. **Warfarin**. FW 308.3 $C_{19}H_{16}O_4$. Abbot Laboratory or equivalent.
13. **Certified Negative Blood**. Previously found to have no interfering peaks. Freeze validated negative blood. Discard after 6 months.
14. **Certified Negative Liver**. Previously found to have no interfering peaks. Freeze validated negative liver. Discard after 6 months.
15. **Certified Negative Brain**. Previously found to have no interfering peaks. Freeze validated negative brain. Discard after 6 months.
16. **Electronic pH meter**.
17. **Laboratory glassware as required**.

***Note**: It is recommended that the primary reference standards used for the preparation of controls and calibrators be obtained from different manufacturers, or that they be prepared from different lot number from the same manufacturer.*

PREPARATION OF CONTROLS

Ibuprofen, naproxen and warfarin 1000 mg/L

1. Accurately weigh 50.0 mg each of ibuprofen, naproxen and warfarin into a clean labeled volumetric flask. Label volumetric flask as follows: 1000 mg/L ibuprofen, naproxen and warfarin control solution. Indicate date prepared, analyst, batch number and expiration date.
2. Add 40 mL of methanol into the 50 mL volumetric flask.
3. Mix solution by mechanical stirrer until dissolved.
4. Remove stirrer and rinse with methanol from squirt bottle. Q.S. to 50 mL mark with methanol.
5. The 1000 mg/L control solution may then be transferred into appropriately labeled headspace vials and sealed with a Teflon septum and aluminum seal. Store at 2-8^{o}C. The headspace vials will now contain the working control solution. On the vials indicate date prepared, expiration date, initials of person who prepared the solution, lot number, solvent, storage condition and bottle number with total number of bottles.
6. A qualitative control containing acetaminophen, salicylic acid, theophylline, and caffeine is extracted with each batch, to provide retention time and UV spectra to identify these compounds if present in case samples. If any of these drugs are qualitatively identified, they will be scheduled for quantitation by the appropriate method.

Note: See Acmp by SPE SOP for detailed information on materials and preparation of Control Reference Solution and spiking of the low control in blank matrix.

PREPARATION OF CALIBRATORS

Ibuprofen, naproxen and warfarin calibrator 1000 mg/L.

1. Accurately weigh 50.0 mg each of ibuprofen, naproxen and warfarin into a clean labeled 50 mL volumetric flask. Label volumetric flask as follows: 1000 mg/L Ibuprofen, naproxen and warfarin control solution. Indicate date prepared, analyst, batch number and expiration date
2. Add 40 mL of methanol into the 50 mL volumetric flask.
3. Mix solution by mechanical stirrer until dissolved.
4. Remove stirrer and rinse with methanol from squirt bottle. Q.S. to 50 mL mark with methanol.
5. The 1000 mg/L calibrator solution may then be transferred into appropriately labeled headspace vials and sealed with a Teflon septum and aluminum seal. Store at 2-8 ^{o}C. The headspace vials will now contain the working calibrator solution. On the vials indicate date prepared, expiration date, initials of person who prepared the solution, lot number, solvent, storage condition and bottle number with total number of bottles.

INTERNAL STANDARD

1. Accurately weigh 50.0 mg of flurbiprofen and transfer to a 50 mL labeled volumetric flask.
2. Add 40 mL of methanol.
3. Stir with magnetic stirrer until dissolved.
4. Remove stirrer and rinse with methanol from squirt bottle. Q.S. to 50 mL mark with methanol.
5. Transfer samples to headspace vials labeled with the lot number, initials of person who prepared the solution, date prepared, expiration date, solvent, storage conditions and bottle number with total number of bottles.
6. Stable for one year. Store at 2-8 ^{0}C.

EXTRACTION SOLVENT

The extraction solvent used is ethyl acetate

PREPARATION OF 10N SODIUM HYDROXIDE

7. Add 400 mL of 50% sodium hydroxide to a 500 mL volumetric flask.
8. Q.S to 500 mL with distilled water and mix well.
9. Transfer the solution to a storage bottle labeled with who prepared the solution, date prepared and expiration date.

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MOBILE PHASE C

1. Add 2400 mL of deionized water to a 4 L graduated volumetric flask.
2. Add 13 mL of 85% phosphoric acid to the 4 L volumetric flask while mixing with a mechanical stirrer for 5 minutes.
3. Add enough 10N sodium hydroxide (approximately 17-18 mL) to increase pH to 3. Check pH with electronic pH meter.
4. Add 1500 mL of acetonitrile to the 4 L volumetric flask.
5. Stir mobile phase for 30 minutes.
6. Store the mobile phase in a 4 gallon brown bottle at room temperature. Label the storage reservoir with the lot number, initials of person who prepared the solution and date prepared. Discard after 3 months. Filter before use.

SPECIMEN PREPARATION

Blood	2.0 mL of the undiluted specimen
Urine	2.0 mL of the undiluted specimen
Brain	2.0 mL of a 1:3 homogenate
Gastric Contents	2.0 mL of a 1:10 dilution
Liver	2.0 mL of a 1:5 homogenate

Dilution of specimens

Specimens are diluted as follows:

Brain 1:3	3.0 g of brain homogenized with 6 mL of deionized water.
Liver 1:5	2.0 g of liver homogenized with 8mL of deionized water.
Gastric 1:10	2.0 mL of liquid *q.s.* to 20 mL of deionized water, or 1.0 g of a solid specimen homogenized with 9 mL of deionized water.

Note: *Use a homogenate which was prepared within two weeks. Do not use homogenates older than two weeks unless low sample size requires it. Discuss with supervisor and note in case record. The entire submitted amount of gastric contents needs to be homogenized prior to sampling.*

Note: *Homogenates of dilution factors other than 1:3 or 1:5 may be used if available. If case is suspected to have a high concentration of analyte, additional dilutions may be analyzed. Record exceptions on the sequence list.*

Note: *Record the total weight of each gastric content.*

EXTRACTION PROCEDURE

1. All reagents, samples, controls and calibrators must equilibrate to room temperature before sampling.
2. Before sampling, label all 50 mL test tubes. The test tube order in the rack must correspond to the order in which samples will be pipetted and injected. Each test tube must be labeled such that the specimen type, aliquot number, laboratory number and any factors unique to a given specimen are prominently written on the test tube. Handwriting must be legible.
3. Pipet 2 mL negative validated blood, negative validated brain or negative validated liver, or deionized water (negative control for urine and gastric extractions) into a 50 mL test tube. Add 5 µL of the working calibrator solution to the test tube. Cap test tube (**Calibrator I**, 2.5 mg/L).
4. Pipet 2 mL negative validated blood, negative validated brain or negative validated liver, or deionized water (negative control for urine and gastric extractions) into a 50 mL test tube. Add 10 µL of the working calibrator solution to the test tube. Cap test tube (**Calibrator II**, 5 mg/L).
5. Pipet 2 mL negative validated blood, negative validated brain or negative validated liver, or deionized water (negative control for urine and gastric extractions) into a 50 mL test tube. Add 20 µL of the working calibrator solution to the test tube. Cap test tube (**Calibrator III,** 10 mg/L).
6. Pipet 2 mL negative validated blood, negative validated brain or negative validated liver, or deionized water (negative control for urine and gastric extractions) into a 50 mL test tube. Add 50 µL of the working calibrator solution to the test tube. Cap test tube (**Calibrator IV,** 25 mg/L).
7. Pipet 2 mL negative validated blood, negative validated brain or negative validated liver, or deionized water (negative control for urine and gastric extractions) into a 50 mL test tube. Cap test tube (negative control).
8. A low and high matrix match quality control sample is run with each batch. Pipet 2 mL negative validated blood, negative validated brain or negative validated liver, or deionized water (negative control for urine and gastric extractions) into a 50 mL test tube. Add 15 µL of the control working solution to a matching negative matrix. This is the 7.5 mg/L control. Add 30 µL of the control working solution to the matching negative matrix in a second test tube. This is the 15 mg/L control. Add 10 µL of 2500 mg/L acetaminophen/salicylic acid: 1000 mg/L theophylline/caffeine control solution to either the 7.5 mg/l control. This is the 25/10 mg/l acmp low control.
9. Pipet 2 mL of specimen(s) into a properly labeled 50 mL test tube. Cap tubes.

   Note: *Open specimen bottles one at a time.*

   Tissue samples may be quantitated by running against blood calibrators provided matrix matched blank and controls are included and pass all QC criteria.

10. Add 25 µL of internal standard solution to each tube. Then add 20 mL of extraction solvent to each tube.
11. Cap tubes with clean screw cap.

12. Mix by Vortex each tube for 15 seconds.
13. Check each tube for any sign of leaks by inverting the tubes a few times.
14. Place tubes on mechanical shaker and shake at high speed for 30 minutes.
15. Centrifuge samples at ≈ 3000 rpm for 10 minutes and then aspirate lower aqueous layer to waste.
16. Add about 3 g of sodium sulfate. Recap tube.
17. Repeat steps 12 to 15.
18. Decant the organic layer to labeled 25 mL beaker.
19. Evaporate samples overnight under hood or under nitrogen stream at 40 °C in the Turbovap.

RECONSTITUTE SAMPLES

Before samples are reconstituted, check to ascertain that all 25 mL beaker are dry. If there is any evidence of extraction solvent in the cup(s), dry using nitrogen.

1. Label 10 by 75 mm disposable borosilicate glass culture tubes.
2. With a calibrated Eppendorf pipet, add 500 microliters of mobile phase to each 25 mL beaker.
3. Add 1mL heptane to each beaker.
4. Vortex each cup at low speed for 15 seconds and transfer the contents to corresponding labeled tube.
5. Centrifuge tubes for 10 minutes at ≈ 3000 rpm.
6. After centrifuging samples, carefully inspect each tube for any evidence of emulsion. If an emulsion exists, add a few drops of sodium chloride to the tube. Repeat steps 4 and 5.
7. Aspirate the upper heptane layer to waste.
8. Transfer about 200 microliters of the reconstituted sample to clearly labeled autosampler vials. The autosampler vial must document sample type, laboratory number, aliquot number, dilution (if applicable) analyst initials and date sample is extracted. The weight and any unique factors about a specimen should also be documented.

INSTRUMENTATION

Instrument #1 Agilent LC 1090 Series HPLC with Autosampler equipped with a Diode-Array Detector.

Column: Supelco Sil LC-18. 7.5 c.m x 4.6 mm. 3 micron particle size.

Integrator: Computer with Agilent Chemstation software.

HPLC Method. **lbfcomb.m**

Instrument #3 or #4 Agilent LC 1100 Series HPLC with Autosampler equipped with a Diode-Array Detector.

Column: Supelco Sil LC-18. 7.5 c.m x 4.6 mm. 3 micron particle size.

Integrator: Computer with Agilent Chemstation software.

HPLC Method. **Ibfcomb.m**

INSTRUMENT SETUP

Information regarding the daily maintenance and standard operation of the LC1100 can be located in the Agilent instrument manuals, the HPLC Maintenance Standard Operation Procedure and the individual method Standard Operation Procedures. For screening and quantitation of HPLC samples, the following procedure must be followed.

1. All appropriate information must be recorded on the autosampler vials. This data will be transferred to the sequence list, which will be compared with the data recorded on the autosampler vials.
2. A calibrator mixture is first injected followed by the calibrators in order of increasing concentration. A blank follows the highest calibrator.
3. Unknown samples are injected next.
4. A quality control sample is placed randomly in the batch.
5. Below is an example of an HPLC sequence for postmortem specimens.

Sequence line	Vial Number	Sample name	Cal. Line	Method Name
1	1	Cal 1 2.5mg/L	1	IBFCOMB.M
2	2	Cal 2 5.0mg/L	2	IBFCOMB.M
3	3	Cal 3 10.0mg/L	3	IBFCOMB.M
4	4	Cal 4 25.0mg/L	4	IBFCOMB.M
5	5	Blood Blank		IBFCOMB.M
6	6	QC 7.5 mg/L		IBFCOMB.M
7	7	1-09-4604 bld.		IBFCOMB.M
8	8	QC 15.0 mg/L		IBFCOMB.M

INSTRUMENT PRE RUN PROCEDURE

LC 1090 Instrument #1 IBF/NAPROXEN Parameters

1. Pump (PV5):

Stop time	15.00 min
Post time	1.00 min
Flow	1.50 mL/min
Min. pressure	10 bar
Max. pressure	400 bar
Solvent A	75.0% (mobile phase C)

Solvent B	0.0% (Bottle B-H_2O)
Solvent C1	25.0% (Methanol)
Third channel	C1
Gradient range	Narrow

2. Injector:

Injection volume	30.0 µL
Draw speed	416.7 µL/min

3. Mobile Phase Time Table:

The run is isocratic. The flow is 1.5 mL/min for 15 minutes run time.

4. Signals:

	Sample, Bw	Reference, Bw	[nm]
A:	215 10	550	6

5. Curve Type: Linear, using 4 points: 2.5 mg/L, 5.0mg/L, 10.0 mg/L, 25.0 mg/L, forced through origin.

6. Spectrum:

Store	All
From	195 nm
To	350 nm
Step	2 nm
Threshold	0.5 mAU

LC 1100 Instrument #3 or #4 IBF/NAPROXEN/WARFARIN Parameters

1. Pump (PV5):

Stop time	15.00 min
Post time	1.00 min
Flow	1.50 mL/min
Min. pressure	10 bar
Max. pressure	400 bar
Solvent A	75.0% (mobile phase C)
Solvent B	0.0% (Bottle B-H_2O)
Solvent C1	25.0% (Methanol)

2. Injector:

Injection volume	15.0 µL

Draw speed	200 µL/min

3. Mobile Phase Time Table:

The run is isocratic. The flow is 1.5 mL/min for 15 minutes run time.

4. Signals:

	Sample, Bw	Reference, Bw	[nm]
A:	215 14	550	6

5. Curve Type: Linear, using 4 points: 2.5 mg/L, 5.0mg/L, 10.0 mg/L, 25.0 mg/L, forced through origin.

6. Spectrum:

Store	All
From	190 nm
To	340 nm
Step	2 nm
Threshold	1.0 mAU

TEST RUN AND SEQUENCE PREPARATION PROCEDURE

In order to ensure the instruments are in working condition, analyst is required to put a test run on the instrument. This ensures that the retention time is appropriate for all the target drugs and checks for contamination of the column (this may be observed by the peak shape in the test run, i.e. a tailing peak may indicate a contaminated column).

Click on **METHOD** and load the **IBFcomb.m** method. Click on **RUNCONTROL**, then **SAMPLE INFO**. In **SAMPLE INFO SCREEN**, enter the **analyst initials** in operator field, verify **DATA File** path is: C:Chem\32\1\Data\. In **Prefix Subdirectory** update the **FILE NAME** to **LC3 (or 4) date of run (MMDDYY)T.** Update counter to 00001. Under **Sample Parameters** note the location of the vial and sample name of test sample (usually Cal 2.5 mg/L). Under **comment field** note IBF Test run. Then click on **Run Method**.

If there is more than one set of calibrators in the current batch (say a batch that requires a quantitative result in two different matrices), then the “Easy Sequence” features must be used as only the Easy Sequence works with the Sequence Queue to run consecutive separate sequences. If there is only one set of calibrators, the below sequence entry procedure may be used.

SEQUENCE PREPARATION PROCEDURE

Note: the following sequence preparation procedure is used when only one set of matrix calibrators are utilized in the sequence. See Easy Sequence Preparation SOP when there are more than one set of matrix calibrators in the sequence.

Click on SEQUENCE and then SEQUENCE PARAMETER. If the instrument is running, analysts can prepare the sequence in the Offline system.

In SAMPLE INFO SCREEN, enter the analyst initials in operator field, the letter following the one from the previous test run in the FILE NAME, date of the run, MMDDYY on SUBDIRECTORY field, Vial Number and Sample name (normally one of the calibrator from an old sequence), Ibf Run on comment field. Then click on OK, Run Control and Run Method.

Click on SEQUENCE and then SEQUENCE PARAMETER. If the instrument is running, analysts can prepare the sequence in the Offline system.

Operator, Subdirectory and **Sequence Comment**

1. **Prefix** field. This determines the name of the data files that will be stored. Except for special circumstances, use the instrument name and the date in the form of LC4MMDD, e.g., LC40411A. If there is more than one sequence in a day, add a serial letter after the day, e.g. LC40411A.
2. On labels to be attached to the sequence note who extracted the sequence, who created the sequence, who loaded and unloaded the sequence and who processed the sequence.
3. **Part of Method to be Run** field. “According to Runtime Checklist”
4. **Wait After Loading New Method** field. Usually zero, but may be changed if the sequence contains samples that need to be run on other methods.
5. **Post Sequence Command Macro**. Unchecked. The Shutdown Method now has the Shutdown Macro run in its Runtime Checklist.
6. **Not Ready Timeout** field. 10 minutes.
7. **Sequence Comment** field. Indicate the initials of the person performing the three steps of the analysis. It should take the form of E-XX/R-YY/S-ZZ, where E stands for extraction, R stands for reconstitution, S stands for sequence, and XX, YY and ZZ stand for the initials for the analyst performing that particular part of the analysis. Indicate the assay name, mobile phase lot number and any information specific to the batch.
8. Click on **Sequence** and then **Sequence Table**. The **Sequence Table** screen contains includes the following columns for instrument #1:

Sequence Line	*Vial Number*	*Sample Name*	*Cal. Line*	*Method Name*
1	1	Cal 1 2.5mg/L	1	IBFCOMB
2	2	Cal 2 5.0mg/L	2	IBFCOMB
3	3	Cal 3 10.0mg/L	3	IBFCOMB
4	4	Cal 4 25.0mg/L	4	IBFCOMB
5	5	Blood Blank		IBFCOMB
6	6	QC 7.5 mg/L		IBFCOMB
7	7	1-11-9999 bld.		IBFCOMB
8	8	QC 15.0 mg/L		IBFCOMB

For the Calibrators, all calibrators should have “Update Response Factors” set to Replace. The “Update Retention Time” field should be set to Replace for the first calibrator and Average for the remaining calibrators.

The Sample Name field should be modified according to the individual specifications for each sample. After the information of each sample is entered, type an appropriate value in the Dilution column if a dilution was made (if original concentration was used, skip the dilution field. If the sequence is the last sequence of the date, put the **SHUTDOWN** in the last Seq Line to clean up the column, followed by instrument shutdown.

Click on OK after all samples have been entered.

At this point, save the sequence into a file named LC4MMDDYY. Click on **SEQUENCE** then **SAVE SEQUENCE TEMPLATE AS**. For example, LC4102711.S or any additional sequence run in the same date in the same instrument will put a letter after the date. For example, LC4102711A.S.

Click on **SEQUENCE,** then **PRINT SEQUENCE,** highlight **SEQUENCE PARAMETERS, SAMPLE INFORMATION PART, METHOD AND INJECTION PART, CALIBRATION PART AND QUANTITATION PART.** Then click **PRINT** to print the sequence on the printer.

Affix preprinted labels for chain-of-custody (Removed by and Returned by) and steps (sequence extracted by, created by, loaded by, unloaded by and processed by). Fill out the necessary information on the stickers.

BATCH ANALYSIS

1. Place sample bottles in the magazine, using the printed copy of the sequence to insure that each bottle is placed in the correct position and that the sample name is checked against the bottle and sequence. If the person loading the samples and comparing sample name is different from the person listed in the sequence, annotate by initialing and dating the sequence.
2. Click on RUN, then click RUN SEQUENCE. Observe the first injection to insure that the system is operating correctly.
3. After the sequence finishes, check that all data files are successfully transferred to the Chemstation. If the files do not transfer successfully, notify the supervisor so proper corrective action can be taken.

4. After the run finishes, the data files will be in the data subdirectory on the local chemstation, and also will be automatically transferred to the NT Server and processed by Target. The files will be in a .b directory under the instrument name with the same name as the sequence file name without the extent. See data processing SOP for data processing instructions.

DATA PROCESSING – FIRST LEVEL REVIEW

All processing and review should be performed on the Chemstation. The processed data files are then archived on the network drive.

Refer to the "Data processing" section of the SOP manual for the details on processing and review of data.

REINJECTION CRITERIA

Infrequently, analyzed samples (and very rarely sequences) may need to be reinjected for a variety of reasons. Subsequent to data review, use the criteria listed below to determine if reinjection of any sample from the sequence is necessary.

1. Poor chromatography
2. If there is an apparent carryover or UID peak
3. Requests made by the appropriate supervisor

If reinjection or other unusual actions are required, annotate this on the sequence list. Any deviation from the standard procedure must be noted, initialed, and dated. If reinjection fails, repeat analysis.

Note: *When samples are reinjected, in addition to the reinjected sample, reinject the blank, a calibrator and the associated QC samples.*

ACCEPTANCE CRITERIA

Subsequent to HPLC analysis, all data is examined and reviewed according to the guidelines below.

1. A least squares regression curve is calculated by the processing method during calibration. Four calibrators (2.5 mg/L, 5 mg/L, 10 mg/L and 25 mg/L) are used to establish the calibration curve. One calibrator may be dropped if the appropriate acceptance criteria are not met. The linear regression line is forced through the origin.
2. Linear regression correlation (r^2) must be equal to or higher than 0.98 for each analyte. If r^2 is below 0.98, only qualitative results may be reported.
3. Internal standard (IS) response comparable to the response for the matrix calibrators (internal standard recovery/response shall be ± 30% of the selected internal standard).. Any specimens with concentrations exceeding the highest calibrator must be re-extracted using appropriate dilution.

4. Positive blood controls must be within ± 20% of the target value. Tissue positive controls must be within ± 30% of the target value.
5. All negative matrix matched controls must have no interfering peaks in the area of the target analyte.
6. Peak shape should be symmetrical and Gaussian in appearance, and the retention times of the analyte peaks are ± 2 % of the calibrator retention times.
7. Sample with final concentrations in excess of 20% more than the highest calibrator must be diluted and re-extracted along with the appropriate matrix.
8. UV spectra of the analyte peaks in question must have the same absorbance curve as the equivalent peak in the respective calibrators. Samples in which co-eluting peaks (UV spectra which do not match the UV spectrum of the corresponding calibrator analyte) are detected are to be confirmed by alternate methods (i.e. TLC or GCMS). If acetaminophen, salicylic acid, caffeine and/or theophylline are presumptively detected by corresponding retention time and UV spectra match, the detection of the analyte is noted on the report and the sample scheduled for the appropriate quantitative method for the analyte.

SECOND LEVEL REVIEW

The Second Level Reviewer will review the processed data in its entirety according to the acceptance criteria. The second level reviewer will also ensure the following;

9. Check chromatography of all injections. Examine the peak shape and note if any peaks show non-Gaussian shape. Identify unresolved peaks and peaks with shoulders on either side. Address any noted problems before proceeding. Consult a supervisor about any unusual events.
10. Check that all significant peaks in the chromatogram are integrated. If the printout allows, check if the baseline used to integrate is appropriate. The analyst should consult with a supervisor about any unusual events, such as the presence of overload peaks
11. Check that all components of each calibrator are present and that each peak is properly assigned. Correct any errors. If any calibration compounds do not extract, or if unexpected multiple peaks are detected for a calibration compound, the analyst must consult with a supervisor.
12. Check the blank for significant peaks that might co-elute with a compound of interest. If any significant peaks are present in a blank for the batch, the run must be rejected. Consult with a supervisor if there are ANY questions.
13. Review QC samples, determine if the controls meet all acceptance criteria and verify the concentration of the components.
14. A copy of the batch calibrators and controls are forwarded to the QC officer, who will enter the results of the QC sample in the QC database. If the batch fails, ensure that the sample chromatograms are annotated, listing the reason for failure. Notify a supervisor and / or the QC manager.
15. Ensure the following information is annotated on the first calibrator's chromatogram or sequence list:
    a. Calibrators and blank reviewed and accepted (or not accepted). Any QC or calibrator failures are annotated on the proper chromatograms.

b. Any deviations from the SOP are noted or any comments are stated in a concise but detailed fashion.

c. Initial(s) and date

d. Regression coefficient (r^2) of the four point calibration curve of each component present in any case in the batch must be greater than or equal to 0.98. Notify a supervisor about any errors and make sure they are corrected before proceeding.

8. Make sure that each control has the appropriate target concentration range label.

9. Review calibrators, controls, and blanks; ensure all acceptable criteria are met.

10. Initial and date the results.

Note: By initialing and dating this document, the analyst certifies that a complete and accurate review was done.

11. Ensure the master copy of the sequence list includes, (from top to bottom): Calibrators, all QC samples and blanks, r^2 report, sequence list, internal standard recovery form and the lot sheet form. It is the responsibility of the analyst to verify that the master copy is legible and is an accurate copy of the originals, with no information cut off at the margins.

12. Retrieve the case file for each sample in the batch and associate the case file with the corresponding chromatogram(s).

13. Review the case's initial chromatogram, if applicable. Determine if the results are consistent with all the other applicable case data to date. For quantitation, it is important to compare the first chromatogram results with the second chromatogram results. The ratio of peak to internal standard for both chromatograms should be examined. If the results are consistent, report the results on the Result Summary Sheet. Date and initial both the chromatogram and the Result Summary Sheet. If the results are not consistent, the inconsistency must be resolved. Consult a supervisor about rescheduling the sample, or other appropriate corrective action.

14. If the chromatogram shows overloaded peaks, or poor recovery of the internal standard, then repeating the sample may be necessary. If the problem is an overload, re-schedule with appropriate dilutions. In cases of poor recovery, the sample, its control, blank, and a calibrator may be re-injected once. If the criteria as listed in batch review are still not met, the sample is re-scheduled. If a case has an unknown or unidentified peak not observed in previous scan results, the case must be transferred to the GCMS section for identification of that peak. All chromatograms must be attached to the case file. Consult with the supervisor if there is any question.

15. Submit the case file for third level review.

Note: *Do not discard any sample paperwork.*

THIRD LEVEL REVIEW (FINAL REVIEW)

The third and final level review can only be performed by the Laboratory Manager. He/she will review the data for the entire case according to all established criteria. They will ensure that screening, confirmatory and quantitative analysis on the case have been completed and reported accurately. As needed, they will also schedule additional analysis and contact the Medical Examiner on the case to discuss any findings and / or review case history.

REPORTING

1. All results must be entered on the result summary form in the case file.
2. Copies of all the calibrators and controls along with a copy of the sequence worksheet must be attached to the original chromatogram of the case, and placed in the case file folder.
3. All negative cases are reported on the result summary form as “Ibuprofen, naproxen and/or warfarin not detected”.
4. Concentrations below 2.5 mg/L are reported as “Ibuprofen, naproxen and/or warfarin less than 2.5 mg/L”.
5. Concentrations greater than 2.5 mg/L are reported truncated to 1 decimal place (e.g. naproxen 7.67 mg/L is reported as 7.6 mg/L).
6. When reporting gastric contents, in addition to the quantitation as mg/kg, the gastric content is also reported as mg total in the stomach content (concentration in mg/kg x weight in kg = total drug in mg).
7. Positive results must be confirmed or substantiated by either repeat analysis or by positive results based on a different analytical principle or in an additional tissue.

REFERENCES

Agilent 1090 and Agilent 1100 Series II HPLC Systems. Installation Guide.

Agilent 1090 and Agilent 1100 Series II HPLC Systems. Users Guide.

Agilent 1090 and Agilent 1100 Series II HPLC Systems. Standard Operating Procedures.

Turbovap. Users Guide.

REVISION HISTORY

Ver 04.20.2015	1. Revision history implemented. 1. Changed position of QC materials from randomly throughout the sequence to every 10th sample. 2. Included an end of run QC for every sequence/sub sequence.
Ver 08.31.2015	1. Revised internal standard acceptance criteria.
Ver 09.14.2015	1. Inclusion of First, Second and Third level review.