



February 18, 2005

John Smith
ABC company
123 Mockingbird Lane
Anytown, USA 55555
(555) 234-5678

Re: Project Number 100.001.001 Selenium Investigation

Dear Mr. Smith,

Attached is the report associated with five (5) wastewater samples submitted for total selenium and selenium speciation on January 22, 2005. All samples were received on January 23, 2005 in acceptable condition. Total selenium analysis was performed in accordance with EPA Method 200.8. Selenium speciation was performed by ion chromatography inductively coupled plasma mass spectrometry (IC-ICP-MS). The overall analysis went very well. Any analytical variances associated with the analysis are addressed in the following report.

If you have any questions, please feel free to contact me at your convenience.

Sincerely,

Tom Jones
Project Manager

ABC Company
123 Mockingbird Lane
Anytown, USA 55555

Project number: 100.001.001
Selenium in Fred's water Investigation
February 18, 2005

1. Sample Reception

Five (5) wastewater samples in 125mL amber high density polyethylene bottles were submitted for total selenium and selenium speciation analysis by EPA Method 200.8 and ASC standard operating procedures, respectively. All samples were received on January 23, 2005. The temperature of the respective transport container upon reception was 3°C. Although no chain of custody seal was applied to the sample shipment all packing materials were intact and no visible signs of tampering were noticeable.

All samples were received in a laminar flow clean hood void of trace metals contamination and ultra-violet radiation. Immediately upon reception, an aliquot of each sample was filtered (0.45µm) and analyzed for selenite, selenate, selenocyanate, methylseleninic acid, and selenomethionine by ion chromatography inductively coupled plasma mass spectrometry (IC-ICP-MS). The original sample container was preserved to pH < 1 with HNO₃, oven digested, and analyzed for total selenium by inductively coupled plasma dynamic reaction cell mass spectrometry (ICP-DRC-MS). Sample aliquots taken for selenium speciation analysis were stored in a cryogenically cooled freezer at 80°C for archival purposes.

2. Sample Preparation

All sample preparation is performed in laminar flow clean hoods known to be free from trace metals contamination. All applied water for dilutions and sample preservatives are monitored for contamination to account for any biases associated with the sample results.

Selenite, Selenate, Selenocyanate, Methylseleninic acid, and Selenomethionine Quantification by IC-ICP-MS Prior to analysis, all samples were filtered with a syringe filter (0.45µm) and injected directly into sealed autosampler vials. No further sample preparation was performed as any chemical alteration of the samples may shift the equilibrium of the system resulting in changes in speciation ratios.

Total Selenium Quantification by ICP-DRC-MS Prior to analysis all original samples were preserved to 1% HNO₃ (v/v), pH < 1, followed by closed vessel oven digestion. All sample fractions were analyzed for total selenium by ICP-DRC-MS.

3. Sample Analysis

All sample analysis is precluded by a minimum of a five-point calibration curve spanning the entire concentration range of interest. Calibration curves are performed at the beginning of each analytical day. All calibration curves, associated with each species of interest, are standardized by linear regression resulting in a response factor. All sample results are **instrument blank corrected** to account for any operational biases associated with the analytical platform.

Prior to sample analysis, all calibration curves are verified using second source standards which are identified as initial calibration verification standards (ICV).

Ongoing instrument performance is identified by the analysis of continuing calibration verification standards (CCV) and continuing calibration blanks (CCB) at a minimal interval of every ten analytical runs.

Selenite, Selenate, Selenocyanate, Methylseleninic acid, and Selenomethionine Quantification by IC-ICP-MS All samples for selenite, selenate, selenocyanate, methylseleninic acid, and selenomethionine quantification were analyzed by ion chromatography inductively coupled plasma mass spectrometry (IC-ICP-MS). Aliquots of each sample are injected onto an anion exchange column and are mobilized by a basic (pH > 7) gradient. The eluting selenium species are then introduced into a radio frequency (RF) plasma where energy-transfer processes cause desolvation, atomization, and ionization. The ions are extracted from the plasma through a differentially-pumped vacuum interface and separated on the basis of their mass-to-charge ratio (m/z) by a mass spectrometer. A solid-state detector detects ions transmitted through the mass analyzer and the resulting current is processed by a data handling system.

Retention times for each eluting species are compared to known standards for species identification.

Total Selenium Quantification by ICP-DRC-MS All samples for total selenium quantification were analyzed by inductively coupled plasma dynamic reaction cell mass spectrometry (ICP-DRC-MS). Aliquots of each sample are introduced into a radio frequency (RF) plasma where energy-transfer processes cause desolvation, atomization, and ionization. The ions are extracted from the plasma through a differentially-pumped vacuum interface and travel through a pressurized chamber (DRC) containing a specific reactive gas which preferentially reacts with interfering ions of the same target mass to charge ratios (m/z). A solid-state detector detects ions transmitted through the mass analyzer, on the basis of their mass-to-charge ratio (m/z), and the resulting current is processed by a data handling system.

4. Analytical Variances

The overall analyses went very well and no significant analytical issues were encountered. All quality control associated with these samples were within acceptance limits.

It should be noted that the estimated method detection limits (eMDLs) for all selenium species are generated from replicate analyses of the lowest standard in the calibration curve. Not all selenium species are present in preparation blanks; therefore, eMDL calculations based on preparation blanks are artificially biased low.

Selenium Speciation and Total Selenium Results for ABC Company

Project Name: Selenium Investigation

Project Number: 100.001.001

Contact: John Smith

Date: February 18, 2005

Report Generated by: Tom Jones

Sample Results

Sample ID	Se(IV)	Se(VI)	SeCN	SeMet	MSe(IV)	Total Se
Well 1	5.60	0.751	ND (<0.005)	0.022	0.010	6.4
Well 2	ND (<0.010)	125	10.5	ND (0.005)	ND (0.005)	137
Well 3	ND (<0.010)	110	30.4	ND (0.005)	ND (0.005)	94.8
Well 4	69.0	15.6	ND (<0.005)	ND (0.005)	5.60	64.8

All results reflect the applied dilution and are reported in µg/L

ND = Not detected at the estimated method detection limit (eMDL)

Selenium Speciation and Total Selenium Results for ABC Company

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Quality Control Summary - Preparation Blank Summary

Analyte (µg/L)	PBW1	PBW2	PBW3	PBW4	Mean	StdDev	eMDL*	eMDL 2x
Se(IV)	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.010
Se(VI)	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.010
SeCN	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.010
SeMe	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.010
MethSe	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.010
Total Se	0.008	0.005	0.005	0.006	0.006	0.001	0.004	0.008

eMDL = Estimated Method Detection Limit

*Please see narrative regarding eMDL calculations

Quality Control Summary - Certified Reference Materials

Analyte (µg/L)	CRM	True Value	Result	Recovery
Se(IV)	LCS	11.43	10.98	96.1
Se(VI)	NIST 1640	21.96	21.54	98.1
SeCN	LCS	10.00	9.99	99.9
SeMe	LCS	10.00	10.03	100.3
MethSe	LCS	10.00	10.58	105.8
Total Se	NIST 1640	21.96	22.51	102.5

Quality Control Summary - Matrix Duplicates

Analyte (µg/L)	Sample ID	Rep 1	Rep 2	Mean	RPD
Se(IV)	Well 4	69.00	68.50	68.75	0.7
Se(VI)	Well 4	15.60	16.20	15.90	3.8
SeCN	Well 4	ND (<0.005)	ND (<0.005)	NC	NC
SeMe	Well 4	ND (<0.005)	ND (<0.005)	NC	NC
MethSe	Well 4	5.600	5.520	5.560	1.4
Total Se	Well 4	64.80	65.37	65.08	0.9

ND = Not detected at the estimated method detection limit (eMDL)

NC = Not calculated due to one or more concentrations below the eMDL.

Quality Control Summary - Matrix Spike/ Matrix Spike Duplicate

Analyte (µg/L)	Sample ID	Spike Conc	MS Result	Recovery	Spike Conc	MSD Result	Recovery	RPD
Se(IV)	Well 4	125.0	195.6	101.5	125.0	197.8	103.2	1.1
Se(VI)	Well 4	125.0	134.7	95.0	125.0	142.5	101.3	5.7
SeCN	Well 4	125.0	123.5	98.8	125.0	128.4	102.7	3.9
SeMe	Well 4	12.50	13.13	105.0	12.50	13.09	104.7	0.3
MethSe	Well 4	12.50	17.80	97.9	12.50	18.00	99.5	1.1
Total Se	Well 4	250.0	312.5	99.0	250.0	335.2	108.0	7.0