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Causes of Failing the Draft ANSI Standard N13.30 Radiobioassay Performance Criterion for Minimum Detectable Amount

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Pacific Northwest Laboratory

Prepared for
U.S. Nuclear Regulatory Commission

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Causes of Failing the Draft ANSI Standard N13.30 Radiobioassay Performance Criterion for Minimum Detectable Amount

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ABSTRACT

The test methods used for Pacific Northwest Laboratory (PNL) bioassay performance tests were evaluated by comparing the minimum detectable amount (MDA) based on performance tests results with the MDA calculated by PNL using the bioassay laboratory's own quality control (QC) data. Two in vitro laboratories and two in vivo laboratories were studied and a correlation between the performance test MDA estimates and the QC data was demonstrated. However, it was often necessary to examine the QC data to identify important characteristics of the blank distribution that affect the MDA calculation, because the MDA equation must be based on the specific analysis and calculational methods of the procedure evaluated. Even when the correct MDA equation is applied, the MDA calculated will have a relatively large confidence interval when only a few replicates are used to estimate the standard deviation. For this reason, a relatively precise estimate of the MDA is generally only available when Poisson statistics may be applied. It was concluded that performance testing alone cannot provide all the information necessary to make an accurate estimate of the measurement process MDA. Review of the laboratory's QC data and the entire measurement procedure will be necessary. Specific recommendations for changes to draft ANSI N13.30, "Performance Criteria for Radiobioassay," are given.

SUMMARY

One of the research projects on occupational radiation protection at Pacific Northwest Laboratory (PNL) (a) concerns the evaluation of draft American National Standards Institute (ANSI) Standard N13.30, "Performance Criteria for Radiobioassay." In support of the evaluation of the draft standard, PNL has conducted performance tests of bioassay laboratories and used the results to verify the appropriateness of the criteria in the draft standard.

Previous reports from PNL have summarized bioassay laboratory performance test results for radionuclides in an artificial urine matrix, artificial fecal samples, and direct measurements (in vivo bioassay) of radioactive material in occupationally exposed individuals. Typically, test results have shown that the minimum detectable amount (MDA) criterion was the one most commonly failed.

For this report, the performance test methods used for the previous reports were evaluated by comparing the MDA calculated from previous MDA performance tests results and the MDA calculated by PNL using the bioassay laboratory's own quality control (QC) data. Four laboratories were chosen for this study. Two in vitro laboratories were evaluated for natural uranium and ^{238}Pu analyses in urine, and two in vivo laboratories for ^{54}Mn and ^{144}Ce in the lung.

Although a correlation between the performance test MDA estimates and the QC data was demonstrated, it was often necessary to examine the QC data to identify important characteristics of the blank distribution that would affect the MDA calculation. Characteristics such as unequal variances of detectors, unstable electronics, and paired samples must all be considered. Furthermore, the MDA equation must be based on the analysis and calculational methods of the procedure evaluated, and no single MDA equation will be appropriate for all analyses.

Even when the correct MDA equation is applied, the MDA calculated will have a relatively large confidence interval when only a few replicates are used to estimate the standard deviation. At least 13 replicates are needed to limit the ratio of the upper-to-lower bound of the 90% confidence interval to 2. For this reason, a relatively precise estimate of the MDA is generally only available when Poisson statistics may be applied.

With the above performance test limitations in mind, the following recommendations were made for determination of the MDA in conjunction with draft ANSI N13.30 performance testing:

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- The bioassay laboratory's own QC data should be used for the MDA calculation in preference to the small data set available from performance testing.
- The MDA equation should be designed specifically for the measurement process being evaluated. If generic MDA equations are developed, the assumptions used should be verified whenever applied.
- Poisson statistics should be assumed for the MDA calculation whenever the Poisson distribution is not rejected for the available data.
- If Poisson statistics are rejected, the standard deviation should be estimated from replicates and a confidence interval should be calculated for the MDA. The laboratory should not be failed if the lower 5% bound of the confidence interval is less the MDA criterion of draft ANSI N13.30. This approach is recommended because of the inherent uncertainty of the replicate based MDA estimate.
- If Gaussian statistics are rejected, the cause of the non-normality should be evaluated and its impact on the MDA estimate determined.

The premise common to all the above recommendations is that performance testing alone cannot provide all of the information necessary to make an accurate estimate of the measurement process MDA. Review of the laboratory's QC data and the entire measurement procedure will also be necessary.

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CONTENTS

ABSTRACT	iii
SUMMARY	v
ACKNOWLEDGMENTS.	vii
INTRODUCTION	1
BASIS FOR THE CALCULATION OF THE MINIMUM DETECTABLE AMOUNT	3
SAMPLE DISTRIBUTION	3
CALCULATION OF THE MINIMUM DETECTABLE AMOUNT	5
CONFIDENCE INTERVAL FOR THE MINIMUM DETECTABLE AMOUNT	7
MINIMUM DETECTABLE AMOUNT COMPARISONS	9
IN VITRO LABORATORIES	9
Natural Uranium in Urine	9
^{238}Pu in Urine	13
IN VIVO LABORATORIES.	17
^{54}Mn in the Lung	21
^{144}Ce in the Lung	23
CONCLUSIONS AND RECOMMENDATIONS	27
REFERENCES	29
APPENDIX A - NATURAL URANIUM LABORATORY QUALITY CONTROL DATA	A.1
APPENDIX B - PACIFIC NORTHWEST LABORATORY IN VITRO PERFORMANCE TEST RESULTS	B.1
APPENDIX C - ^{238}PU LABORATORY QUALITY CONTROL DATA	C.1
APPENDIX D - PACIFIC NORTHWEST LABORATORY IN VIVO PERFORMANCE TEST RESULTS.	D.1

FIGURES

1	Laboratory A Natural Uranium Cumulative Probability	10
2	Laboratory B Natural Uranium Cumulative Probability	10
3	Laboratory A Natural Uranium MDAs	12
4	Laboratory B Natural Uranium MDAs	12
5	Laboratory A ^{238}Pu Cumulative Probability	14
6	Laboratory B ^{238}Pu Cumulative Probability	14
7	Laboratory A ^{238}Pu MDAs	16
8	Laboratory B ^{238}Pu MDAs	16
9	Laboratory C Blank Gamma Spectra.	18
10	Laboratory D Blank Gamma Spectra	18
11	Laboratory C ^{54}Mn Cumulative Probability	19
12	Laboratory D ^{54}Mn Cumulative Probability	19
13	Laboratory C ^{144}Ce Cumulative Probability	20
14	Laboratory D ^{144}Ce Cumulative Probability	20
15	Laboratory C ^{54}Mn MDAs	22
16	Laboratory D ^{54}Mn MDAs	22
17	Laboratory C ^{144}Ce MDAs	25
18	Laboratory D ^{144}Ce MDAs	25

TABLES

1	Five Percent Rejection Levels for Poisson Goodness of Fit.	5
2	Power of Chi-Square Test to Identify Non-Poisson Variability	5
3	Factors for Estimating the MDA Confidence Intervals	7
4	Natural Uranium Minimum Detectable Amounts	11
5	^{238}Pu Minimum Detectable Amounts	15
6	^{54}Mn Minimum Detectable Amounts	21
7	^{144}Ce Minimum Detectable Amounts	24
A.1	Natural Uranium Laboratory Quality Control Data	A.1
B.1	Pacific Northwest In Vitro Performance Test Results	B.1
C.1	^{238}Pu Laboratory Quality Control Data	C.1
D.1	Pacific Northwest Laboratory In Vivo Performance Test Results	D.1

INTRODUCTION

One of the research projects on occupational radiation protection at Pacific Northwest Laboratory (PNL) (a) concerns the evaluation of draft American National Standards Institute (ANSI) Standard N13.30, "Performance Criteria for Radiobioassay" (ANSI 1989). This draft standard specifies performance criteria against which results of performance tests of radio-bioassay laboratories may be compared. In support of evaluation of the draft standard, PNL has conducted performance tests of bioassay laboratories at U.S. Department of Energy (DOE) facilities, DOE-contractor facilities, and other facilities throughout the United States. The results of these studies were used to verify the appropriateness of the criteria selected by the Standards Committee's Working Group in developing ANSI N13.30.

Previous reports from PNL have summarized bioassay laboratory performance test results for radionuclides in an artificial urine matrix (Robinson, Fisher, and Hadley 1984; MacLellan, Traub, and Fisher 1988), artificial fecal samples (MacLellan 1988), and direct measurements (in vivo bioassay) of radioactive material in occupationally exposed individuals (Robinson et al. 1986). In these previous reports it was reported that the minimum detectable amount (MDA) criterion was the one most commonly failed during performance tests. An evaluation of the test methods used during performance testing was conducted by PNL for the U.S. Nuclear Regulatory Commission to attempt to determine the cause of these failures. The basis for calculating the MDA, MDA comparison, and the conclusions of the test method evaluation and the associated recommendations are discussed in this report.

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BASIS FOR THE CALCULATION OF THE MINIMUM DETECTABLE AMOUNT

Calculated detection limits require knowledge of many parameters that are often poorly defined. Measurement of the activity concentration that is routinely achievable depends not only on the instrument characteristics, but also on the characteristics of the sample being measured and the measurement procedure used. The routinely achievable detection level only has meaning when the instrument, analytical method, and type of sample are specified (Collé et al. 1980). A calculated MDA based on historical data should be considered an *a priori* indication of a routinely detectable amount and not an *a posteriori* determined quantity for a specific analysis.

Furthermore, it is necessary to define the acceptable probability of non-detection. Draft ANSI N13.30 (ANSI 1989) defines the minimum detectable activity as "the smallest amount of a radionuclide in a sample that will be detected with a β probability of non-detection (Type II error) while accepting an α probability of erroneously detecting that radionuclide in an appropriate blank sample (Type I error). For this standard, the α and β probabilities are both set at 0.05." In other words, a critical level, which limits to 5% the probability of falsely accepting a truly negative result, is determined. Then, the minimum detectable activity is set at a level above the critical level, where the probability of falsely rejecting a truly positive result is also less than 5%.

The MDA is usually estimated by evaluating the variability observed in the measurement of the appropriate blanks. The specific form of the MDA equation will depend on the assumptions made about the sample distribution. Whether the MDA is used to compare measurement systems or to demonstrate procedure capabilities for regulatory purposes, it is important to remember that the MDA is a reliable estimate of capabilities only when all assumptions of the equation are met.

SAMPLE DISTRIBUTION

A major assumption underlying the MDA calculation procedure is that the estimated net signal is an independent random variable having a known distribution (Currie 1984). It is necessary to know (or have a statistical estimate for) the standard deviation of the estimated net signal in order to calculate the decision and detection levels.

The best estimate of the MDA occurs when the standard deviation of the blank is known, such as when the blank population is Poisson distributed. When the blank and sample analyses are not independent measurements (e.g., baseline spectrum and gamma peak), the data should be treated as paired results. In this case the non-Poisson errors for each sample-blank pair are assumed to be the same and cancel when the net value is calculated, which allows Poisson statistics to be employed.

When samples are not paired, the chi-square test may be used to determine whether the data are Poisson distributed (Remington and Schork 1970). The sample variance (s^2) equals $\sum(x_i - \bar{x})^2/(n-1)$ and the variance of a Poisson distribution equals the mean (\bar{x}). The ratio of the two estimates of the variance may be expressed as follows:

$$s^2/\sigma^2 = \left[\sum_{i=1}^n (x_i - \bar{x})^2/(n-1) \right] / \bar{x} \quad (1)$$

where n equals the number of replicate measurements and x_i represents an observed result. Because

$$\chi^2 = \sum_{i=1}^n (x_i - \bar{x})^2 / \bar{x} \quad (2)$$

substituting Equation (2) into Equation (1) and \bar{x} for σ^2 results in the following:

$$\frac{s^2}{\bar{x}} = \chi^2 / (n-1) \quad (3)$$

Equation (3) may, therefore, be used to test whether the sample variance is significantly different than the mean, and thereby whether a Poisson distribution is appropriate.

Because we are usually only concerned when variability is in excess of the Poisson estimate, a one-sided test for significance is applied. The hypothesis that the distribution is Poisson is rejected when the ratio of the sample variance and the mean exceed the value in the third column of Table 1. The power of this test (probability of detecting a true variance that is greater than the mean) may be estimated using the data in Table 2 (Remington and Schork 1970).

If the hypothesis that the distribution is Poisson is rejected, the hypothesis that the data are normally distributed should be tested using the Shapiro and Wilk W test (Anderson and McLean 1974) or graphically using probability paper (when normally distributed data are plotted on probability paper they lie in a straight line).

When normality is accepted, the standard deviation may be estimated from the sample distribution. When normality is rejected, the cause for the rejection should be investigated to the extent that the data will allow. If the deviation from normality is extreme (i.e., bi-modal or skewed distributions) the calculated MDA will not correctly estimate the procedure detection capabilities.

TABLE 1. Five Percent Rejection Levels for Poisson Goodness of Fit

Sample Size	χ^2	$\chi^2 / (n-1)$
2	3.841	3.84
3	5.991	3.00
4	7.815	2.61
5	9.488	2.37
6	11.070	2.21
7	12.592	2.10
8	14.067	2.01
9	15.507	1.94
10	16.919	1.88

Source: Remington and Schork (1970).

TABLE 2. Power of Chi-Square Test to Identify Non-Poisson Variability

Sample Size	σ^2/mean		
	1.1	1.4	1.54
5	0.69	0.90	0.95
10	0.72	0.96	0.99

CALCULATION OF THE MINIMUM DETECTABLE AMOUNT

When a Gaussian or Poisson distribution is assumed, the minimum detectable count (MDC) has the following relationship to the net blank standard deviation (s_0), gross blank standard deviation (s_b), gross sample standard deviation at the MDC (s_s), and the standard normal variate (z).

$$\text{MDC} = z \cdot s_0 + z(s_b^2 + s_s^2)^{\frac{1}{2}} \quad (4)$$

The concepts on which this equation is based are discussed in the draft standard (ANSI 1989) and will not be repeated here.

The total variance of a sample containing an amount of radioactive material equal to the MDA (s_s^2) may be separated into two components. The variance component attributable to the radioactive material of interest (MDC) is Poisson distributed and is estimated by the mean. The remaining variance (s_b^2) of the blank sample is assumed for this derivation to be normally distributed. The variance of the net sample count equals the sum of the gross sample (s_s^2) and blank (s_b^2) variances. Using this substitution, Equation (4) is changed as follows:

$$\text{MDC} = z \cdot s_0 + z(s_b^2 + s_b^2 + \text{MDC})^{\frac{1}{2}} \quad (4a)$$

Because the net blank is determined by subtracting one blank count from another, the variance of the net blank (s_0^2) equals twice the variance of the gross blank (s_b^2) and Equation (4a) may be rewritten as follows:

$$MDC = z \cdot s_0 + z(s_0^2 + MDC)^{\frac{1}{2}} \quad (4b)$$

After the $z \cdot s_0$ term of Equation (4b) is moved to the other side of the equal sign and both sides of the equation are squared, the more familiar form of the MDA equation is produced by solving Equation (4d) algebraically, as follows:

$$(MDC - z \cdot s_0)^2 = z^2 \cdot (s_0^2 + MDC) \quad (4c)$$

$$MDC^2 - 2z \cdot s_0 \cdot MDC + z^2 \cdot s_0^2 = z^2 \cdot (s_0^2 + MDC) \quad (4d)$$

$$MDC^2 = z^2 \cdot s_0^2 + z^2 \cdot MDC + 2z \cdot s_0 \cdot MDC - z^2 \cdot s_0^2 \quad (4e)$$

$$MDC = z^2 + 2z \cdot s_0 \quad (4f)$$

When Type I and Type II errors are limited to 5% and the net blank variance is assumed to equal twice the blank variance, the equation reduces to the following form:

$$MDC = 2.71 + 4.65 \cdot s_b \quad (5)$$

In order to limit Type II errors (false negatives) to 5% for very low blank count rates, the 2.71 term is usually rounded to 3. This is appropriate when Poisson statistics apply because the probability of obtaining zero counts is about 5% when the true mean is three.

The MDA is determined by dividing the MDC by the appropriate conversion factors. The MDA equation for paired observations is then as follows:

$$MDA = (1 + \Delta K) [4.65 \cdot s_b + 3] / KT \quad (6)$$

where K = the calibration factor supplied by the performance laboratory for the measurement process, in counts per unit time per unit activity.

ΔK = the estimated fractional systematic error in the calibration factor K . This author recommends that the reciprocal of the sum of one plus the performance test estimate of the relative bias (B_r) should be used as an estimator of $(1 + \Delta K)$.

s_b = the standard deviation of the gross blank count

T = the sample count time.

The value of the net blank standard deviation, s_0 , is estimated by the product of the sample standard deviation and a factor (η), where η equals the square root of $(1 + 1/b)$ and (b) is the ratio of the background and sample count times (Currie 1984). The calibration factor, K , is equal to the

product of the detector counting efficiency, chemical yield when appropriate, and the physical conversion factor for nuclear transformations per unit activity (i.e., decays per minute per nanocurie). This value would normally be supplied by the service laboratory. When the total baseline counts exceed about 1000 counts, the 3 term will be insignificant and may be dropped from the equation.

If the analytical results represent a gross count (as with uranium mass analyses) b equals zero and η equals one. The equation for this case then becomes

$$MDA = (1 + \Delta K) [3.29 \cdot s_b + MBV + 3] / KT \quad (7)$$

where MBV is the mean blank value and the other terms are defined the same as above. The MBV is added to the equation because gross rather than net values are being used.

CONFIDENCE INTERVAL FOR THE MINIMUM DETECTABLE AMOUNT

Because the performance criteria estimates may be based on as few as five replicates, it is important to calculate their confidence intervals. The random variable $(n-1)s^2/\sigma^2$ follows the chi-square distribution with $n-1$ degrees of freedom (Remington and Schork 1970). To obtain the 5% lower bound and 95% upper bound for a standard deviation related term, the s_b term should be divided by the value from the third and fifth columns of Table 3, respectively. These boundary values should then be used in the appropriate MDA equation to obtain the 90% confidence interval.

TABLE 3. Factors for Estimating the MDA Confidence Intervals

Replicates, n	$\chi^2(0.95)$	$[\chi^2/(n-1)]^{\frac{1}{2}}$	$\chi^2(0.05)$	$[\chi^2/(n-1)]^{\frac{1}{2}}$
2	3.841	1.96	0.00393	0.063
3	5.991	1.73	0.103	0.227
4	7.815	1.61	0.352	0.343
5	9.488	1.54	0.711	0.422
6	11.070	1.49	1.145	0.479
7	12.592	1.45	1.635	0.522
8	14.067	1.42	2.167	0.556
9	15.507	1.39	2.733	0.584
10	16.919	1.37	3.325	0.608

Source: Remington and Schork (1970).

MINIMUM DETECTABLE AMOUNT COMPARISONS

The performance test methods were evaluated by comparing the MDA calculated from previous MDA performance test results and the MDA calculated by PNL using the bioassay laboratory's own quality control (QC) data. Four laboratories were chosen for this study, two in vitro laboratories and two in vivo laboratories. The QC data for the in vitro laboratories consisted of the results of blank samples analyzed for two common radionuclides. For the in vivo laboratories, collected data consisted of gamma spectra from individuals considered free from radioactive contaminants, information on the energy windows used by the analysis program for the appropriate photons of two common analyses, and appropriate calibration factors.

IN VITRO LABORATORIES

Two in vitro bioassay laboratories that provide a broad range of analyses were selected from the list of past performance test participants for further study. Appropriate laboratory personnel were then contacted and asked to make their QC data available for review. After an initial review of the data, natural uranium and ^{238}Pu analysis data were selected for further evaluation. The QC data were then used to calculate an MDA for each analysis, and the MDA from the QC data were compared with the MDAs calculated from performance test data.

Natural Uranium in Urine

The natural uranium QC data from Laboratories A and B are listed in Appendix A. Prior to calculating *a priori* MDAs based on these data, the sample distributions were investigated. One result from Laboratory A was deleted when three standard deviations were used as the outlier test. No data were deleted from Laboratory B.

Following the removal of the outliers, the data were plotted in relation to cumulative percent. The scale used for the cumulative percent observed was the expected Z value, where Z equals the quantity of the observed value minus the mean, divided by the standard deviation of the population, $(x-\mu)/\sigma$ (see Figures 1 and 2). For both laboratories, the variance of the blank data was less than the mean value and the Poisson distribution was accepted (Remington and Schork 1970).

The bounds for the confidence interval for the natural uranium MDA were calculated using the following equation

$$\text{MDA} = [3.29 \cdot s_b \cdot (\chi^2 / (n-1))^{\frac{1}{2}}] / [1 + Br] \quad (8)$$

The multiplier for the standard deviation in Equation (8) is 3.29 rather than 4.65 because the gross uranium mass rather than the net mass is reported for the fluorometric analysis. The MDAs calculated using Equation (8) and the data from Appendix A are shown in Table 4. The values of the F test for

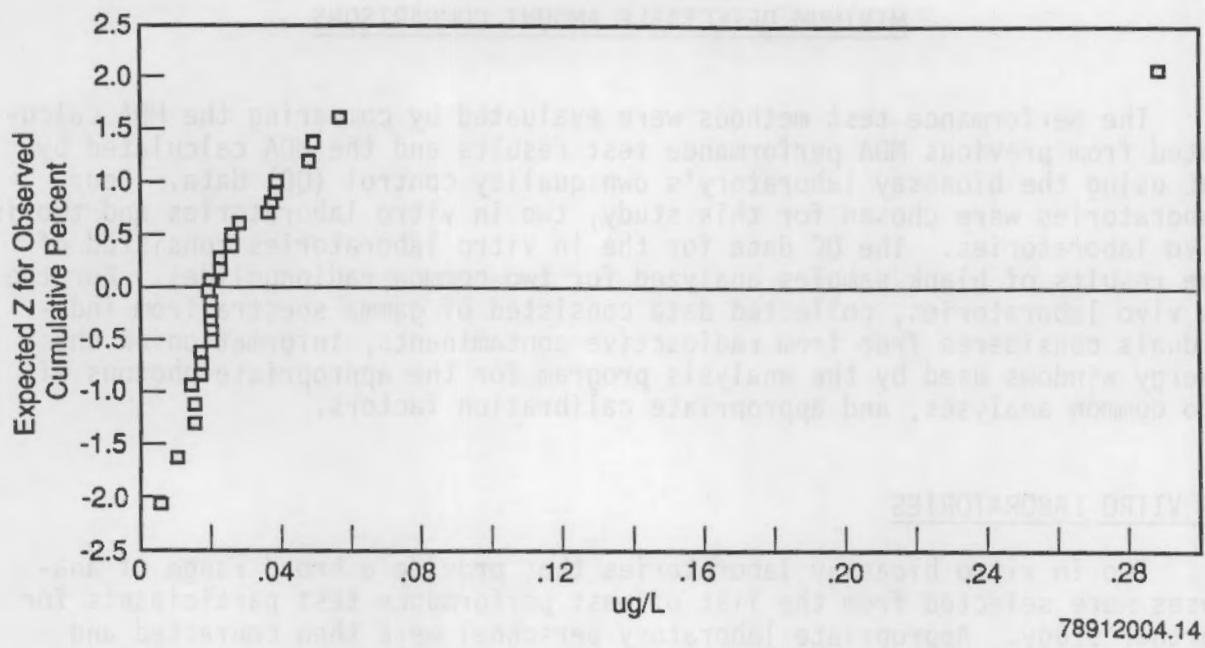


FIGURE 1. Laboratory A Natural Uranium Cumulative Probability

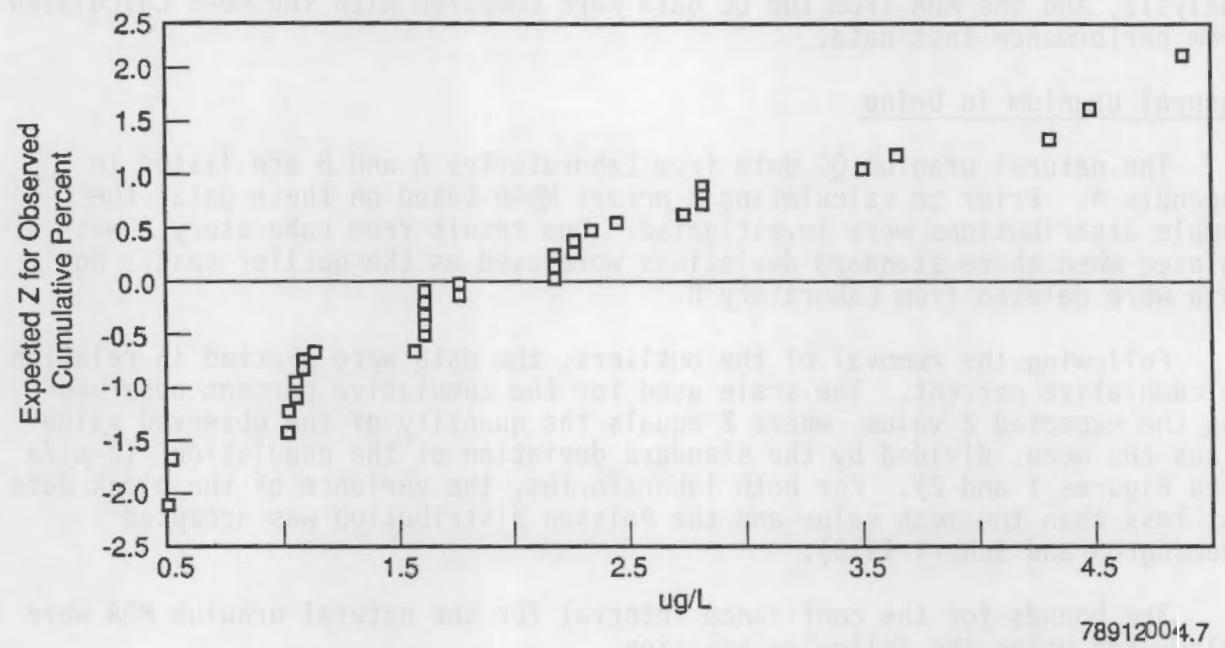


FIGURE 2. Laboratory B Natural Uranium Cumulative Probability

TABLE 4. Natural Uranium Minimum Detectable Amounts

Laboratory A	n	Br	S _b , μg/L	Natural Uranium MDAs and Confidence Interval Corrected for Bias, μg/L		
				5%	Mean	95%
QC Data	28	--	0.012	0.042	0.051	0.66
Test Data	3	-0.227	0.006	0.015	0.025	0.11
Calculated F: 4.0 F _{0.05} (27,2): 19.5						
Laboratory B				5%	Mean	95%
QC Data	33	--	1.10	3.52	4.22	5.32
Test Data	3	-0.142	1.15	2.58	4.41	19.4
Calculated F: 1.80 F _{0.05} (32,2): 19.5						

unequal variances are also shown. This test is used to test the hypothesis that the true variances of two populations, and therefore the estimated MDAs, are the same. The variances of the QC and test data were not considered significantly different unless the calculated F value was greater than the tabulated F at the 95 percentile for the given degrees of freedom.

The calculated MDAs are presented graphically in Figures 3 and 4. The diagonal line represents perfect agreement between the two estimates of the MDA. The estimates were not considered significantly different if either confidence interval crossed the diagonal.

Table 4 also shows the MDAs calculated from the performance test data (MacLellan, Traub, and Fisher 1988). Two MDA equations were used in that report:

$$MDA(1) = (4.65s_b + 3)/K \quad (9)$$

where s_b is the standard deviation of the blank counts and K is the calibration factor, and

$$MDA(2) = 4.65s_B \quad (10)$$

where s_B is the standard deviation of the equivalent blank activity. Equation (10) was incorrectly applied in the report of Round One in vitro performance test results (Robinson, Fisher, and Hadley 1984) because the equivalent blank activity is a net quantity and the square-root-of-two term is not needed to estimate the standard deviation of the net blank (i.e.,

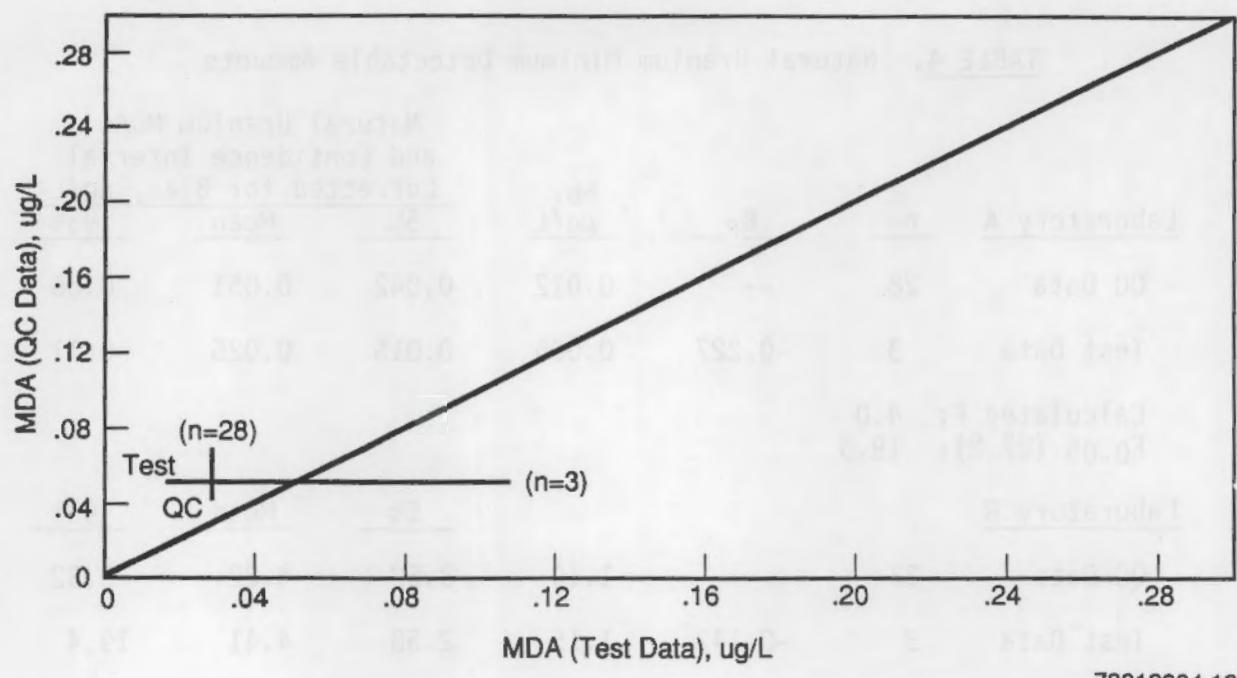


FIGURE 3. Laboratory A Natural Uranium MDAs

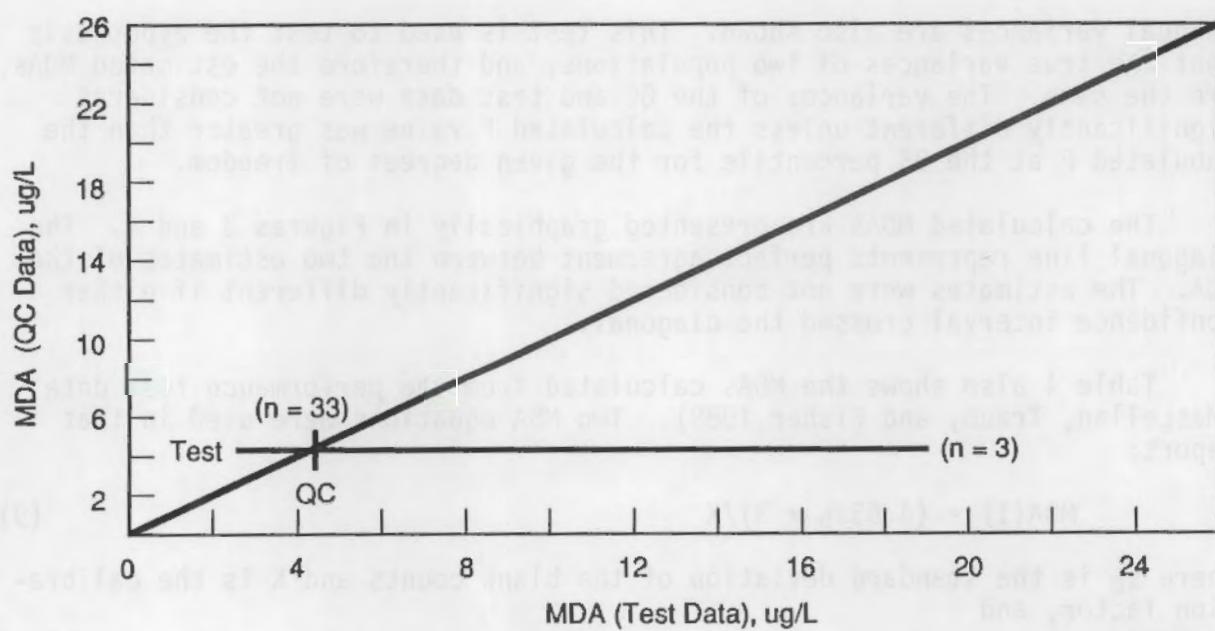


FIGURE 4. Laboratory B Natural Uranium MDAs

$s_B = \sqrt{2 \cdot s_B}$). The MDA(2) values from that report should therefore be interpreted as

$$MDA(2) = 4.65 \cdot \sqrt{2 \cdot s_B / K} \quad (11)$$

When Equations (9) and (11) are both solved for s_B and set equal to each other, the new equation may be solved for K (calibration factor), as follows:

$$K = 3 / [MDA(1) - MDA(2) / \sqrt{2}] \quad (12)$$

The MDA values in Appendix F of the performance test report (MacLellan, Traub, and Fisher 1988; refer to Appendix B of this report) were used with the above equations to recalculate the MDA using the methods of this report. For fluorometric analysis of uranium, the gain of the fluorometer is usually set so that the calibration factor equals one. The units (μg) are therefore read out directly and Equation (12) is not needed.

The variances of the QC and performance test blank data, for both laboratories, are not significantly different as measured by the F test for unequal variances. The MDAs estimated by the performance test and QC data therefore are also not significantly different. The confidence intervals for the performance-test-estimated MDA are larger due to the small size of the data set. Although not significantly different, the MDA estimates for Laboratory A by the QC data are about twice the MDA using the test data. This difference is most likely due to the composition of the blanks analyzed. The performance test used an artificial matrix with a water base and the samples did not have any added uranium in the blanks. The QC blanks for Laboratory A were natural urine and therefore contained natural uranium from environmental sources. The variability for this environmental activity was significantly greater than the variability for the artificial blanks and therefore raised the MDA accordingly.

ANSI N13.30 specifies that the acceptable MDA for natural uranium is 5 $\mu\text{g}/\text{L}$. Both laboratories would pass this criterion using the equations described in this report, although with the small sample size used for the performance test the calculated MDA for Laboratory B would have almost a 50% probability of being greater than the criterion (see Table 4).

238Pu in Urine

The 238Pu QC data from Laboratories A and B are listed in Appendix C. One result from Laboratory A was deleted from the data set as an outlier because it was greater than three standard deviations from the mean value. The data set for Laboratory B contained fewer than 26 members and the Dixon criterion for outliers was used (Snedecor and Cochran 1967). This test also resulted in the deletion of one result from Laboratory B. The data were again plotted in relation to the Z value, $(x - \mu) / \sigma$ (see Figures 5 and 6). Data from both laboratories failed the test for Poisson distribution at the 5% level. The clumping of results around the means is indicative of bias in the procedures for both laboratories. Standard deviations estimated directly from Figures 5 and 6 suggest that the calculated MDA is about 25% low for Laboratory A and unaffected for Laboratory B.

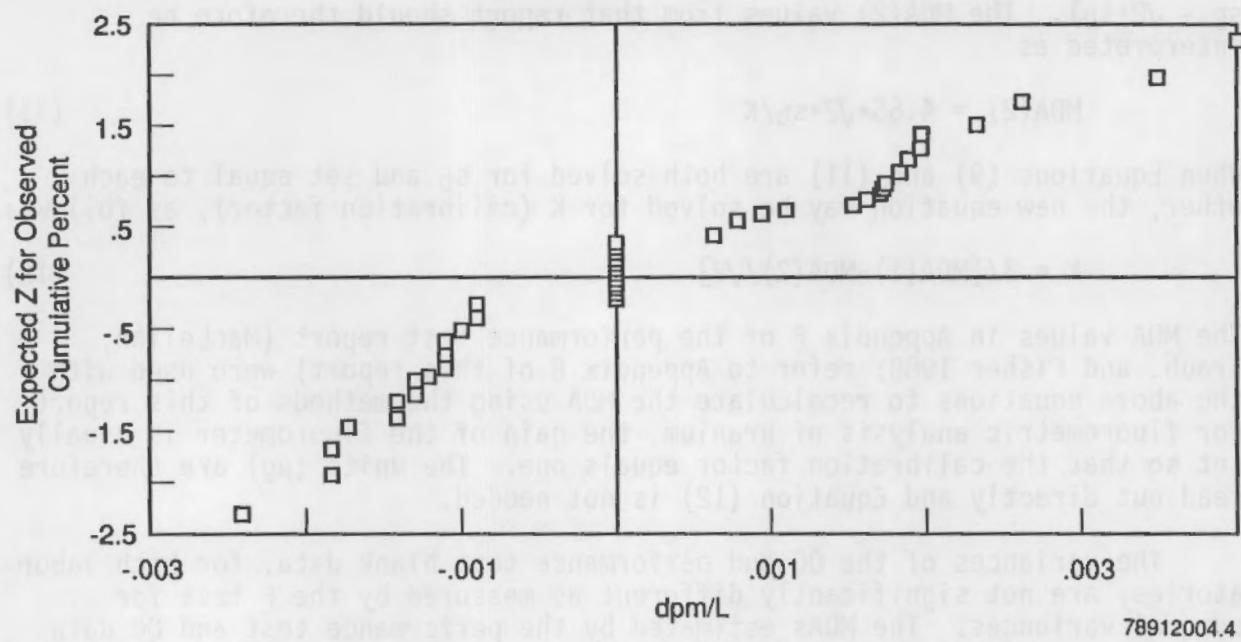


FIGURE 5. Laboratory A 238Pu Cumulative Probability

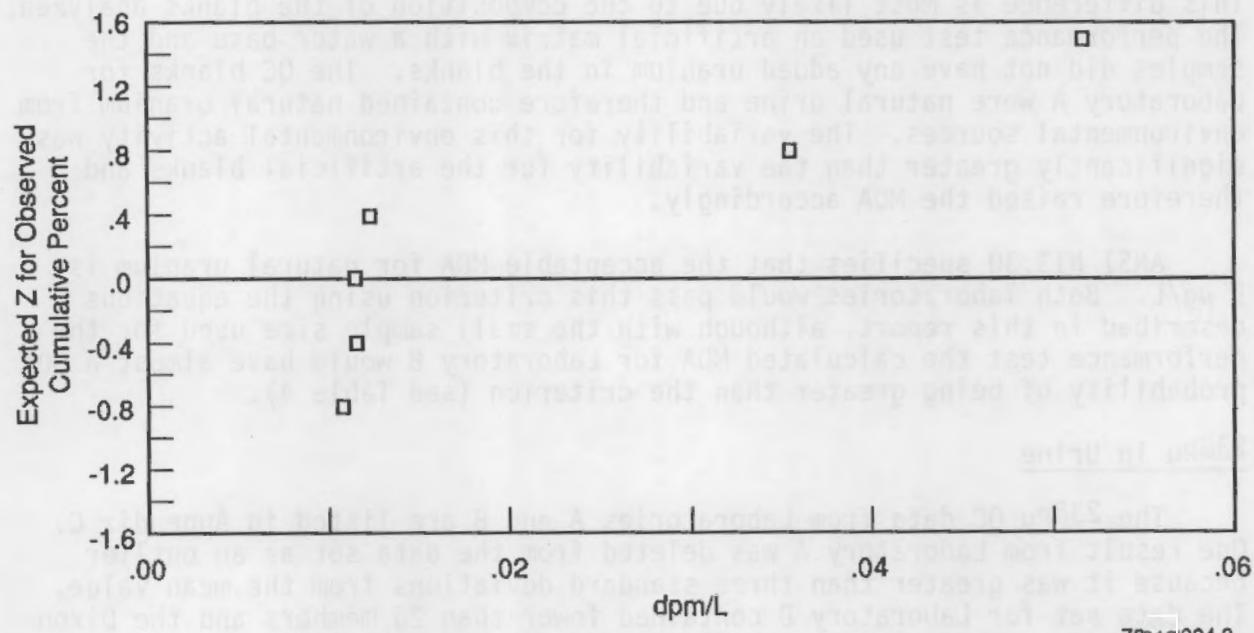


FIGURE 6. Laboratory B 238Pu Cumulative Probability

The confidence interval for the ^{238}Pu MDA was calculated using the following equation:

$$\text{MDA} = [4.65 \cdot s_b \cdot (\chi^2 / (n-1))^{\frac{1}{2}}] / [1 + B_r] \quad (13)$$

The MDAs calculated using Equation (13) and the data from Appendix C are shown in Table 5. The table also shows the MDAs calculated from the performance test data (MacLellan, Traub, and Fisher 1988; refer to Appendix B) in a manner similar to that described for the natural uranium samples. The calculated MDAs are represented graphically in Figures 7 and 8.

The MDAs estimated by the performance test and QC data for each laboratory are not significantly different at the 5% level as measured by the F test for unequal variances. The confidence intervals for the MDAs both overlap, further supporting the correlation of the estimates.

Although the QC and test data standard deviations are not significantly different, it is unusual for the standard deviation for the QC data ($n = 49$) to be more than three times greater than the test data standard deviation. This is thought to result from combining blank count data from two groups of detectors with significantly different background levels. One group of detectors has a very low background that is nearly zero; the other group of detectors has a slightly higher background. The pooled standard deviation of these counts is larger than the standard deviation for either group and the MDA estimated from the data is therefore inflated.

TABLE 5. ^{238}Pu Minimum Detectable Amounts

<u>n</u>	<u>B_r</u>	<u>s_b, pCi/L</u>	238Pu MDAs		
			<u>5%</u>	<u>Mean</u>	<u>95%</u>
<u>Laboratory A</u>					
QC Data	49	--	0.0010	0.0042	0.0049
Test Data	3	-0.052	0.0003	0.0009	0.0015
Calculated F: 11.11 F _{0.05} (48,2): 19.5					
<u>Laboratory B</u>					
QC Data	7	--	0.0178	0.057	0.083
Test Data	3	-0.003	0.0401	0.109	0.187
Calculated F: 5.08 F _{0.05} (2,6): 5.141					

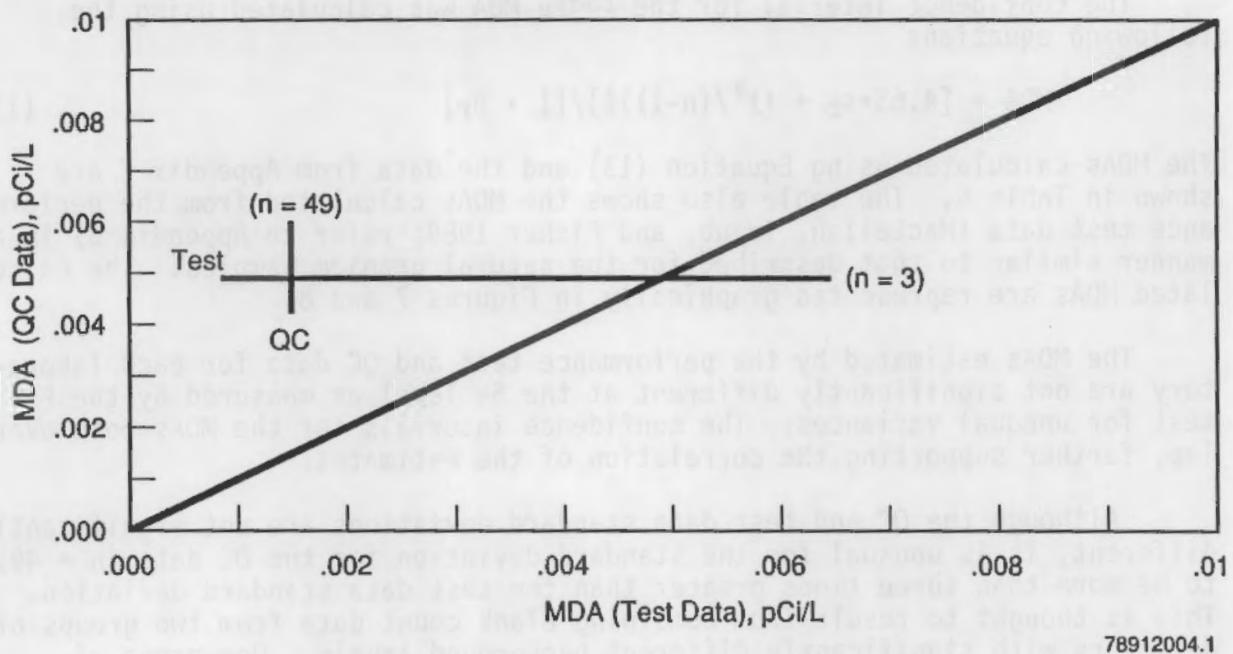


FIGURE 7. Laboratory A ^{238}Pu MDAs (90% confidence intervals)

78912004.1

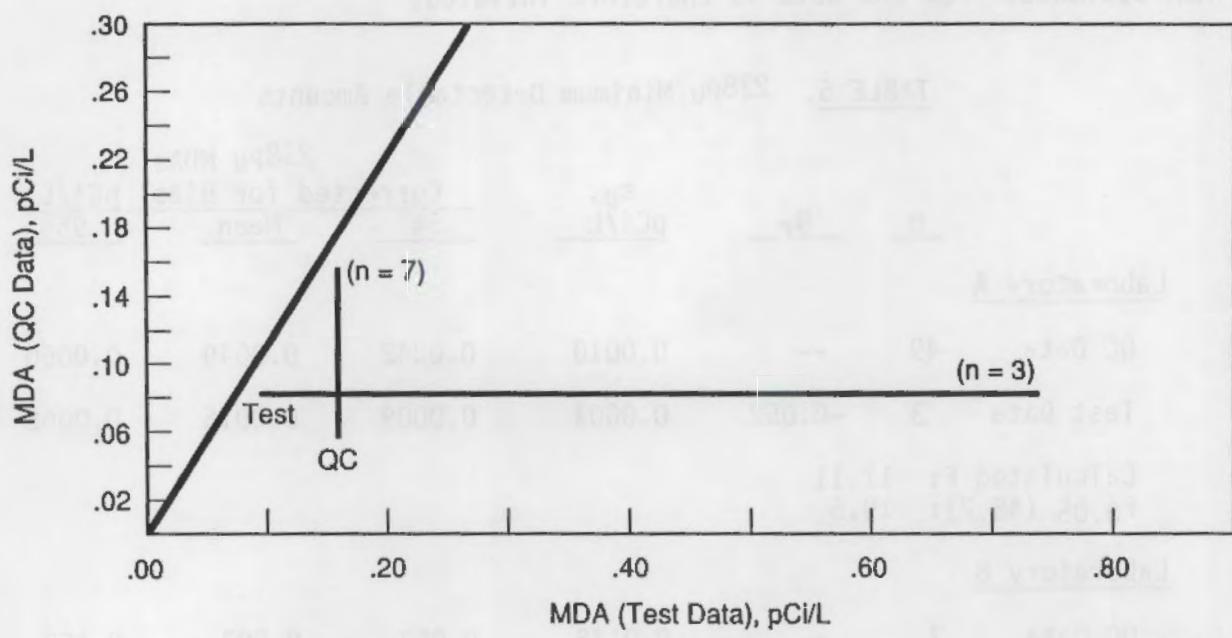


FIGURE 8. Laboratory B ^{238}Pu MDAs (90% confidence intervals)

ANSI N13.30 specifies that the acceptable MDA for ^{238}Pu is 0.06 pCi/L. Laboratory A would pass this criterion using the equations described in this report. Laboratory B would not pass the MDA criterion based on the performance test data. From the QC data it may be inferred that there is only about a 5% chance that the true MDA is 0.06 $\mu\text{g}/\text{L}$ or less.

IN VIVO LABORATORIES

Two in vivo bioassay laboratories (Laboratory C and D) were also selected from the list of past performance test participants for further study. Appropriate laboratory personnel were contacted and asked to supply QC data consisting of bioassay gamma spectra for 10 individuals considered free from contamination. The analyses selected for further study were for estimation of ^{54}Mn and ^{144}Ce in the lung. The blank spectra were used to calculate an MDA for each analysis, and the MDAs from the QC data were compared with the MDAs calculated from performance test data. The blank spectra from Laboratories C and D are shown in Figures 9 and 10. Because each spectral peak is naturally paired with its baseline, distributions were assumed to be Poisson. Cumulative probability plots for Laboratory C and D are shown in Figures 11, 12, 13 and 14.

The determination of MDAs for in vivo analyses is complicated by the features of the software programs used for data analysis. An important parameter used by many software programs is the sensitivity factor. When the operator changes the value of this parameter, it is equivalent to changing the α probability of false non-detection. In vivo laboratories often increase this parameter above the 5% level to compensate for the cumulative probability of a false positive when multiple peaks are scanned in the same spectrum. When the α and β levels are not set at the same value, the solution to Equation (4) is more complicated, as follows:

$$\text{MDC} = L_c + (k_\beta^2/2) \{ 1 + (1 + 4L_c/k_\beta^2 + 4L_c^2/k_\beta^2 \cdot k_\alpha^2)^{\frac{1}{2}} \} \quad (14)$$

where L_c is the decision level ($k_\alpha s_0$). When L_c is set to 3σ , the cumulative probability of a false positive result is limited to 5% for up to 40 individual peaks.

The MDA equivalent of Equation (14) is

$$\text{MDA} = [L_c + (k_\beta^2/2) \{ 1 + (1 + 4L_c/k_\beta^2 + 4L_c^2/k_\beta^2 \cdot k_\alpha^2)^{\frac{1}{2}} \}] / [KT \cdot (1 + Br)] \quad (15)$$

and when k_α is 3 and k_β is 1.645 the equation reduces to

$$\text{MDA} = [3 \cdot s_0 + 1.35 \{ 1 + (1 + 4.43 \cdot s_0 + 1.48 \cdot f^{\frac{1}{2}}) \}] / [KT \cdot (1 + Br)] \quad (16)$$

For this study, the standard deviation of the baseline (s_b) in the region of interest of the spectrum was estimated in two ways: 1) by the square root of the average sum of the channels for the blank spectra (Poisson), and 2) by the calculated standard deviation for the sums (Gaussian). The standard deviations for the QC data were then compared with the results obtained from the second round of in vivo bioassay performance

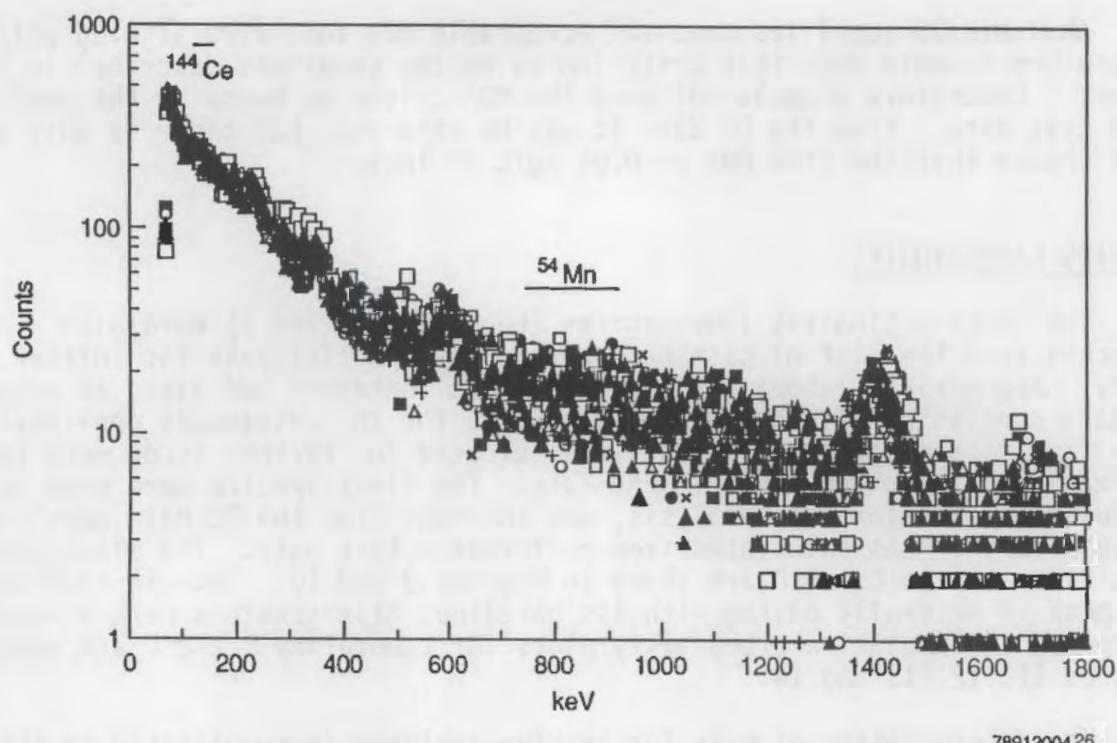


FIGURE 9. Laboratory C Blank Gamma Spectra

78912004.26

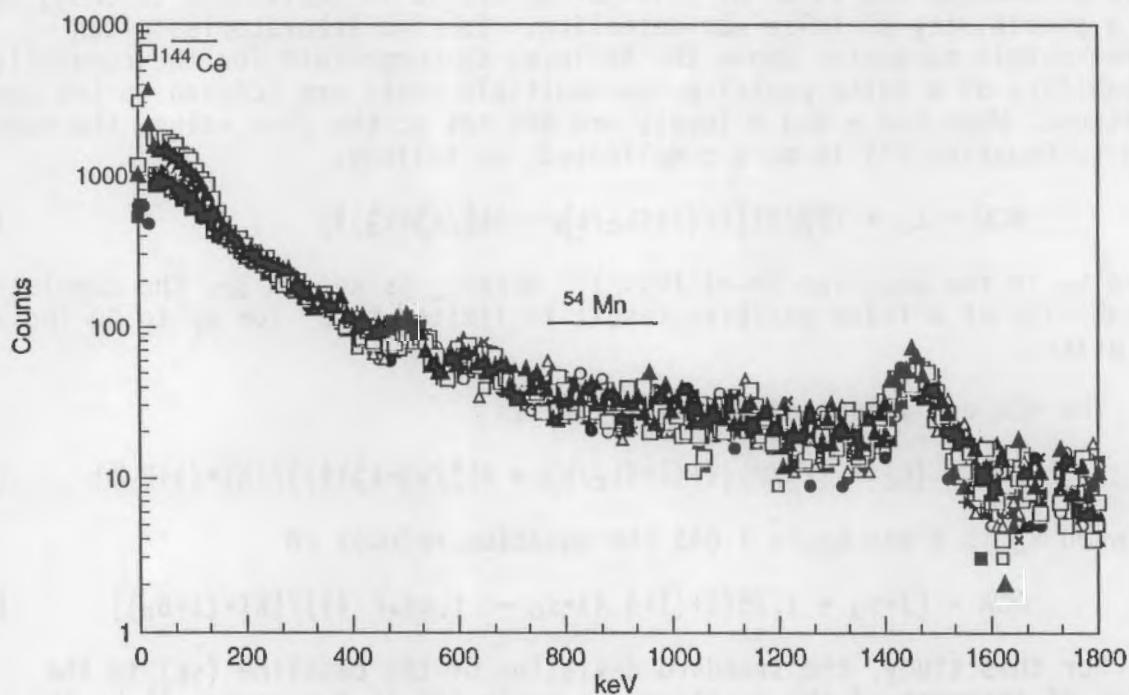


FIGURE 10. Laboratory D Blank Gamma Spectra

78912004.25

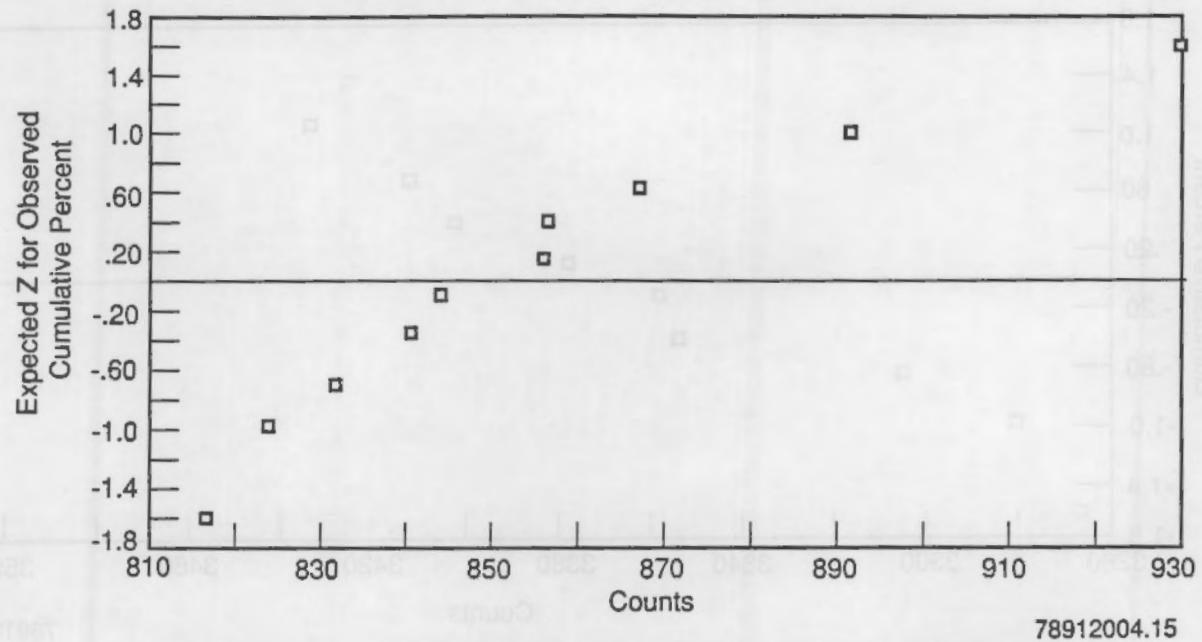


FIGURE 11. Laboratory C ^{54}Mn Cumulative Probability

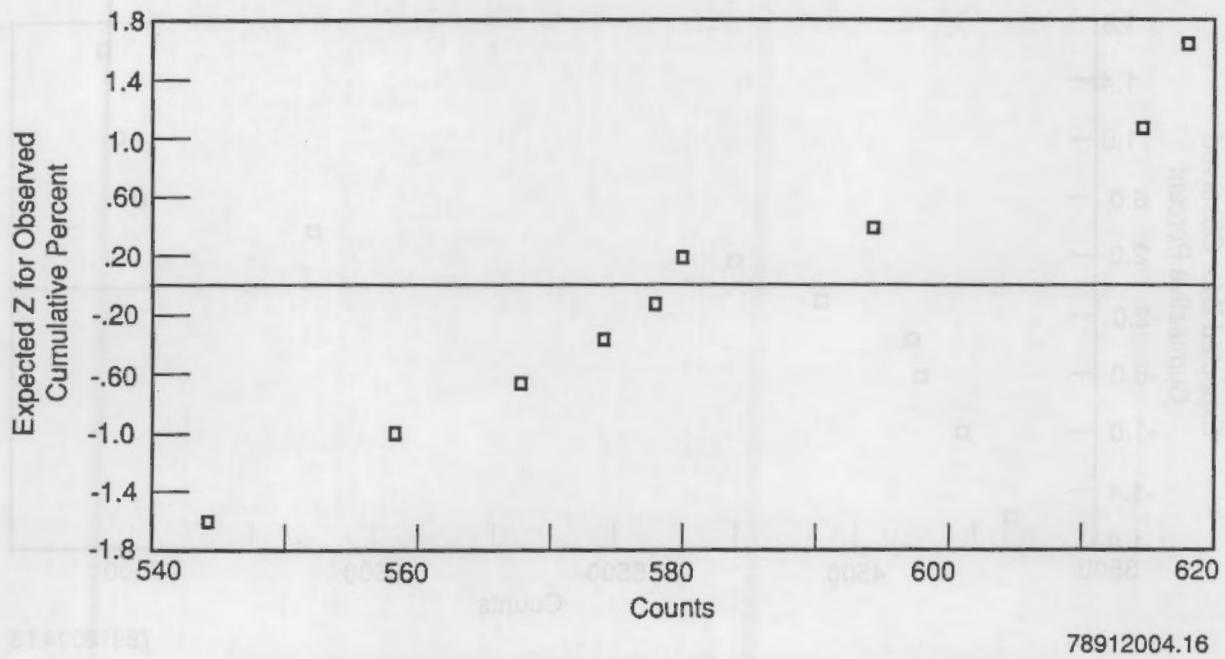


FIGURE 12. Laboratory D ^{54}Mn Cumulative Probability

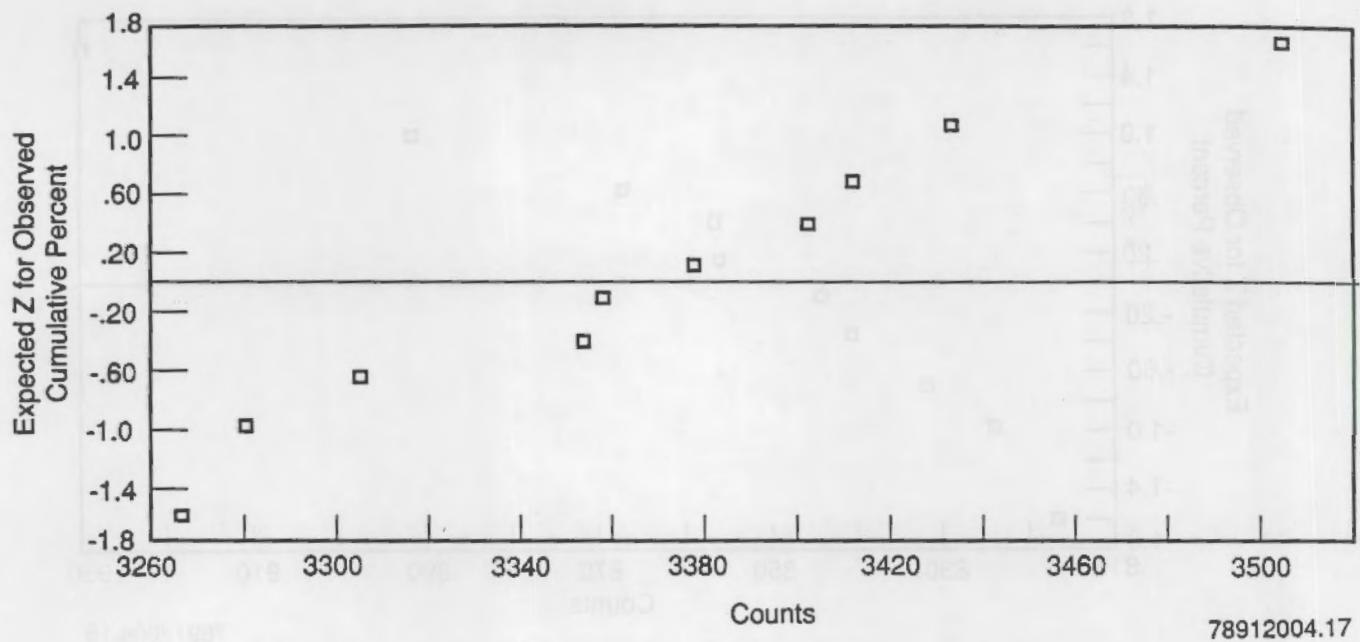


FIGURE 13. Laboratory C ^{144}Ce Cumulative Probability

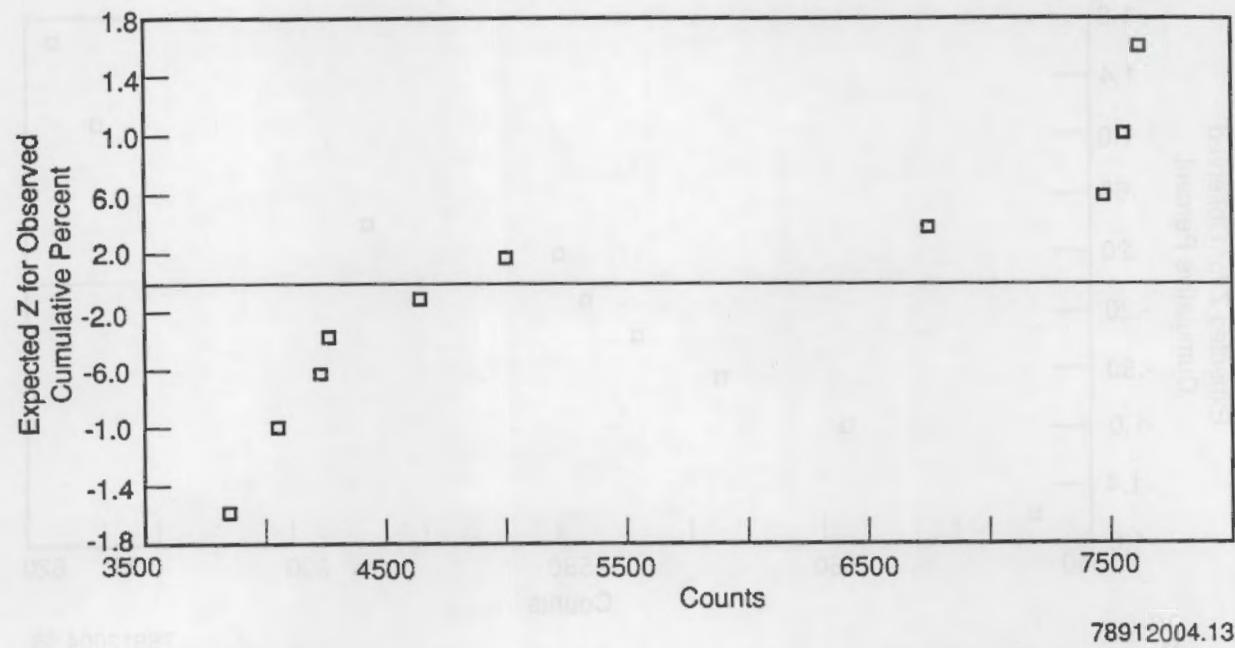


FIGURE 14. Laboratory D ^{144}Ce Cumulative Probability

tests recently conducted by PNL (see Appendix D). Phantom preparation for the second round of performance tests was similar to preparation for the first round of testing (Robinson et al. 1986). The results of the second round of in vivo performance tests will be published in a future PNL report.

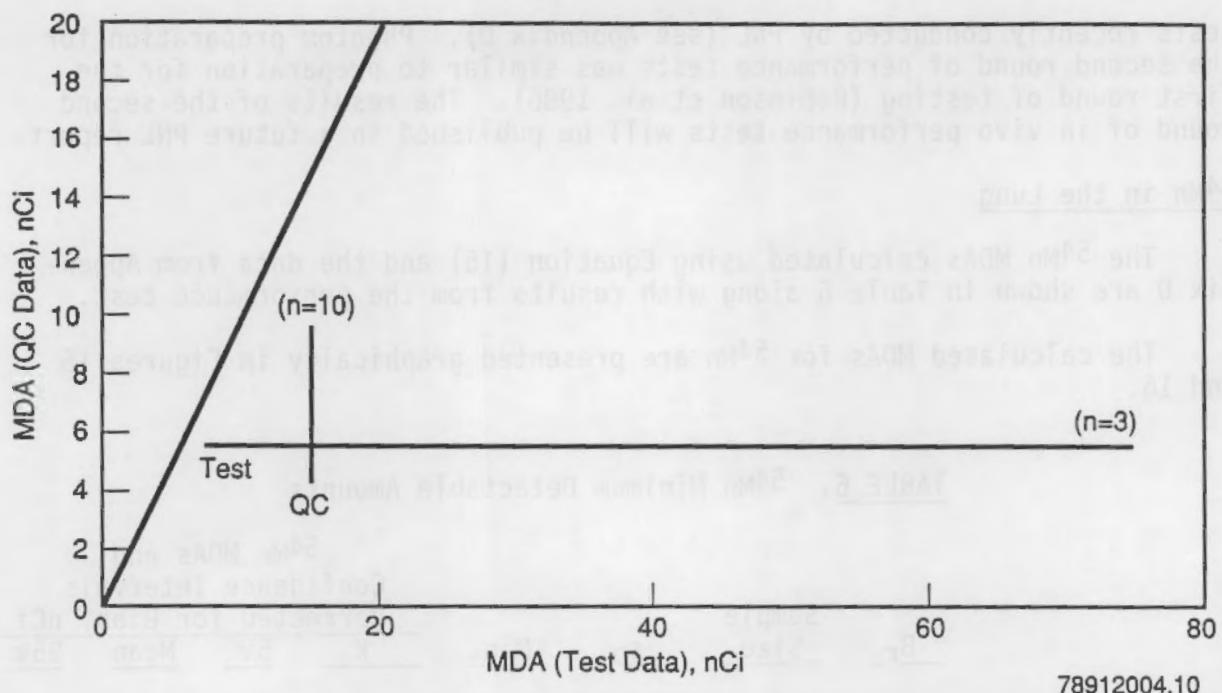
54Mn in the Lung

The ^{54}Mn MDAs calculated using Equation (16) and the data from Appendix D are shown in Table 6 along with results from the performance test.

The calculated MDAs for ^{54}Mn are presented graphically in Figures 15 and 16.

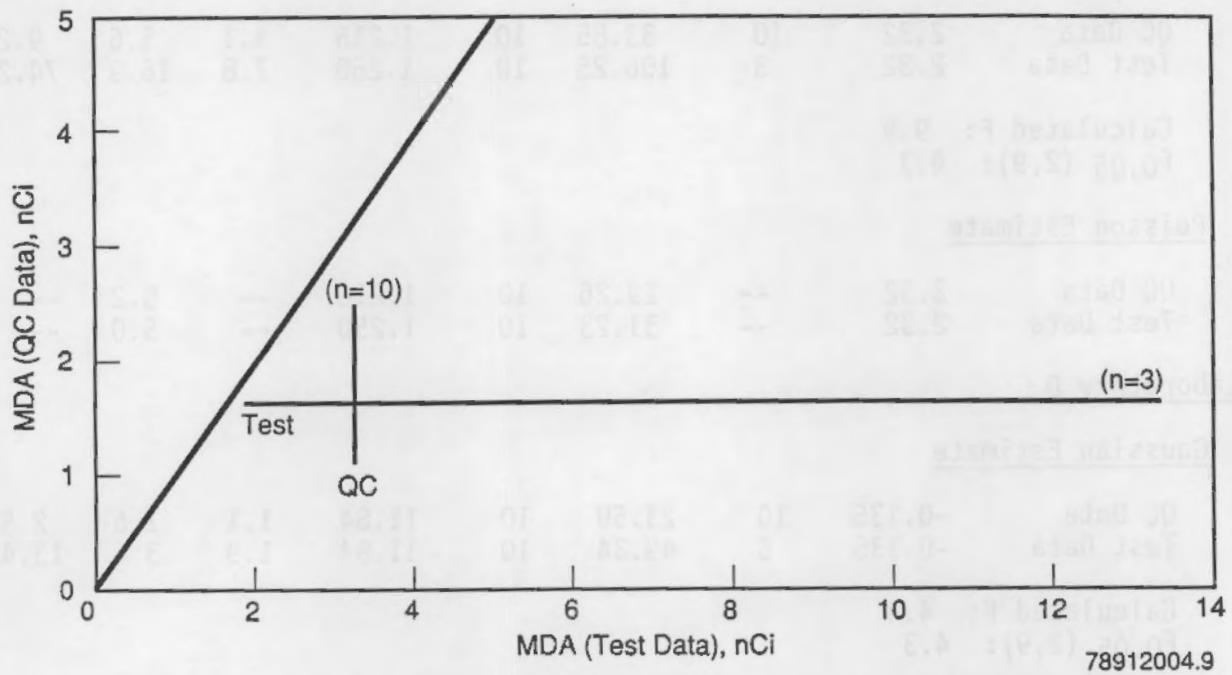
TABLE 6. ^{54}Mn Minimum Detectable Amounts

<u>Br</u>	<u>Sample Size</u>	<u>sb</u>	<u>Min.</u>	54Mn MDAs and Confidence Intervals Corrected for Bias, nCi						
				<u>K</u>	<u>5%</u>	<u>Mean</u>	<u>95%</u>			
<u>Laboratory C</u>										
<u>Gaussian Estimate</u>										
QC Data	2.32	10	33.85	10	1.216	4.1	5.6			
Test Data	2.32	3	106.25	10	1.250	7.8	16.9			
Calculated F: 9.9 F _{0.05 (2,9)} : 4.3										
<u>Poisson Estimate</u>										
QC Data	2.32	--	29.26	10	1.216	--	5.2			
Test Data	2.32	--	31.23	10	1.250	--	5.0			
<u>Laboratory D</u>										
<u>Gaussian Estimate</u>										
QC Data	-0.135	10	23.59	10	11.84	1.1	1.6			
Test Data	-0.135	5	49.34	10	11.84	1.9	3			
Calculated F: 4.4 F _{0.05 (2,9)} : 4.3										
<u>Poisson Estimate</u>										
QC Data	-0.135	--	24.15	10	11.84	--	1.6			
Test Data	-0.135	--	24.31	10	11.84	--	1.6			



78912004.10

FIGURE 15. Laboratory C ^{54}Mn MDAs (90% confidence intervals)



78912004.9

FIGURE 16. Laboratory D ^{54}Mn MDAs (90% confidence intervals)

For both Laboratories C and D, the standard deviation estimated from the replicate counts is significantly larger than the other estimate of the standard deviation. These differences are significant at the 99% and 95% levels, respectively. The differences are believed to result partially from the application of Gaussian statistics where a Poisson distribution is more appropriate.

The replicate estimated Gaussian standard deviation includes the uncertainty components that result from changes between analyses. These uncertainties should not be included when the peak count is paired with the baseline count from the same spectrum. The probability of a error in the variance estimate is largest when the number of replicates is small, as was the case with the performance test.

144Ce in the Lung

The ^{144}Ce MDAs calculated using Equation (16) and the data from Appendix C are shown in Table 7 along with results from the performance test.

The calculated MDAs for ^{144}Ce are presented graphically in Figures 17 and 18.

The QC data and test data estimates of the Poisson-based blank standard deviation are not significantly different for either laboratory, and the QC data estimate for Laboratory C is not significantly different from the Poisson-based estimates. However, the QC data for Laboratory D have a much larger standard deviation than the Poisson estimates.

Review of Figure 10 reveals a split in the baseline data in the ^{144}Ce region of interest. This split is most likely due to a change in the response of the instrumentation electronics. The pooled standard deviation of the two subpopulations is larger than the standard deviation for either group and the MDA estimated from the data is therefore inflated. The test estimated standard deviations for both laboratories are again significantly larger than the Poisson estimates, similar to the ^{54}Mn data.

TABLE 7. ^{144}Ce Minimum Detectable Amounts

<u>Laboratory C</u>	<u>Br</u>	<u>Sample Size</u>	<u>sb</u>	<u>Min.</u>	<u>^{144}Ce MDAs and Confidence Intervals</u>				
					<u>Corrected for Bias, nCi</u>	<u>K</u>	<u>5%</u>	<u>Mean</u>	<u>95%</u>
<u>Gaussian Estimate</u>									
QC data	1.93	10	73.55	10	0.242	50.3	68.7	112.6	
Test data	1.93	3	576.05	10	0.240	311.7	538.8	2371.7	
Calculated F: 61.3									
F _{0.05} (2,9): 4.3									
<u>Poisson Estimate</u>									
QC data	1.93	-	58.15	10	0.242	-	54.4	-	
Test data	1.93	-	60.92	10	0.242	-	57.5	-	
<u>Laboratory D</u>									
<u>Gaussian Estimate</u>									
QC data	0.126	10	1587.16	10	13.76	49.2	67.3	110.7	
Test data	0.126	5	150.30	10	13.76	3.7	6.4	28.1	
Calculated F: 111.5									
F _{0.05} (9,2): 19.4									
<u>Poisson Estimate</u>									
QC data	0.126	-	74.42	10	13.76	-	3.2	-	
Test data	0.126	-	84.01	10	13.76	-	3.6	-	

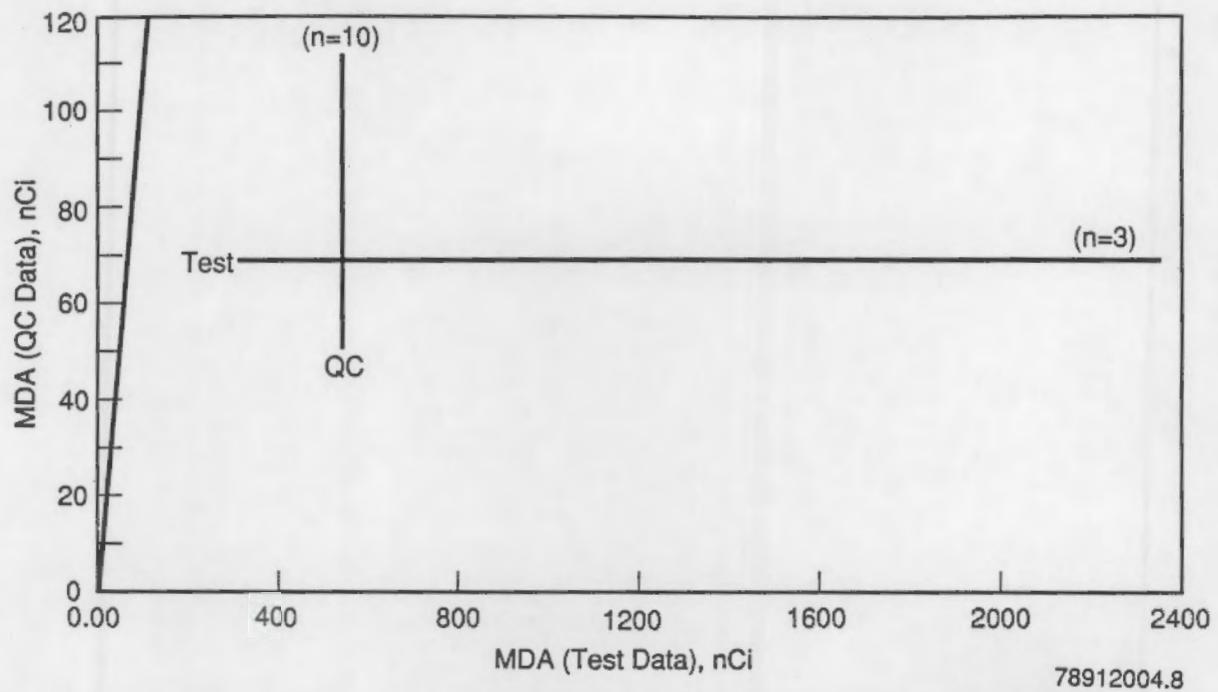


FIGURE 17. Laboratory C ^{144}Ce MDAs (90% confidence intervals)

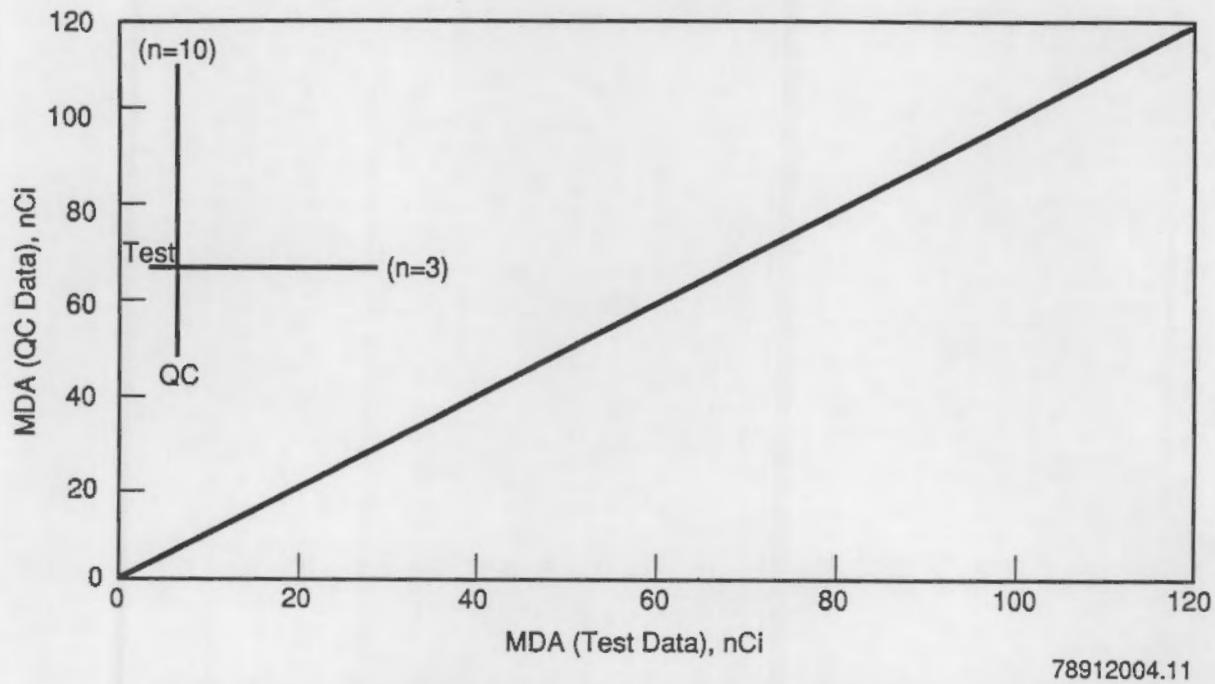


FIGURE 18. Laboratory D ^{144}Ce MDAs (90% confidence intervals)



FIGURE 17. Polarization C NACe MOs (80# count/dose intervals)

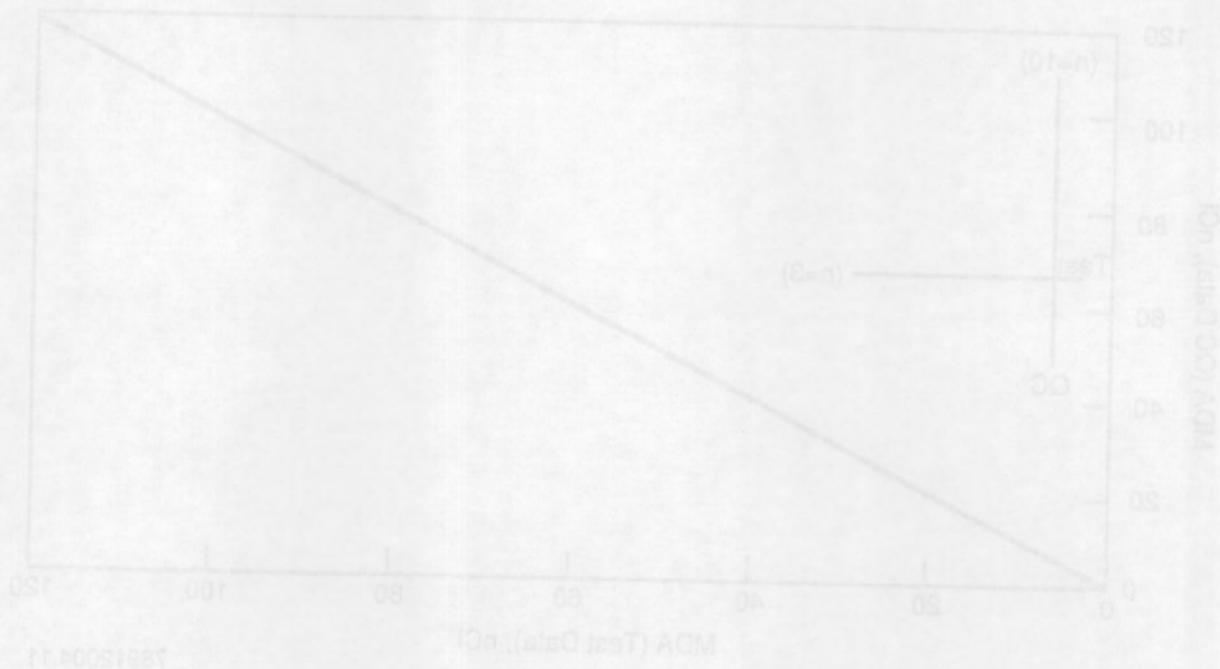


FIGURE 18. Polarization D NACe MOs (80# count/dose intervals)

CONCLUSIONS AND RECOMMENDATIONS

A relationship between the performance test MDA estimates and the QC data has been demonstrated. However, it is often necessary to examine the QC data to identify important characteristics of the blank distribution that will affect the MDA calculation. Characteristics such as unequal variances of detectors, unstable electronics, and paired samples must all be considered. The MDA equation must be based on the analysis and calculational methods of the procedure evaluated. No single MDA equation will be appropriate for all analyses.

Even when the correct MDA equation is applied, the MDA calculated will have a relatively large confidence interval when relatively few replicates are used to estimate the standard deviation. At least 13 replicates are needed to limit to 2 the ratio of the upper to lower bound of the 90% confidence interval (Currie 1984). For this reason, a relatively precise estimate of the MDA is generally only available when Poisson statistics may be applied.

With the above performance test limitations in mind, the following recommendations are made for determination of the MDA in conjunction with draft ANSI N13.30 performance testing.

- The bioassay laboratory's own QC data should be used for the MDA calculation in preference to the small data set available from performance testing.
- The MDA equation should be designed specifically for the measurement process being evaluated (e.g., fluorometry, radioactivity counting, *in vivo* gamma counting). If generic MDA equations are developed, the assumptions used should be verified whenever one is applied.
- Poisson statistics should be assumed for the MDA calculation whenever the Poisson distribution is not rejected for the available data.
- If Poisson statistics are rejected, the standard deviation should be estimated from replicates and a confidence interval should be calculated for the MDA. The laboratory should not be failed if the lower 5% bound of the confidence interval is less than the MDA criterion of draft ANSI N13.30. This approach is recommended because of the inherent uncertainty of the replicate-based MDA estimate.

The premise that performance testing alone cannot provide all the information necessary to make an accurate estimate of the measurement process MDA is common to all of the above recommendations. Review of the laboratory's QC data and the entire measurement procedure will be necessary also.

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APPENDIX A

NATURAL URANIUM LABORATORY QUALITY CONTROL DATA

APPENDIX A

NATURAL URANIUM LABORATORY QUALITY CONTROL DATA

The natural uranium quality control data for Laboratories A and B are listed in Table A.1.

TABLE A.1. Natural Uranium Laboratory Quality Control Data

Laboratory A(a)				Laboratory B(b)			
Result	Rank	Cumulative Percent	Z	Result	Rank	Cumulative Percent	Z
0.0071	1	0.017857	-2.1	0.516666	1	0.015151	-2.17
0.0109	2	0.053571	-1.61	0.536538	2	0.045454	-1.69
0.0141	3	0.089285	-1.35	0.996428	3	0.075757	-1.435
0.0144	4	0.125	-1.15	0.996428	4	0.106060	-1.245
0.0144	5	0.160714	-0.965	1.033333	5	0.136363	-1.1
0.0162	6	0.196428	-0.855	1.033333	6	0.166666	-0.965
0.0171	7	0.232142	-0.73	1.073076	7	0.196969	-0.852
0.0173	8	0.267857	-0.62	1.073076	8	0.227272	-0.745
0.019	9	0.303571	-0.515	1.116	9	0.257575	-0.65
0.0195	10	0.339285	-0.423	1.55	10	0.287878	-0.558
0.0196	11	0.375	-0.319	1.609615	11	0.318181	-0.475
0.0198	12	0.410714	-0.227	1.609615	12	0.348484	-0.39
0.0199	13	0.446428	-0.135	1.609615	13	0.378787	-0.306
0.0206	14	0.482142	-0.045	1.609615	14	0.409090	-0.23
0.021	15	0.517857	0.045	1.609615	15	0.439393	-0.152
0.0219	16	0.553571	0.135	1.74375	16	0.469696	-0.0753
0.0222	17	0.589285	0.227	1.74375	17	0.5	0
0.024	18	0.625	0.319	2.146153	18	0.530303	0.0753
0.0246	19	0.660714	0.423	2.146153	19	0.560606	0.152
0.0261	20	0.696428	0.515	2.146153	20	0.590909	0.23
0.0355	21	0.732142	0.62	2.232	21	0.621212	0.306
0.0365	22	0.767857	0.73	2.232	22	0.651515	0.39
0.0378	23	0.803571	0.855	2.325	23	0.681818	0.475
0.0386	24	0.839285	0.965	2.426086	24	0.712121	0.558
0.0477	25	0.875	1.15	2.7	25	0.742424	0.65
0.05	26	0.910714	1.35	2.79	26	0.772727	0.745
0.0562	27	0.946428	1.61	2.79	27	0.803030	0.852
0.29	28	0.982142	2.1	2.79	28	0.833333	0.965
				3.4875	29	0.863636	1.1
				3.616666	30	0.893939	1.245
				4.292307	31	0.924242	1.435
				4.464	32	0.954545	1.69
				4.8825	33	0.984848	2.17

(a) For Laboratory A: Mean = 0.034 and SD = 0.052
 One outlier removed: Mean = 0.025 and SD = 0.012
 (b) For Laboratory B: Mean = 2.1 and SD = 1.1

APPENDIX A

NATIONAL URANIUM LABORATORY QUALITY CONTROL DATA

The following narrative quality control data for Laboratory Quality Control A and B are listed in Table A.1.

TABLE A.1. National Uranium Laboratory Quality Control Data

S	Sample	Constitutive	Sporadic (a)			Sporadic (a)		
			Percent	Rank	Percent	Rank	Percent	Rank
11.5	11.0121	0.216028	1	-5.1	0.011252	1	0.00211	0
11.0	0.011252	0.216028	2	-1.0	0.022021	2	0.01010	0
11.422	0.022021	0.216028	3	-1.2	0.033251	3	0.01010	0
11.548	0.033251	0.216028	4	-1.12	0.044458	4	0.01010	0
11.548	0.044458	0.216028	5	-1.12	0.055665	5	0.01010	0
11.1	0.055665	0.216028	6	-1.12	0.066872	6	0.01010	0
11.1	0.066872	0.216028	7	-0.28	0.078074	7	0.01010	0
11.1	0.078074	0.216028	8	-0.28	0.089275	8	0.01010	0
11.1	0.089275	0.216028	9	-0.28	0.100476	9	0.01010	0
11.1	0.100476	0.216028	10	-0.28	0.111678	10	0.01010	0
11.1	0.111678	0.216028	11	-0.28	0.122879	11	0.01010	0
11.1	0.122879	0.216028	12	-0.28	0.134081	12	0.01010	0
11.1	0.134081	0.216028	13	-0.28	0.145283	13	0.01010	0
11.1	0.145283	0.216028	14	-0.28	0.156484	14	0.01010	0
11.1	0.156484	0.216028	15	-0.28	0.167686	15	0.01010	0
11.1	0.167686	0.216028	16	-0.28	0.178888	16	0.01010	0
11.1	0.178888	0.216028	17	-0.28	0.180089	17	0.01010	0
11.1	0.180089	0.216028	18	-0.28	0.191291	18	0.01010	0
11.1	0.191291	0.216028	19	-0.28	0.202493	19	0.01010	0
11.1	0.202493	0.216028	20	-0.28	0.213695	20	0.01010	0
11.1	0.213695	0.216028	21	-0.28	0.224897	21	0.01010	0
11.1	0.224897	0.216028	22	-0.28	0.236099	22	0.01010	0
11.1	0.236099	0.216028	23	-0.28	0.247299	23	0.01010	0
11.1	0.247299	0.216028	24	-0.28	0.258499	24	0.01010	0
11.1	0.258499	0.216028	25	-0.28	0.269699	25	0.01010	0
11.1	0.269699	0.216028	26	-0.28	0.280899	26	0.01010	0
11.1	0.280899	0.216028	27	-0.28	0.292099	27	0.01010	0
11.1	0.292099	0.216028	28	-0.28	0.303299	28	0.01010	0
11.1	0.303299	0.216028	29	-0.28	0.314499	29	0.01010	0
11.1	0.314499	0.216028	30	-0.28	0.325699	30	0.01010	0
11.1	0.325699	0.216028	31	-0.28	0.336899	31	0.01010	0
11.1	0.336899	0.216028	32	-0.28	0.348099	32	0.01010	0
11.1	0.348099	0.216028	33	-0.28	0.359299	33	0.01010	0
11.1	0.359299	0.216028	34	-0.28	0.370499	34	0.01010	0
11.1	0.370499	0.216028	35	-0.28	0.381699	35	0.01010	0
11.1	0.381699	0.216028	36	-0.28	0.392899	36	0.01010	0
11.1	0.392899	0.216028	37	-0.28	0.404099	37	0.01010	0
11.1	0.404099	0.216028	38	-0.28	0.415299	38	0.01010	0
11.1	0.415299	0.216028	39	-0.28	0.426499	39	0.01010	0
11.1	0.426499	0.216028	40	-0.28	0.437699	40	0.01010	0
11.1	0.437699	0.216028	41	-0.28	0.448899	41	0.01010	0
11.1	0.448899	0.216028	42	-0.28	0.459999	42	0.01010	0
11.1	0.459999	0.216028	43	-0.28	0.471199	43	0.01010	0
11.1	0.471199	0.216028	44	-0.28	0.482399	44	0.01010	0
11.1	0.482399	0.216028	45	-0.28	0.493599	45	0.01010	0
11.1	0.493599	0.216028	46	-0.28	0.504799	46	0.01010	0
11.1	0.504799	0.216028	47	-0.28	0.515999	47	0.01010	0
11.1	0.515999	0.216028	48	-0.28	0.527199	48	0.01010	0
11.1	0.527199	0.216028	49	-0.28	0.538399	49	0.01010	0
11.1	0.538399	0.216028	50	-0.28	0.549599	50	0.01010	0
11.1	0.549599	0.216028	51	-0.28	0.560799	51	0.01010	0
11.1	0.560799	0.216028	52	-0.28	0.571999	52	0.01010	0
11.1	0.571999	0.216028	53	-0.28	0.583199	53	0.01010	0
11.1	0.583199	0.216028	54	-0.28	0.594399	54	0.01010	0
11.1	0.594399	0.216028	55	-0.28	0.605599	55	0.01010	0
11.1	0.605599	0.216028	56	-0.28	0.616799	56	0.01010	0
11.1	0.616799	0.216028	57	-0.28	0.627999	57	0.01010	0
11.1	0.627999	0.216028	58	-0.28	0.639199	58	0.01010	0
11.1	0.639199	0.216028	59	-0.28	0.650399	59	0.01010	0
11.1	0.650399	0.216028	60	-0.28	0.661599	60	0.01010	0
11.1	0.661599	0.216028	61	-0.28	0.672799	61	0.01010	0
11.1	0.672799	0.216028	62	-0.28	0.683999	62	0.01010	0
11.1	0.683999	0.216028	63	-0.28	0.695199	63	0.01010	0
11.1	0.695199	0.216028	64	-0.28	0.706399	64	0.01010	0
11.1	0.706399	0.216028	65	-0.28	0.717599	65	0.01010	0
11.1	0.717599	0.216028	66	-0.28	0.728799	66	0.01010	0
11.1	0.728799	0.216028	67	-0.28	0.739999	67	0.01010	0
11.1	0.739999	0.216028	68	-0.28	0.751199	68	0.01010	0
11.1	0.751199	0.216028	69	-0.28	0.762399	69	0.01010	0
11.1	0.762399	0.216028	70	-0.28	0.773599	70	0.01010	0
11.1	0.773599	0.216028	71	-0.28	0.784799	71	0.01010	0
11.1	0.784799	0.216028	72	-0.28	0.795999	72	0.01010	0
11.1	0.795999	0.216028	73	-0.28	0.807199	73	0.01010	0
11.1	0.807199	0.216028	74	-0.28	0.818399	74	0.01010	0
11.1	0.818399	0.216028	75	-0.28	0.829599	75	0.01010	0
11.1	0.829599	0.216028	76	-0.28	0.840799	76	0.01010	0
11.1	0.840799	0.216028	77	-0.28	0.851999	77	0.01010	0
11.1	0.851999	0.216028	78	-0.28	0.863199	78	0.01010	0
11.1	0.863199	0.216028	79	-0.28	0.874399	79	0.01010	0
11.1	0.874399	0.216028	80	-0.28	0.885599	80	0.01010	0
11.1	0.885599	0.216028	81	-0.28	0.896799	81	0.01010	0
11.1	0.896799	0.216028	82	-0.28	0.907999	82	0.01010	0
11.1	0.907999	0.216028	83	-0.28	0.919199	83	0.01010	0
11.1	0.919199	0.216028	84	-0.28	0.930399	84	0.01010	0
11.1	0.930399	0.216028	85	-0.28	0.941599	85	0.01010	0
11.1	0.941599	0.216028	86	-0.28	0.952799	86	0.01010	0
11.1	0.952799	0.216028	87	-0.28	0.963999	87	0.01010	0
11.1	0.963999	0.216028	88	-0.28	0.975199	88	0.01010	0
11.1	0.975199	0.216028	89	-0.28	0.986399	89	0.01010	0
11.1	0.986399	0.216028	90	-0.28	0.997599	90	0.01010	0
11.1	0.997599	0.216028	91	-0.28	1.008799	91	0.01010	0
11.1	1.008799	0.216028	92	-0.28	1.019999	92	0.01010	0
11.1	1.019999	0.216028	93	-0.28	1.031199	93	0.01010	0
11.1	1.031199	0.216028	94	-0.28	1.042399	94	0.01010	0
11.1	1.042399	0.216028	95	-0.28	1.053599	95	0.01010	0
11.1	1.053599	0.216028	96	-0.28	1.064799	96	0.01010	0
11.1	1.064799	0.216028	97	-0.28	1.075999	97	0.01010	0
11.1	1.075999	0.216028	98	-0.28	1.087199	98	0.01010	0
11.1	1.087199	0.216028	99	-0.28	1.098399	99	0.01010	0
11.1	1.098399	0.216028	100	-0.28	1.109599	100	0.01010	0

(p) Lot Laboratory B: Mean = 0.992 and SD = 0.111
 (q) Lot Laboratory A: Mean = 0.992 and SD = 0.101
 (r) Lot Laboratory A: Mean = 0.992 and SD = 0.101

APPENDIX B

PACIFIC NORTHWEST LABORATORY IN VITRO PERFORMANCE TEST RESULTS

APPENDIX B

PACIFIC NORTHWEST LABORATORY IN VITRO PERFORMANCE TEST RESULTS

Table B.1 lists the results of the in vitro performance tests performed by Pacific Northwest Laboratory using natural uranium and ^{238}Pu analysis data from Laboratories A and B for evaluation. Quality control data were used to calculate the minimum detectable amounts for each analysis.

TABLE B.1. Pacific Northwest Laboratory In Vitro Performance Test Results

<u>Laboratory</u>	<u>Br</u>	<u>MDA, $\mu\text{g/L}$</u>	
		<u>MDA(1)</u>	<u>MDA(2)</u>
<u>Natural Uranium Blank Urine Data</u>			
A	-0.277	Insufficient data	0.0268
B	-0.142	Insufficient data	5.37
<u>^{238}Pu Blank Urine Count Data</u>			
A	-0.0521	0.00424	0.00177
B	-0.0027	0.504	0.264

Source: MacLellan et al. 1988; Appendix F

APPENDIX B

PARALLEL MORTINELT LABORATORY IN VITRO PERMEABILITY TEST RESULTS

Table B.1 gives the results of the parallel permeation tests described in Table B.1 of the Interlaboratory Comparison of In Vitro Permeability Test Results and 386a Appendix B data by parallel Mortinelt and 8 for comparison. Only counts data were used to show how comparable are the two methods for each substance.

TABLE B.1. PARALLEL MORTINELT LABORATORY IN VITRO PERMEABILITY TEST RESULTS

Sample	MDA (1)	MDA (2)	Parallel Mortinelt	386a
386a Glucagon count data				
8850.0	10500.0	10500.0	10500.0	A
235	235	235	235	B
386a Glucagon count data				
55100.0	55100.0	55100.0	55100.0	A
485.0	485.0	485.0	485.0	B

Source: Maclellan et al., 1989, Appendix B

APPENDIX C

238PU LABORATORY QUALITY CONTROL DATA

APPENDIX C

238PU LABORATORY QUALITY CONTROL DATA

The 238Pu quality control data for Laboratories A and B are listed in Table C.1.

TABLE C.1. 238Pu Laboratory Quality Control Data

Laboratory A(a)

<u>Result</u>	<u>Rank</u>	<u>Cumulative Percent</u>	<u>Z</u>	<u>Result</u>	<u>Rank</u>	<u>Cumulative Percent</u>	<u>Z</u>
-0.0024	1	0.01	-2.326	0	26	0.51	0.0251
-0.0018	2	0.03	-1.881	0	27	0.53	0.0753
-0.0018	3	0.05	-1.645	0	28	0.55	0.1257
-0.0017	4	0.07	-1.476	0	29	0.57	0.1764
-0.0014	5	0.09	-1.341	0	30	0.59	0.2275
-0.0014	6	0.11	-1.227	0	31	0.61	0.2793
-0.0013	7	0.13	-1.1264	0	32	0.63	0.3319
-0.0013	8	0.15	-1.036	0.00061	33	0.65	0.3853
-0.0012	9	0.17	-0.9542	0.00075	34	0.67	0.4399
-0.0011	10	0.19	-0.8779	0.00095	35	0.69	0.4959
-0.0011	11	0.21	-0.8064	0.00115	36	0.71	0.5534
-0.0011	12	0.23	-0.7388	0.0014	37	0.73	0.6128
-0.0010	13	0.25	-0.6745	0.0015	38	0.75	0.6745
-0.0009	14	0.27	-0.6128	0.0016	39	0.77	0.7388
-0.0009	15	0.29	-0.5534	0.00162	40	0.79	0.8064
0	16	0.31	-0.4959	0.00163	41	0.81	0.8779
0	17	0.33	-0.4399	0.00174	42	0.83	0.9542
0	18	0.35	-0.3853	0.00185	43	0.85	1.036
0	19	0.37	-0.3319	0.00195	44	0.87	1.1264
0	20	0.39	-0.2793	0.00197	45	0.89	1.227
0	21	0.41	-0.2275	0.0023	46	0.91	1.341
0	22	0.43	-0.1764	0.00255	47	0.93	1.476
0	23	0.45	-0.1257	0.0035	48	0.95	1.645
0	24	0.47	-0.0753	0.00399	49	0.97	1.881
0	25	0.49	-0.0251	0.00627	50	0.99	2.326

TABLE C.1. (contd)

Laboratory B(b)

Blank Counts	Instrument BKGD	Min.	dpm/pCi	dpm	pCi/L	Rank	Cumulative Percent	Z
2.0000	2	400	0.201	0.0000	0.000	1	0.0625	-1.53
2.0000	0	400	0.214	0.0233	0.011	2	0.1875	-0.89
3.0000	1	400	0.193	0.0259	0.012	3	0.3125	-0.49
2.0000	1	400	0.092	0.0271	0.012	4	0.4375	-0.152
4.0000	2	400	0.168	0.0297	0.013	5	0.5625	0.152
5.0000	1	400	0.125	0.0800	0.036	6	0.6875	0.49
12.0000	2	400	0.219	0.1143	0.052	7	0.8125	0.89
17.0000	1	400	0.121	0.3314	0.150	8	0.9375	1.53

(a) Mean = 0.00034

SD = 0.00165

 $s_b = SD/\sqrt{2} = 0.0012$

Data with one outlier removed

Mean = 0.00022

SD = 0.00142

 $s_b = 0.0010$

(b) Mean = 5.88 counts

SD = 5.59 counts

Mean = 0.036 pCi/L

SD = 0.049 pCi/L

Data with one outlier removed

Mean = 4.29 counts

SD = 3.59 counts

Mean = 0.0194 pCi/L

SD = 0.0178 pCi/L

APPENDIX D

PACIFIC NORTHWEST LABORATORY IN VIVO PERFORMANCE TEST RESULTS

APPENDIX D

PACIFIC NORTHWEST LABORATORY IN VIVO PERFORMANCE TEST RESULTS

Table D.1 lists the results of the second round of in vivo bioassay performance tests conducted by Pacific Northwest Laboratory using ^{54}Mn and ^{144}Ce blank phantom count data.

TABLE D.1. Pacific Northwest Laboratory In Vivo Performance Test Results

Laboratory	Test No.	Gross Counts	Time	Efficiency	Assay, nCi	Relative Bias		
						5%	Mean	95%
<u>54Mn Blank Phantom Count Data</u>								
C	1	943	10.0	1.160	3.7100	0.35	0.74	1.13
C	2	889	10.0	1.260	0.7100			
C	3	1094	10.0	1.330	1.0500			
D	1	654	10.0	11.840	-0.2500	-0.19	-0.13	-0.07
D	2	591	10.0	11.840	-0.0600			
D	3	623	10.0	11.840	0.1000			
D	4	526	10.0	11.840	0.3200			
D	5	568	10.0	11.840	0.3000			
<u>144Ce Blank Phantom Count Data</u>								
C	1	4206	10.0	0.240	23.3300	1.42	1.71	2.01
C	2	3079	10.0	0.240	24.5800			
C	3	3850	10.0	0.240	12.5000			
D	1	7092	10.0	13.760	0.9900	-0.09	0.13	0.35
D	2	6977	10.0	13.760	0.7700			
D	3	7162	10.0	13.760	0.6400			
D	4	6843	10.0	13.760	0.6500			
D	5	7218	10.0	13.760	1.2700			

APPENDIX D

BACULUS NORTHWEST LABORATORY IN VIVO PERLON-500 TEST RESULTS

TABLE D.1. Lists the results of the second round of *in vivo* process cell counts conducted by Pacific Northwest Laboratory under BACULUS Northwest contract number 00000000000000000000000000000000 and

TABLE D.1. *In vivo* bacterial count data, *in vivo* perlonaurea test results

Test	Sample No.	Eros Count	Time	Efficacy	Table D1a: <i>In vivo</i> bacterial count data	
					Assay	Qualitative Inference
C	1	1	10.0	0.01	3.5100	C
C	2	1	10.0	0.01	0.3100	C
C	3	1	10.0	0.01	1.0200	C
C	4	1	10.0	0.01	0.0200	C
C	5	1	10.0	0.01	0.0200	C
C	6	1	10.0	0.01	0.0200	C
C	7	1	10.0	0.01	0.0200	C
C	8	1	10.0	0.01	0.0200	C
C	9	1	10.0	0.01	0.0200	C
C	10	1	10.0	0.01	0.0200	C
C	11	1	10.0	0.01	0.0200	C
C	12	1	10.0	0.01	0.0200	C
C	13	1	10.0	0.01	0.0200	C
C	14	1	10.0	0.01	0.0200	C
C	15	1	10.0	0.01	0.0200	C
C	16	1	10.0	0.01	0.0200	C
C	17	1	10.0	0.01	0.0200	C
C	18	1	10.0	0.01	0.0200	C
C	19	1	10.0	0.01	0.0200	C
C	20	1	10.0	0.01	0.0200	C
C	21	1	10.0	0.01	0.0200	C
C	22	1	10.0	0.01	0.0200	C
C	23	1	10.0	0.01	0.0200	C
C	24	1	10.0	0.01	0.0200	C
C	25	1	10.0	0.01	0.0200	C
C	26	1	10.0	0.01	0.0200	C
C	27	1	10.0	0.01	0.0200	C
C	28	1	10.0	0.01	0.0200	C
C	29	1	10.0	0.01	0.0200	C
C	30	1	10.0	0.01	0.0200	C
C	31	1	10.0	0.01	0.0200	C
C	32	1	10.0	0.01	0.0200	C
C	33	1	10.0	0.01	0.0200	C
C	34	1	10.0	0.01	0.0200	C
C	35	1	10.0	0.01	0.0200	C
C	36	1	10.0	0.01	0.0200	C
C	37	1	10.0	0.01	0.0200	C
C	38	1	10.0	0.01	0.0200	C
C	39	1	10.0	0.01	0.0200	C
C	40	1	10.0	0.01	0.0200	C
C	41	1	10.0	0.01	0.0200	C
C	42	1	10.0	0.01	0.0200	C
C	43	1	10.0	0.01	0.0200	C
C	44	1	10.0	0.01	0.0200	C
C	45	1	10.0	0.01	0.0200	C
C	46	1	10.0	0.01	0.0200	C
C	47	1	10.0	0.01	0.0200	C
C	48	1	10.0	0.01	0.0200	C
C	49	1	10.0	0.01	0.0200	C
C	50	1	10.0	0.01	0.0200	C
C	51	1	10.0	0.01	0.0200	C
C	52	1	10.0	0.01	0.0200	C
C	53	1	10.0	0.01	0.0200	C
C	54	1	10.0	0.01	0.0200	C
C	55	1	10.0	0.01	0.0200	C
C	56	1	10.0	0.01	0.0200	C
C	57	1	10.0	0.01	0.0200	C
C	58	1	10.0	0.01	0.0200	C
C	59	1	10.0	0.01	0.0200	C
C	60	1	10.0	0.01	0.0200	C
C	61	1	10.0	0.01	0.0200	C
C	62	1	10.0	0.01	0.0200	C
C	63	1	10.0	0.01	0.0200	C
C	64	1	10.0	0.01	0.0200	C
C	65	1	10.0	0.01	0.0200	C
C	66	1	10.0	0.01	0.0200	C
C	67	1	10.0	0.01	0.0200	C
C	68	1	10.0	0.01	0.0200	C
C	69	1	10.0	0.01	0.0200	C
C	70	1	10.0	0.01	0.0200	C
C	71	1	10.0	0.01	0.0200	C
C	72	1	10.0	0.01	0.0200	C
C	73	1	10.0	0.01	0.0200	C
C	74	1	10.0	0.01	0.0200	C
C	75	1	10.0	0.01	0.0200	C
C	76	1	10.0	0.01	0.0200	C
C	77	1	10.0	0.01	0.0200	C
C	78	1	10.0	0.01	0.0200	C
C	79	1	10.0	0.01	0.0200	C
C	80	1	10.0	0.01	0.0200	C
C	81	1	10.0	0.01	0.0200	C
C	82	1	10.0	0.01	0.0200	C
C	83	1	10.0	0.01	0.0200	C
C	84	1	10.0	0.01	0.0200	C
C	85	1	10.0	0.01	0.0200	C
C	86	1	10.0	0.01	0.0200	C
C	87	1	10.0	0.01	0.0200	C
C	88	1	10.0	0.01	0.0200	C
C	89	1	10.0	0.01	0.0200	C
C	90	1	10.0	0.01	0.0200	C
C	91	1	10.0	0.01	0.0200	C
C	92	1	10.0	0.01	0.0200	C
C	93	1	10.0	0.01	0.0200	C
C	94	1	10.0	0.01	0.0200	C
C	95	1	10.0	0.01	0.0200	C
C	96	1	10.0	0.01	0.0200	C
C	97	1	10.0	0.01	0.0200	C
C	98	1	10.0	0.01	0.0200	C
C	99	1	10.0	0.01	0.0200	C
C	100	1	10.0	0.01	0.0200	C
C	101	1	10.0	0.01	0.0200	C
C	102	1	10.0	0.01	0.0200	C
C	103	1	10.0	0.01	0.0200	C
C	104	1	10.0	0.01	0.0200	C
C	105	1	10.0	0.01	0.0200	C
C	106	1	10.0	0.01	0.0200	C
C	107	1	10.0	0.01	0.0200	C
C	108	1	10.0	0.01	0.0200	C
C	109	1	10.0	0.01	0.0200	C
C	110	1	10.0	0.01	0.0200	C
C	111	1	10.0	0.01	0.0200	C
C	112	1	10.0	0.01	0.0200	C
C	113	1	10.0	0.01	0.0200	C
C	114	1	10.0	0.01	0.0200	C
C	115	1	10.0	0.01	0.0200	C
C	116	1	10.0	0.01	0.0200	C
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