44908

RESULTS OF ACUTE AND CHRONIC TOXICITY TESTING WITH SODIUM PERCHLORATE

Prepared for:

Armstrong Laboratory
AL/OEMH
2402 E Drive
Brooks AFB, Texas 78235-5114

Prepared by:

EA Engineering, Science, and Technology, Inc.
15 Loveton Circle
Sparks, Maryland 21152

November 1998 *EA Project 70003.10*

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Date

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1. INTRODUCTION

At the request of Armstrong Laboratory, EA Engineering, Science, and Technology performed acute and chronic toxicity tests with sodium perchlorate ($NaClO_4$) using selected freshwater and terrestrial test species. Acute toxicity tests were conducted with *Daphnia magna* (water flea), *Pimephales promelas* (fathead minnow), and *Eisenia foetida* (red worm) in order to assess the acute lethality of perchlorate to each test species. Chronic toxicity tests were performed with *Ceriodaphnia dubia* (water flea), *P. promelas*, and *Lactuca sativa* (buttercrunch lettuce). The objectives of the chronic toxicity testing were to assess the chronic lethality of perchlorate to the three test species and to determine the inhibition of reproduction (*C. dubia*) and growth, as biomass (*P. promelas* and *L. sativa*), of the test organisms as compared to the control.

Initial rangefinding toxicity testing was conducted with each test species in order to broadly assess the acute and chronic toxicity of perchlorate to the test species. Based on the results of these rangefinding tests, an appropriate concentration series for each test species was selected for conducting the definitive acute and chronic toxicity tests. This report summarizes the results of both the rangefinding and definitive acute and chronic toxicity testing.

2. METHODS AND MATERIALS

2.1 TEST MATERIAL

The test material was perchlorate (ClO_4), administered as sodium perchlorate ($NaClO_4$). Stocks of ClO_4 were prepared from reagent grade (99%+ pure) $NaClO_4$ and deionized water, and these stocks were used to dose the test solutions and soils for the acute and chronic toxicity tests.

2.2 TEST ORGANISMS

Daphnia magna (water flea) were raised in EA's Culture Facility in Sparks, Maryland using dilute mineral water (DMW) at 20°C as the culture media, with a 16-hour light/8-hour dark photoperiod. The cultures were fed daily in a manner described in the ASTM Standard Guide (1997a) and thinned as necessary to maintain maximum young production while inhibiting ephippia production. In addition to the normal feeding regime of a yeast/cereal leaves/trout chow suspension (YCT), the adults were provided with the algae *Selenastrum capricornutum*. The day before test initiation, gravid adults were segregated from the cultures to ensure that neonates (young) produced were less than 24 hours old for initiation of the acute toxicity tests. Neonates were fed YCT supplemented with algae prior to use in toxicity testing.

Pimephales promelas (fathead minnow) were also obtained from EA's Culture Facility. Brood organisms were maintained in recirculating dechlorinated tap water at 20°C in 10-gallon aquaria. For the chronic toxicity tests, eggs produced from the brood system were removed from the brood aquaria and placed into dilute mineral water at 25°C for the incubation period. Newly hatched larvae, less than 24 hours old, from lots FH 8-9/7-8 and FH 8-9/28-29 were used in the chronic rangefinding and chronic definitive toxicity testing, respectively. Juvenile organisms (up to 14 days old) were maintained in dechlorinated tap water at 20°C and were fed brine shrimp nauplii (*Artemia* sp., less than 24 hours old) a minimum of once daily. Prior to use in the acute toxicity tests, the juveniles were gradually acclimated to dilute mineral water. The *P. promelas*, lot FH 8-8/26-27 and lot FH 8-9/11-12, were 12-13 days old (hatched within single 24-hour periods) when used to initiate the acute rangefinding and acute definitive toxicity testing,

respectively.

Ceriodaphnia dubia were obtained from EA's Culture Facility. The *C. dubia* were cultured in dilute mineral water, and the cultures were kept in an environmentally controlled room at 25°C with a 16-hour light/8-hour dark photoperiod. Organisms were fed daily a suspension of yeast/cereal leaves/trout chow supplemented with the algae *Selenastrum capricornutum*, as described in US EPA (1993), and thinned as necessary to maintain healthy, productive cultures. Adults were separated from the bulk cultures at least one week prior to test initiation and placed in individual 30-ml plastic cups (15-ml volume) in brood boards. Gravid adults were reisolated the evening before the initiation of the toxicity test to ensure that neonates produced were less than 24 hours old for test initiation. For use in the chronic toxicity testing, the neonates were released within an 8-hour period from the time of reisolation from broods of eight or more.

The *Eisenia foetida* (red worm) were acquired from Smith Worms (Boston, Georgia). Upon receipt at EA, the worms were held at 20°C in the supplied bedding material until used in the acute toxicity tests. Organism lot EF-008 was received on 1 October 1998 and was used in the acute rangefinding test on 2 October 1998. Lot EF-009, received on 8 October, was used to initiate the acute toxicity definitive assay on 9 October.

The buttercrunch lettuce seeds (*Lactuca sativa*) were obtained from Meyer Seed Company (Baltimore, Maryland). The seeds (lot K-409) were maintained in cool, dark, air-tight storage until used in the toxicity tests. Prior to use in testing, the seeds were examined for hull integrity and size. Empty hulls or seeds with split, cracked or damaged hulls were not used for toxicity testing. Seeds were visually sorted for uniformity in size, color, and shape for use in testing.

2.3 DILUTION WATER AND DILUTION MEDIA

The dilution water used for the acute and chronic freshwater testing with *D. magna*, *P. promelas*, and *C. dubia* was 20 percent dilute mineral water (DMW). Individual 20-L batches

of this water were made by passing 16 L of deionized water through activated carbon, adding 4 L of bottled Perrier® water, and aerating the mixture overnight. The water was stored at 20°C under gentle aeration until needed for testing.

For the red worm toxicity testing, an artificial soil was prepared by combining 10 percent sphagnum moss, 20 percent kaolinite clay, and 70 percent silica sand on a dry weight basis (Harris, et. al. 1990). The pH of the artificial soil was adjusted to pH 6-7 with the addition of calcium carbonate prior to use in testing. The artificial soil was hydrated to 26-35 percent with the addition of the perchlorate test solutions. Deionized water was used to hydrate the artificial soil for the control.

The lettuce toxicity tests utilized commercial potting soil and commercial sand as the dilution media. The soil and sand were used individually in rangefinding and definitive assays to evaluate any differences in perchlorate toxicity in the two dilution medias.

2.4 TOXICITY TEST OPERATIONS AND PERFORMANCE

Toxicity testing was performed in accordance with US EPA (1993 and 1994) and ASTM (1997a, 1997b, and 1997c) guidance, and methodology followed EA's standard toxicity testing protocols (EA 1996) which are included in Attachment I. A graded concentration series of ClO_4 was selected for each acute and chronic definitive test based on the results of preliminary rangefinding tests. Each toxicity test included a series of five ClO_4 concentrations and a dilution water/dilution media control. An additional sodium (Na) control, introduced as NaCl, was included with each toxicity test. Prior to preparation of test solutions, aliquots of dilution water were brought to the proper test temperature using a water bath. For the terrestrial testing, the artificial soil, commercial potting soil, and sand were allowed to equilibrate to ambient air temperature prior to use in testing. Aqueous test concentrations were prepared by measuring volumes of test material with pipets or small graduated cylinders, adding to a volumetric flask or larger graduated cylinder, and bringing to final volume with dilution water/media. Each test solution was mixed and split equally into the replicate test vessels.

Copies of original data sheets which include all mortality observations and water quality measurements are presented in Attachment II, and copies of statistical analyses are included in Attachment III. The Report Quality Assurance Record is presented in Attachment IV.

2.4.1 *Daphnia magna* Acute Toxicity Testing

The acute toxicity tests with *D. magna* were conducted in 30-ml plastic cups with 25 ml of test solution per cup. The tests utilized four replicates per concentration with five organisms per replicate. The *D. magna* neonates (less than 24 hours old) were randomly introduced into the test cups for a total of 20 organisms exposed per concentration. The organisms were not fed during the test exposure period.

Test chambers were maintained in an environmentally controlled chamber at 20±1°C with a 16-hour light/8-hour dark photoperiod. Organism counts and water quality parameters were monitored and recorded daily on each test concentration. To avoid injury to the test organisms, water quality parameters (temperature, pH, dissolved oxygen, and conductivity) were measured in a fifth replicate test cup containing test solution without organisms. Based on the number of surviving organisms per concentration at the end of the 48-hour exposure period, the median lethal concentration (LC50) was calculated using the Spearman Karber, Trimmed Spearman Karber, or probit analysis methods.

2.4.2 *Pimephales promelas* Acute Toxicity Testing

The *P. promelas* acute toxicity testing utilized 1-L polypropylene beakers as the exposure vessels. Each beaker contained 250 ml of test solution, and there were two beakers per concentration. Ten *P. promelas* juveniles were randomly loaded into each replicate beaker for a total of 20 organisms per concentration. The test organisms were not fed during the 96-hour exposure period.

The *P. promelas* acute toxicity tests were conducted at 20±1°C with a 16-hour light/8-hour dark photoperiod. Observations on mortality were recorded at test initiation and termination, and at each 24-hour intermediate observation period. Temperature, pH, dissolved oxygen, and conductivity measurements were recorded daily on one replicate of every concentration. Using the total number of dead organisms per concentration at the end of the 96-hour exposure period, the median lethal concentration (LC50) was calculated for each test.

2.4.3 *Eisenia foetida* Acute Toxicity Testing

The *E. foetida* acute toxicity tests were performed in 1-L wide-mouth glass jars equipped with screw-top lids. Each jar contained 400 g of test soil and ten organisms. There were three replicate jars per concentration. The test chambers were placed in an environmentally controlled chamber and maintained at 25±1°C for the 14-day exposure period. Because earthworms burrow into the soil to avoid light, the photoperiod for these tests was continuous illumination in order to maximize organism contact with the soil. Daily observations were made on all test chambers, and any organisms not in contact with the sample were gently placed back onto the surface of the soil. Temperature in the chamber was recorded daily on a surrogate vessel containing soil. In addition, pH and percent moisture was measured on each concentration at initiation and termination of the definitive acute toxicity tests.

The number of surviving worms was recorded on Day 7 and at test termination on Day 14. Death was defined by a lack of response to a gentle prod with a glass rod. Since earthworms decompose rapidly in soil, those organisms not found were presumed and recorded as dead. Based on the survival data, 7-day and 14-day LC50s were calculated for the toxicity tests.

2.4.4 *Ceriodaphnia dubia* Chronic Toxicity Testing

Chronic toxicity tests with *C. dubia* were conducted in 30-ml plastic cups with 15 ml of test solution per cup. Each test concentration had ten replicate cups with one organism per cup. To

initiate the chronic toxicity test, one brood of eight of more *C. dubia* neonates was used per test row according to US EPA (1994) known parentage blocking technique. The organisms were fed daily during testing with 0.2 ml suspension of yeast/cereal leaves/trout chow supplemented with algae (*S. capricornutum*). Daily renewals of test solution were performed by carefully transferring the test organism from each test cup into a new cup containing freshly prepared test solution. During the daily transfer process, observations of mortality were recorded along with the number of neonates produced per organism. Temperature, pH, dissolved oxygen, and conductivity measurements were recorded on each concentration at test initiation and termination, and daily on the test solutions before and after renewal. The chronic toxicity test was terminated when at least 60 percent of the surviving control organisms had produced three broods, with a mean of at least 15 neonates per control organism.

Following US EPA (1994) guidance, statistical analyses were performed on the survival and reproduction data to determine if any test concentration was significantly different from the control (P=0.05). The short-term chronic toxicity test endpoints reported are expressed as the No Observed Effect Concentration (NOEC), the Lowest Observed Effect Concentration (LOEC), and the Chronic Value (ChV). Additionally, a 25 percent Inhibition Concentration (IC25) was calculated for each test. The definitions of these chronic endpoints follow US EPA (1994) and are as follows:

- The NOEC is the highest concentration of toxicant to which organisms are exposed in a full life-cycle or partial life-cycle test, which causes no statistically significant adverse effect on the observed parameter (usually hatchability, survival, growth, and reproduction).

- The LOEC is the lowest concentration of toxicant to which organisms are exposed in a life-cycle or partial life-cycle test, which causes a statistically significant adverse effect on the observed parameters (usually hatchability, survival, growth, and reproduction).

- The ChV is a value lying between the NOEC and LOEC, derived by calculating the

geometric mean of the NOEC and LOEC. The term is sometimes used interchangeably with Maximum Acceptable Toxicant Concentration (MATC).

- Inhibition Concentration (ICp) - A point estimate of the toxicant concentration that causes a given percent reduction in a non-quantal biological measurement such as fecundity or growth. For example, an IC25 is the estimate concentration of toxicant that causes a 25 percent reduction in mean young per female or some other non-quantal biological measurement.

In addition, a 48-hour LC50 was calculated from each *C. dubia* chronic toxicity test.

2.4.5 *Pimephales promelas* Chronic Toxicity Testing

The *P. promelas* chronic toxicity tests were conducted in 1-L polypropylene beakers with each beaker containing 250 ml test solution. Each concentration had four replicates of ten organisms, for a total of 40 organisms exposed per concentration. The *P. promelas* larvae were fed 0.15 to 0.25 ml (ration increased with age) of a 0.05 g/ml suspension of newly hatched brine shrimp nauplii (*Artemia* sp., less than 24 hours old) three times daily. The test solution in each beaker was renewed daily with freshly prepared test dilution. The daily solution renewals were performed by siphoning 80 percent of the old test solution from each test chamber taking care to remove debris from the bottom of the chamber, and then slowly siphoning new test solution into the chamber.

Observations of mortality were recorded daily. Temperature, pH, dissolved oxygen, and conductivity measurements were recorded on one replicate of each concentration at test initiation and termination, and daily on the test solutions before and after solution renewal.
At the end of the 7-day exposure period, the surviving larvae were placed in pre-weighed, oven-dried aluminum pans (one pan per replicate) and dried at 100°C for a minimum of six hours. The total organism dry weight per replicate was divided by the number of originally exposed organisms to obtain a mean biomass for each replicate.

The results of the *P. promelas* chronic toxicity tests were statistically analyzed according to EPA (1994) guidance to determine if any test concentration was significantly different from the

control with respect to survival or biomass (P=0.05). The results of the chronic toxicity test were reported as the NOEC, the LOEC, the ChV, and the IC25. A 96-hour LC50 was also calculated based on the 96-hour survival values.

2.4.6 *Lactuca sativa* Chronic Toxicity Testing

The *L. sativa* chronic toxicity tests were conducted in 6-inch diameter polypropylene pots, five replicate pots per concentration, with approximately 1,500 g of media (sand or soil) per pot. Ten seeds were planted in each pot, marking the initiation of the toxicity test. The seeds were arranged equally spaced in the pot and covered with a thin layer of soil. Deionized water was added to each pot, wetting the entire surface, taking care not to disturb the planted seeds. The pots were kept covered with plastic wrap until the seeds germinated. The number of germinated seeds was monitored daily.

The pots were maintained in an environmentally controlled room at 25±1°C under wide spectrum fluorescent light, with a 16-hour light/8-hour dark photoperiod. Monitoring of the toxicity test included monitoring the number of live plants per replicate and recording daily the temperature, light level, and humidity of the environmental room. Test vessels were watered daily, or as needed, with deionized water. Hoagland nutrient solution was applied to all of the replicates every Monday through Friday starting on Day 4 to provide necessary nutrients for maintaining plant growth.

After 18 days, the number of seedlings in each pot was thinned to five to allow for unrestricted growth, while still maintaining enough biomass for dry weight measurements at test termination. The toxicity tests were terminated after 28 days from test initiation. At test termination, the number of surviving plants per replicate was recorded, and the total above ground biomass of the plants from each replicate was carefully harvested and placed into pre-weighed aluminum pans. The plants were dried a minimum of 48 hours in an oven at 100°C and then weighed. The total dry weight per replicate was divided by the number of surviving plants in that replicate at test termination to obtain a mean dry weight. The percent germination, percent survival, and mean dry weight data were statistically analyzed to determine which test

concentrations, if any, were significantly different from the control (P=0.05).

2.5 REFERENCE TOXICANT TESTS

In conformance with EA's quality assurance/quality control program, reference toxicant tests were performed with each species tested. For in-house cultured organisms (i.e., *D. magna*, *C. dubia*, and *P. promelas*), reference toxicant tests were performed monthly. For organisms acquired from an outside source, a reference toxicant test was conducted on each lot of acquired organisms. The results of each reference toxicant test were compared to EA's established control chart limits.

2.6 ARCHIVES

Original data sheets, records, memoranda, notes, and computer printouts are archived at EA's Baltimore Office in Sparks, Maryland. These data will be retained for a period of 5 years unless a longer period of time is requested by Armstrong Laboratory.

3. RESULTS AND DISCUSSION

A summary of the water quality parameters measured (temperature, pH, dissolved oxygen and conductivity) during the rangefinding and definitive acute toxicity testing with aquatic species is presented in Table 1. The results of the water flea, *Daphnia magna* static acute toxicity rangefinding test with sodium perchlorate are summarized in Table 2. The test concentrations are expressed as nominal mg/L (ppm) CLO_4, and the dilution water was 20 percent dilute mineral water. The test concentration series for the rangefinding test was 1, 10, 100, 1000 and 5000 mg/L CLO_4 and control. A sodium chloride control was included, with the sodium concentration (1155 mg/L Na) matching that in the highest perchlorate concentration of 5000 mg/L CLO_4. There was 0, 35 and 95 percent *D. magna* survival in the 5000, 1000 and 100 mg/L CLO_4 test concentrations, respectively. The resulting probit 48-hour LC50 was 601 mg/L CLO_4, and the 95 percent confidence interval (95% C.I.) for the LC50 was 340-973 mg/L CLO_4.

The results of the *D. magna* definitive acute toxicity test are also presented in Table 2. The definitive acute toxicity test nominal concentration series was 155, 280, 490, 870 and 1550 mg/L CLO_4, control and sodium control. The 48-hour *D. magna* LC50 (and 95% C.I.) for the definitive acute toxicity test was 490 (406-591) mg/L CLO_4. There was 100 percent survival in the control and the sodium control in both the rangefinding and definitive acute toxicity tests.

Table 3 presents the results of the sodium perchlorate rangefinding and definitive acute toxicity testing with fathead minnow *Pimephales promelas*. The rangefinding test employed a test concentration series of 1, 10, 100, 1000 and 5000 mg/L CLO_4, a control and a 1155 mg/L Na control. The 96-hour LC50 (and 95% C.I.) for the *P. promelas* rangefinding test was 1128 (743-1712) mg/L CLO_4. The definitive acute toxicity test concentration series consisted of 420, 650, 1000, 1550, 2400 mg/L CLO_4, control and 554 mg/L Na control. The sodium perchlorate was slightly less toxic in the definitive acute toxicity test. In the rangefinding test, there was 65 percent survival in the 1000 mg/L treatment, while in the definitive test there was 65 percent survival in the 1550 mg/L CLO_4 treatment. The resulting 96-hour LC50 (and 95% C.I.) for the definitive test was 1655 (1507-1817) mg/L CLO_4.

A summary of the environmental parameters measured during the red worm, *Eisenia foetida*, test is presented in Table 4, and the test results with sodium perchlorate are presented in Table 5. In the rangefinding test, there was 83 percent survival in the 3750 mg/L CLO_4 concentration at 7 and 14 days, and there was 0 percent survival at 7500 mg/L. The 7- and 14-day LC50s (and 95% C.I.) in the rangefinding test were 4725 (4299-5192) mg/L CLO_4. The sodium perchlorate definitive acute toxicity test with *E. foetida* produced results very similar to the rangefinding test. The *E. foetida* 7- and 14-day LC50s (and 95% C.I.) in the definitive test were both 4450 (4213-4701) mg/L CLO_4. In the rangefinding test, the sodium control corresponding to 15000 mg/L CLO_4 (3465 mg/L Na) was toxic to *E. foetida*. The sodium chloride concentration at that treatment level was 8801 mg/L NaCl, and was apparently above the toxic threshold for NaCl. The sodium control in the definitive test (2009 mg/L Na; 5103 mg/L NaCl) resulted in 93 percent survival at 14-days and was below the acutely toxic threshold for NaCl.

Table 6 presents the results of the sodium perchlorate chronic toxicity testing with the water flea *Ceriodaphnia dubia*. In the rangefinding chronic toxicity test, the chronic No Observed Effect Concentration (NOEC) was 10 mg/L CLO_4, the Lowest Observed Effect Concentration (LOEC) was 100 mg/L CLO_4, and the resulting Chronic Value (ChV) was 31.6 mg/L CLO_4. There was 100 percent *C. dubia* mortality at 100 mg/L CLO_4 in the rangefinding test. The results of the *C. dubia* definitive chronic toxicity test were in agreement with the rangefinding test results. The NOEC again was 10 mg/L, the LOEC was the next higher concentration, 33 mg/L, and the resulting ChV was 18.2 mg/L CLO_4. Based on the dose response data, the IC25 derived in the definitive test (17.0 mg/L) appears to be a better chronic toxicity estimate than the IC25 derived in the rangefinding test (2.2 mg/L). For each test, survival in the sodium control was 70 percent, and young production was not significantly reduced compared to the respective control. The 48-hour LC50 in the rangefinding test was 202 mg/L ClO_4, while the 48-hour LC50 in the definitive chronic toxicity test was 66 mg/L ClO_4.

The results of the fathead minnow, *P. promelas*, chronic toxicity test are summarized in Table 7. The rangefinding perchlorate test concentrations ranged from 1 to 2000 mg/L CLO_4. At the end of the 7-day test period, there was zero percent survival in the 1000 and 2000 mg/L

concentrations. In fact, complete mortality was observed in the 2000 mg/L concentrations by Day 4 (96 hours), and in the 1000 mg/L concentration by Day 6. At 96 hours, there was 15 percent survival in the 1000 mg/L test concentration compared to 65 percent survival at 1000 mg/L CLO_4 in the acute toxicity rangefinding test with *P. promelas*. This comparison suggests that the less than 24 hours old larvae evaluated in the chronic toxicity test were slightly more acutely sensitive to perchlorate than were the 12-13 day old larvae used in the acute toxicity test. The NOEC, LOEC and ChV for the *P. promelas* chronic toxicity rangefinding test were 100, 1000, and 316 mg/L CLO_4, respectively. A significant negative effect was observed in the sodium control (NaCl) corresponding to the sodium concentration in the 2000 mg/L CLO_4 concentration.

The *P. promelas* definitive chronic toxicity test evaluated perchlorate concentrations ranging from 87 to 870 mg/L. A significant (P=0.05) effect on survival was observed at 280 mg/L CLO_4 where there was 68 percent survival compared to 100 percent survival in the control. There was no effect on survival or growth at the next lowest perchlorate concentration (155 mg/L); thus, the NOEC, LOEC, and ChV for the fathead minnow chronic test were 155, 280, and 208 mg/L CLO_4, respectively. The IC25s for the rangefinding test (264 mg/L) and the definitive test (212 mg/L) were quite similar given the differences in the test concentration series ranges. In the definitive test, the sodium control (201 mg/L Na; 510 mg/L NaCl) again, was adversely affected with respect to survival (13 percent). The 96-hour LC50s for the *P. promelas* rangefinding and definitive chronic toxicity tests were 397 and 614 mg/L $Cl0_4$, respectively.

The environmental parameters measured during the lettuce (*Lactuca sativa*) 28-day growth tests with sodium perchlorate are presented in Table 8, and the results of the tests are reported in Table 9. The reported endpoints are percent germination, 28-day percent survival, and mean dry weight at the end of the 28-day exposure period. The percent survival is based on the number of plants that germinated in each pot, not on the number of seeds that were planted. For the soil test and the sand test, percent germination was significantly reduced only at the highest test concentration of 2400 mg/kg CLO_4. In the soil test, there was zero percent survival in the 1000 and 2400 mg/kg concentrations at Day 28; however, there was 74 percent survival in the next lowest test

concentration (420 mg/L) which was not significantly different than the control. In the sand test, survival was significantly lower than the control in the 420 mg/kg concentration (17 percent survival), but was not significantly affected at the next lower concentration of 180 mg/kg (61 percent survival).

With respect to the growth endpoint, the mean dry weights of plants in the lowest sodium perchlorate concentrations tested in both the soil and sand tests were significantly different (P=0.05) from their respective control dry weight. In the soil test, the mean dry weight of plants exposed to the lowest perchlorate concentration of 80 mg/kg (0.083 g/plant) was 74.8 percent of dry weight of the soil control treatment (0.111 g/plant), and was significantly different than the control at P=0.05. Thus, the LOEC for the soil test was 80 mg/kg CLO_4 and the NOEC and ChV were both less than 80 mg/kg. The IC25 for the lettuce growth test in soil was 78 mg/kg CLO_4. Based on mean dry weight, the Na control in the soil test was adversely affected (0.081 g/plant).

In the sand test, the lowest perchlorate concentration of 80 mg/kg (0.094 g/plant) was very similar to mean dry weight of the 80 mg/kg in the soil test (0.083 g/plant), but was only 51.4 percent of the respective sand control (0.183 g/plant). Similar to the soil test the LOEC, NOEC, and ChV were 80, <80 and <80 mg/kg CLO_4, respectively. However, because there was a greater difference between the 80 mg/kg CLO_4 and control in the sand test, the IC25 for the sand test was 41 mg/kg as compared to 78 mg/kg in the soil test. The mean control dry weight per plant in the soil test was 0.111 g, whereas mean control dry weight in the sand test was 0.183 g per plant. Visual observations during the performance of the test indicated that initially, growth rate was more rapid in the soil test, however by the end of 28 days, the sand control growth exceeded the soil control. The Na control in the sand test was not significantly affected with respect to dry weight (0.134 g/plant).

The results of reference toxicant testing conducted on commercially purchased lots of test organisms, as well as on in-house cultured species, are presented in Table 10. For *Daphnia magna*, *Ceriodaphnia dubia* and *Pimephales promelas*, the tests were part of the monthly reference toxicant testing program for cultured species. The values for those species were all within the acceptable control chart limits. For *Eisenia foetida* and *Lactuca sativa*, the testing was conducted on the lots of organisms used in testing. Again, the reference toxicant test values fell

within the acceptable control chart limits.

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TITLE: TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
FILE: F:\LS\423PPSUR.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 4

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	0.9000	0.9000
1	CONTROL	3	1.0000	1.0000
1	CONTROL	4	1.0000	1.0000
2	1	1	1.0000	1.0000
2	1	2	1.0000	1.0000
2	1	3	0.9000	0.9000
2	1	4	1.0000	1.0000
3	10	1	1.0000	1.0000
3	10	2	1.0000	1.0000
3	10	3	1.0000	1.0000
3	10	4	1.0000	1.0000
4	100	1	0.9000	0.9000
4	100	2	1.0000	1.0000
4	100	3	1.0000	1.0000
4	100	4	1.0000	1.0000

TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
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SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	4	0.900	1.000	0.975
2	1	4	0.900	1.000	0.975
3	10	4	1.000	1.000	1.000
4	100	4	0.900	1.000	0.975

TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
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SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.003	0.050	0.025	5.13
2	1	0.003	0.050	0.025	5.13
3	10	0.000	0.000	0.000	0.00
4	100	0.003	0.050	0.025	5.13

TITLE: TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
FILE: F:\LS\423PPSUA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	0.9000	0.9000
1	CONTROL	3	1.0000	1.0000
1	CONTROL	4	1.0000	1.0000
2	Na CONTROL	1	0.3000	0.3000
2	Na CONTROL	2	0.2000	0.2000
2	Na CONTROL	3	0.1000	0.1000
2	Na CONTROL	4	0.3000	0.3000

TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\423PPSUA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	4	0.900	1.000	0.975
2	Na CONTROL	4	0.100	0.300	0.225

TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\423PPSUA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.003	0.050	0.025	5.13
2	Na CONTROL	0.009	0.096	0.048	42.55

TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\423PPSUA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.065

W = 0.853

Critical W (P = 0.05) (n = 8) = 0.818
Critical W (P = 0.01) (n = 8) = 0.749

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\423PPSUA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

F-Test for equality of two variances

GROUP	IDENTIFICATION	VARIANCE	F
1	CONTROL	0.007	
2	Na CONTROL	0.015	2.260

Critical F = 47.50 (P=0.01, 3, 3)

Since F <= Critical F, FAIL TO REJECT Ho: Equal Variances.

TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\423PPSUA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	1.567	1.567	144.776
Within (Error)	6	0.065	0.011	
Total	7	1.632		

Critical F value = 5.99 (0.05,1,6)
Since F > Critical F REJECT Ho: All equal

TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\423PPSUA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.371	0.975		
2	Na CONTROL	0.486	0.225	12.032	*

2 Sample t table value = 1.94 (1 Tailed Value, P=0.05, df=6,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.371	0.975		
2	Na CONTROL	0.486	0.225	12.032	*

2 Sample t table value = 2.01 (1 Tailed Value, P=0.05, df=5,1)

TN-98-423 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\423PPSUA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	4			
2	Na CONTROL	4	0.073	7.5	0.750

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	4			
2	Na CONTROL	4	0.077	7.9	0.750

TITLE: TN-98-423 ARMSTRONG P.PROMELAS BIOMASS
FILE: F:\LS\423PPGRO.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 4

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.8750	0.8750
1	CONTROL	2	0.7310	0.7310
1	CONTROL	3	0.9010	0.9010
1	CONTROL	4	0.8450	0.8450
2	1	1	0.7950	0.7950
2	1	2	0.8960	0.8960
2	1	3	0.7190	0.7190
2	1	4	0.9560	0.9560
3	10	1	0.8690	0.8690
3	10	2	0.8540	0.8540
3	10	3	0.8830	0.8830
3	10	4	0.8490	0.8490
4	100	1	0.6990	0.6990
4	100	2	0.8240	0.8240
4	100	3	0.8580	0.8580
4	100	4	0.7270	0.7270

TN-98-423 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\423PPGRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	4	0.731	0.901	0.838
2	1	4	0.719	0.956	0.842
3	10	4	0.849	0.883	0.864
4	100	4	0.699	0.858	0.777

TN-98-423 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\423PPGRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.006	0.075	0.037	8.94
2	1	0.011	0.105	0.053	12.51
3	10	0.000	0.015	0.008	1.78
4	100	0.006	0.076	0.038	9.79

```
TN-98-423  ARMSTRONG  P.PROMELAS  BIOMASS
File: F:\LS\423PPGRO.ARM       Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D =    0.068

W =    0.977

Critical W (P = 0.05) (n = 16) = 0.887
Critical W (P = 0.01) (n = 16) = 0.844
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.
```

```
TN-98-423  ARMSTRONG  P.PROMELAS  BIOMASS
File: F:\LS\423PPGRO.ARM       Transform: NO TRANSFORMATION

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    6.59

-------------------------------------------------------------------------------
Table Chi-square value =   11.34  (alpha = 0.01, df =   3)
Table Chi-square value =    7.81  (alpha = 0.05, df =   3)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-423 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\423PPGRO.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	3	0.017	0.006	0.973
Within (Error)	12	0.068	0.006	
Total	15	0.085		

Critical F value = 3.49 (0.05,3,12)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-423 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\423PPGRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.838	0.838		
2	1	0.842	0.842	-0.066	
3	10	0.864	0.864	-0.483	
4	100	0.777	0.777	1.145	

Dunnett table value = 2.29 (1 Tailed Value, P=0.05, df=12,3)

TN-98-423 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\423PPGRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	4			
2	1	4	0.122	14.6	-0.003
3	10	4	0.122	14.6	-0.026
4	100	4	0.122	14.6	0.061

TITLE: TN-98-423 ARMSTRONG P.PROMELAS BIOMASS
FILE: F:\LS\423PPGRA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.8750	0.8750
1	CONTROL	2	0.7310	0.7310
1	CONTROL	3	0.9010	0.9010
1	CONTROL	4	0.8450	0.8450
2	Na CONTROL	1	0.0720	0.0720
2	Na CONTROL	2	0.0360	0.0360
2	Na CONTROL	3	0.0220	0.0220
2	Na CONTROL	4	0.0650	0.0650

TN-98-423 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\423PPGRA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	4	0.731	0.901	0.838
2	Na CONTROL	4	0.022	0.072	0.049

TN-98-423 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\423PPGRA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.006	0.075	0.037	8.94
2	Na CONTROL	0.001	0.024	0.012	48.58

Conc. ID	1	2	3	4	5	6
Conc. Tested	0	1	10	100	1000	2000
Response 1	.875	.795	.869	.699	0	0
Response 2	.731	.896	.854	.824	0	0
Response 3	.901	.719	.883	.858	0	0
Response 4	.845	.956	.849	.727	0	0

*** Inhibition Concentration Percentage Estimate ***
Toxicant/Effluent: TN-98-423 ARMSTRONG BIOMASS
Test Start Date: Test Ending Date:
Test Species: P.PROMELAS
Test Duration: 7 DAYS
DATA FILE: 423PPARM.icp
OUTPUT FILE: 423PPARM.i25

Conc. ID	Number Replicates	Concentration	Response Means	Std. Dev.	Pooled Response Means
1	4	0.000	0.838	0.075	0.848
2	4	1.000	0.842	0.105	0.848
3	4	10.000	0.864	0.015	0.848
4	4	100.000	0.777	0.076	0.777
5	4	1000.000	0.000	0.000	0.000
6	4	2000.000	0.000	0.000	0.000

The Linear Interpolation Estimate: 263.5376 Entered P Value: 25

Number of Resamplings: 200
The Bootstrap Estimates Mean: 259.8536 Standard Deviation: 35.9757
Original Confidence Limits: Lower: 185.4108 Upper: 325.0000
Expanded Confidence Limits: Lower: 138.5346 Upper: 361.8774
Resampling time in Seconds: 0.06 Random_Seed: 3257335

TN-98-424 ARMSTRONG LAB D.MAGNA-RANGEFINDER SODIUM PERCHLORATE

****

CONC.	NUMBER EXPOSED	NUMBER DEAD	PERCENT DEAD	BINOMIAL PROB.(PERCENT)
5000	20	20	100	LESS THAN 0.001
1000	20	13	65	13.15878
100	20	1	5	2.002717E-03
10	20	0	0	LESS THAN 0.001
1	20	0	0	LESS THAN 0.001

THE BINOMIAL TEST SHOWS THAT 100 AND 5000 CAN BE USED AS STATISTICALLY SOUND CONSERVATIVE 95 PERCENT CONFIDENCE LIMITS BECAUSE THE ACTUAL CONFIDENCE LEVEL ASSOCIATED WITH THESE LIMITS IS GREATER THAN 95 PERCENT.

AN APPROXIMATE LC50 OF 604.5117 IS OBTAINED BY NONLINEAR INTERPOLATION BETWEEN 100 AND 1000

RESULTS CALCULATED USING THE MOVING AVERAGE METHOD

SPAN	G	LC50	95 PERCENT CONFIDENCE LIMITS	
4	3.921942E-02	393.4311	215.9287	796.5165
3	4.595932E-02	469.5655	285.3651	804.9796
2	6.572948E-02	583.0807	358.5826	900.5203
1	.2127725	604.5124	354.5157	1463.161

RESULTS CALCULATED USING THE PROBIT METHOD

ITERATIONS	G	H	CHI-SQUARE	PROBABILITY
6	.1630274	1	.637749	.8877388

SLOPE = 2.299999

95 PERCENT CONFIDENCE LIMITS = 1.371336 AND 3.228661

LC50 = 600.9359

95 PERCENT CONFIDENCE LIMITS = 340.2152 AND 973.3384

****

TITLE: TN-98-447 ARMSTRONG LETTUCE-SOIL GERMINATION
FILE: F:\LS\447GERM.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 6

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.5000	0.5000
1	CONTROL	2	0.8000	0.8000
1	CONTROL	3	1.0000	1.0000
2	80	1	0.9000	0.9000
2	80	2	1.0000	1.0000
2	80	3	0.9000	0.9000
3	180	1	1.0000	1.0000
3	180	2	0.9000	0.9000
3	180	3	0.8000	0.8000
4	420	1	0.9000	0.9000
4	420	2	0.7000	0.7000
4	420	3	0.9000	0.9000
5	1000	1	0.5000	0.5000
5	1000	2	0.4000	0.4000
5	1000	3	0.8000	0.8000
6	2400	1	0.1000	0.1000
6	2400	2	0.0000	0.0000
6	2400	3	0.0000	0.0000

TN-98-447 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\447GERM.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.500	1.000	0.767
2	80	3	0.900	1.000	0.933
3	180	3	0.800	1.000	0.900
4	420	3	0.700	0.900	0.833
5	1000	3	0.400	0.800	0.567
6	2400	3	0.000	0.100	0.033

TN-98-447 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\447GERM.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.063	0.252	0.145	32.83
2	80	0.003	0.058	0.033	6.19
3	180	0.010	0.100	0.058	11.11
4	420	0.013	0.115	0.067	13.86
5	1000	0.043	0.208	0.120	36.74
6	2400	0.003	0.058	0.033	173.21

```
TN-98-447  ARMSTRONG  LETTUCE-SOIL  GERMINATION
File: F:\LS\447GERM.ARM       Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D =    0.420

W =    0.977

Critical W (P = 0.05) (n = 18) = 0.897
Critical W (P = 0.01) (n = 18) = 0.858
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-447  ARMSTRONG  LETTUCE-SOIL  GERMINATION
File: F:\LS\447GERM.ARM       Transform: ARC SINE(SQUARE ROOT(Y))

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    3.77

-------------------------------------------------------------------------------
Table Chi-square value =   15.09  (alpha = 0.01, df =   5)
Table Chi-square value =   11.07  (alpha = 0.05, df =   5)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-447 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\447GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	5	2.495	0.499	14.258
Within (Error)	12	0.420	0.035	
Total	17	2.915		

Critical F value = 3.11 (0.05,5,12)
Since F > Critical F REJECT Ho: All equal

TN-98-447 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\447GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.102	0.767		
2	80	1.303	0.933	-1.321	
3	180	1.256	0.900	-1.012	
4	420	1.163	0.833	-0.403	
5	1000	0.859	0.567	1.587	
6	2400	0.213	0.033	5.816	*

Dunnett table value = 2.50 (1 Tailed Value, P=0.05, df=12,5)

TN-98-447 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\447GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	80	3	0.361	47.1	-0.167
3	180	3	0.361	47.1	-0.133
4	420	3	0.361	47.1	-0.067
5	1000	3	0.361	47.1	0.200
6	2400	3	0.361	47.1	0.733

TITLE: TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
FILE: F:\LS\447SUR.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 4

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
2	80	1	1.0000	1.0000
2	80	2	1.0000	1.0000
2	80	3	1.0000	1.0000
3	180	1	1.0000	1.0000
3	180	2	1.0000	1.0000
3	180	3	1.0000	1.0000
4	420	1	0.8900	0.8900
4	420	2	0.4300	0.4300
4	420	3	0.8900	0.8900

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	1.000	1.000	1.000
2	80	3	1.000	1.000	1.000
3	180	3	1.000	1.000	1.000
4	420	3	0.430	0.890	0.737

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.000	0.000	0.00
2	80	0.000	0.000	0.000	0.00
3	180	0.000	0.000	0.000	0.00
4	420	0.071	0.266	0.153	36.05

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.179

W = 0.650

Critical W (P = 0.05) (n = 12) = 0.859
Critical W (P = 0.01) (n = 12) = 0.805

Data FAIL normality test. Try another transformation.

Warning - The first three homogeneity tests are sensitive to non-normal data and should not be performed.

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Hartley's test for homogeneity of variance
Bartlett's test for homogeneity of variance

These two tests can not be performed because at least one group has zero variance.

Data FAIL to meet homogeneity of variance assumption.
Additional transformations are useless.

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	3	0.278	0.093	4.158
Within (Error)	8	0.179	0.022	
Total	11	0.457		

Critical F value = 4.07 (0.05,3,8)
Since F > Critical F REJECT Ho: All equal

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	80	1.412	1.000	0.000	
3	180	1.412	1.000	0.000	
4	420	1.060	0.737	2.884	*

Dunnett table value = 2.42 (1 Tailed Value, P=0.05, df=8,3)

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	80	3	0.167	16.7	0.000
3	180	3	0.167	16.7	0.000
4	420	3	0.167	16.7	0.263

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

WILCOXON'S RANK SUM TEST W/ BONFERRONI ADJUSTMENT - Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	RANK SUM	CRIT. VALUE	REPS	SIG
1	CONTROL	1.412				
2	80	1.412	10.50	None	3	
3	180	1.412	10.50	None	3	
4	420	1.060	6.00	None	3	

Critical values use k = 3, are 1 tailed, and alpha = 0.05

TITLE: TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
FILE: F:\LS\447SURA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
2	420	1	0.8900	0.8900
2	420	2	0.4300	0.4300
2	420	3	0.8900	0.8900

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SURA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	1.000	1.000	1.000
2	420	3	0.430	0.890	0.737

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SURA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.000	0.000	0.00
2	420	0.071	0.266	0.153	36.05

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SURA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.179

W = 0.814

Critical W (P = 0.05) (n = 6) = 0.788
Critical W (P = 0.01) (n = 6) = 0.713

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SURA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	0.186	0.186	4.158
Within (Error)	4	0.179	0.045	
Total	5	0.364		

Critical F value = 7.71 (0.05,1,4)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SURA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	420	1.060	0.737	2.039	

2 Sample t table value = 2.13 (1 Tailed Value, P=0.05, df=4,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	420	1.060	0.737	2.039	

2 Sample t table value = 6.31 (1 Tailed Value, P=0.05, df=1,1)

TN-98-447 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\447SURA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	420	3	0.228	22.8	0.263

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	420	3	0.874	87.4	0.263

TITLE: TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
FILE: F:\LS\447GRO.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 4

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.1095	0.1095
1	CONTROL	2	0.1070	0.1070
1	CONTROL	3	0.1171	0.1171
2	80	1	0.0968	0.0968
2	80	2	0.0683	0.0683
2	80	3	0.0829	0.0829
3	180	1	0.0144	0.0144
3	180	2	0.0074	0.0074
3	180	3	0.0177	0.0177
4	420	1	0.0195	0.0195
4	420	2	0.0038	0.0038
4	420	3	0.0255	0.0255

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.107	0.117	0.111
2	80	3	0.068	0.097	0.083
3	180	3	0.007	0.018	0.013
4	420	3	0.004	0.025	0.016

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.005	0.003	4.71
2	80	0.000	0.014	0.008	17.25
3	180	0.000	0.005	0.003	39.65
4	420	0.000	0.011	0.006	68.76

```
TN-98-447  ARMSTRONG  LETTUCE-SOIL  DRY WEIGHT
File: F:\LS\447GRO.ARM       Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D =    0.001

W =    0.980

Critical W (P = 0.05) (n = 12) = 0.859
Critical W (P = 0.01) (n = 12) = 0.805
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-447  ARMSTRONG  LETTUCE-SOIL  DRY WEIGHT
File: F:\LS\447GRO.ARM       Transform: NO TRANSFORMATION

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    2.46

-------------------------------------------------------------------------------
Table Chi-square value =   11.34  (alpha = 0.01, df =   3)
Table Chi-square value =    7.81  (alpha = 0.05, df =   3)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GRO.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	3	0.022	0.007	74.871
Within (Error)	8	0.001	0.000	
Total	11	0.022		

Critical F value = 4.07 (0.05,3,8)
Since F > Critical F REJECT Ho: All equal

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.111	0.111		
2	80	0.083	0.083	3.568	*
3	180	0.013	0.013	12.267	*
4	420	0.016	0.016	11.879	*

Dunnett table value = 2.42 (1 Tailed Value, P=0.05, df=8,3)

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	80	3	0.019	17.4	0.029
3	180	3	0.019	17.4	0.098
4	420	3	0.019	17.4	0.095

TITLE: TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
FILE: F:\LS\447GROA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.1095	0.1095
1	CONTROL	2	0.1070	0.1070
1	CONTROL	3	0.1171	0.1171
2	Na CONTROL	1	0.0770	0.0770
2	Na CONTROL	2	0.0949	0.0949
2	Na CONTROL	3	0.0713	0.0713

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GROA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.107	0.117	0.111
2	Na CONTROL	3	0.071	0.095	0.081

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GROA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.005	0.003	4.71
2	Na CONTROL	0.000	0.012	0.007	15.22

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GROA.ARM Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality

D = 0.000

W = 0.924

Critical W (P = 0.05) (n = 6) = 0.788
Critical W (P = 0.01) (n = 6) = 0.713

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GROA.ARM Transform: NO TRANSFORMATION

F-Test for equality of two variances

GROUP	IDENTIFICATION	VARIANCE	F
1	CONTROL	0.000	
2	Na CONTROL	0.000	5.554

Critical F = 199.00 (P=0.01, 2, 2)

Since F <= Critical F, FAIL TO REJECT Ho: Equal Variances.

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GROA.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	0.001	0.001	15.152
Within (Error)	4	0.000	0.000	
Total	5	0.002		

Critical F value = 7.71 (0.05,1,4)
Since F > Critical F REJECT Ho: All equal

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GROA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.111	0.111		
2	Na CONTROL	0.081	0.081	3.893	*

2 Sample t table value = 2.13 (1 Tailed Value, P=0.05, df=4,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.111	0.111		
2	Na CONTROL	0.081	0.081	3.893	*

2 Sample t table value = 2.92 (1 Tailed Value, P=0.05, df=2,1)

TN-98-447 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\447GROA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.016	14.8	0.030

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.023	20.3	0.030

Conc. ID	1	2	3	4
Conc. Tested	0	80	180	420
Response 1	.10946	.09684	.01438	.01946
Response 2	.10702	.06832	.00744	.00383
Response 3	.11706	.08286	.01766	.02550

*** Inhibition Concentration Percentage Estimate ***
Toxicant/Effluent: TN-98-447 ARMSTRONG
Test Start Date: Test Ending Date:
Test Species: L.SATIVA
Test Duration: 28-DAYS
DATA FILE: 447LSARM.icp
OUTPUT FILE: 447LSARM.i25

Conc. ID	Number Replicates	Concentration	Response Means	Std. Dev.	Pooled Response Means
1	3	0.000	0.111	0.005	0.111
2	3	80.000	0.083	0.014	0.083
3	3	180.000	0.013	0.005	0.015
4	3	420.000	0.016	0.011	0.015

The Linear Interpolation Estimate: 78.0028 Entered P Value: 25

Number of Resamplings: 200
The Bootstrap Estimates Mean: 75.9028 Standard Deviation: 11.4153
Original Confidence Limits: Lower: 53.3384 Upper: 94.5931
Expanded Confidence Limits: Lower: 26.2075 Upper: 112.8423
Resampling time in Seconds: 0.05 Random_Seed: -17237079

TITLE: TN-98-448 ARMSTRONG LETTUCE-SAND GERMINATION
FILE: F:\LS\448GERM.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 6

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.8000	0.8000
1	CONTROL	2	0.6000	0.6000
1	CONTROL	3	0.9000	0.9000
2	80	1	0.8000	0.8000
2	80	2	0.9000	0.9000
2	80	3	0.8000	0.8000
3	180	1	0.8000	0.8000
3	180	2	0.9000	0.9000
3	180	3	0.7000	0.7000
4	420	1	0.9000	0.9000
4	420	2	0.9000	0.9000
4	420	3	1.0000	1.0000
5	1000	1	0.7000	0.7000
5	1000	2	0.8000	0.8000
5	1000	3	1.0000	1.0000
6	2400	1	0.3000	0.3000
6	2400	2	0.4000	0.4000
6	2400	3	0.5000	0.5000

TN-98-448 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\448GERM.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.600	0.900	0.767
2	80	3	0.800	0.900	0.833
3	180	3	0.700	0.900	0.800
4	420	3	0.900	1.000	0.933
5	1000	3	0.700	1.000	0.833
6	2400	3	0.300	0.500	0.400

TN-98-448 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\448GERM.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.023	0.153	0.088	19.92
2	80	0.003	0.058	0.033	6.93
3	180	0.010	0.100	0.058	12.50
4	420	0.003	0.058	0.033	6.19
5	1000	0.023	0.153	0.088	18.33
6	2400	0.010	0.100	0.058	25.00

```
TN-98-448  ARMSTRONG  LETTUCE-SAND  GERMINATION
File: F:\LS\448GERM.ARM       Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D =    0.247

W =    0.968

Critical W (P = 0.05) (n = 18) = 0.897
Critical W (P = 0.01) (n = 18) = 0.858
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-448  ARMSTRONG  LETTUCE-SAND  GERMINATION
File: F:\LS\448GERM.ARM       Transform: ARC SINE(SQUARE ROOT(Y))

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    2.55

-------------------------------------------------------------------------------
Table Chi-square value =   15.09  (alpha = 0.01, df =   5)
Table Chi-square value =   11.07  (alpha = 0.05, df =   5)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-448 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\448GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	5	0.666	0.133	6.472
Within (Error)	12	0.247	0.021	
Total	17	0.913		

Critical F value = 3.11 (0.05,5,12)
Since F > Critical F REJECT Ho: All equal

TN-98-448 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\448GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.081	0.767		
2	80	1.154	0.833	-0.629	
3	180	1.116	0.800	-0.299	
4	420	1.303	0.933	-1.900	
5	1000	1.170	0.833	-0.763	
6	2400	0.683	0.400	3.393	*

Dunnett table value = 2.50 (1 Tailed Value, P=0.05, df=12,5)

TN-98-448 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\448GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	80	3	0.276	36.0	-0.067
3	180	3	0.276	36.0	-0.033
4	420	3	0.276	36.0	-0.167
5	1000	3	0.276	36.0	-0.067
6	2400	3	0.276	36.0	0.367

TITLE: TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
FILE: F:\LS\448SUR.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 4

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
2	80	1	1.0000	1.0000
2	80	2	1.0000	1.0000
2	80	3	1.0000	1.0000
3	180	1	0.7500	0.7500
3	180	2	0.7800	0.7800
3	180	3	0.2900	0.2900
4	420	1	0.0000	0.0000
4	420	2	0.2200	0.2200
4	420	3	0.3000	0.3000

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	1.000	1.000	1.000
2	80	3	1.000	1.000	1.000
3	180	3	0.290	0.780	0.607
4	420	3	0.000	0.300	0.173

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.000	0.000	0.00
2	80	0.000	0.000	0.000	0.00
3	180	0.075	0.275	0.159	45.27
4	420	0.024	0.155	0.090	89.62

```
TN-98-448  ARMSTRONG  LETTUCE-SAND  SURVIVAL
File: F:\LS\448SUR.ARM       Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D =    0.263

W =    0.835

Critical W (P = 0.05) (n = 12) = 0.859
Critical W (P = 0.01) (n = 12) = 0.805
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-448  ARMSTRONG  LETTUCE-SAND  SURVIVAL
File: F:\LS\448SUR.ARM       Transform: ARC SINE(SQUARE ROOT(Y))

Hartley's test for homogeneity of variance
Bartlett's test for homogeneity of variance
-------------------------------------------------------------------------------

These two tests can not be performed because at least one group has
zero variance.

Data FAIL to meet homogeneity of variance assumption.
Additional transformations are useless.

-------------------------------------------------------------------------------
```

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	3	2.084	0.695	21.148
Within (Error)	8	0.263	0.033	
Total	11	2.347		

Critical F value = 4.07 (0.05,3,8)
Since F > Critical F REJECT Ho: All equal

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	80	1.412	1.000	0.000	
3	180	0.899	0.607	3.463	*
4	420	0.409	0.173	6.779	*

Dunnett table value = 2.42 (1 Tailed Value, P=0.05, df=8,3)

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	80	3	0.219	21.9	0.000
3	180	3	0.219	21.9	0.393
4	420	3	0.219	21.9	0.827

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

WILCOXON'S RANK SUM TEST W/ BONFERRONI ADJUSTMENT - Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	RANK SUM	CRIT. VALUE	REPS	SIG
1	CONTROL	1.412				
2	80	1.412	10.50	None	3	
3	180	0.899	6.00	None	3	
4	420	0.409	6.00	None	3	

Critical values use k = 3, are 1 tailed, and alpha = 0.05

TITLE: TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
FILE: F:\LS\448SURA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
2	180	1	0.7500	0.7500
2	180	2	0.7800	0.7800
2	180	3	0.2900	0.2900

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	1.000	1.000	1.000
2	180	3	0.290	0.780	0.607

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.000	0.000	0.00
2	180	0.075	0.275	0.159	45.27

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.165

W = 0.840

Critical W (P = 0.05) (n = 6) = 0.788
Critical W (P = 0.01) (n = 6) = 0.713

Data PASS normality test at P=0.01 level. Continue analysis.

BARTLETT'S TEST ABORTED (DIVISION BY ZERO)

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	0.394	0.394	9.565
Within (Error)	4	0.165	0.041	
Total	5	0.559		

Critical F value = 7.71 (0.05,1,4)
Since F > Critical F REJECT Ho: All equal

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	180	0.899	0.607	3.093	*

2 Sample t table value = 2.13 (1 Tailed Value, P=0.05, df=4,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	180	0.899	0.607	3.093	

2 Sample t table value = 6.31 (1 Tailed Value, P=0.05, df=1,1)

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	180	3	0.215	21.5	0.393

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	180	3	0.847	84.7	0.393

TITLE: TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
FILE: F:\LS\448SURB.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
2	420	1	0.0000	0.0000
2	420	2	0.2200	0.2200
2	420	3	0.3000	0.3000

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURB.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	1.000	1.000	1.000
2	420	3	0.000	0.300	0.173

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURB.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.000	0.000	0.00
2	420	0.024	0.155	0.090	89.62

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURB.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.098

W = 0.875

Critical W (P = 0.05) (n = 6) = 0.788
Critical W (P = 0.01) (n = 6) = 0.713

Data PASS normality test at P=0.01 level. Continue analysis.

BARTLETT□S TEST ABORTED (DIVISION BY ZERO)

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURB.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	1.509	1.509	61.609
Within (Error)	4	0.098	0.025	
Total	5	1.607		

Critical F value = 7.71 (0.05,1,4)
Since F > Critical F REJECT Ho: All equal

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURB.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	420	0.409	0.173	7.849	*

2 Sample t table value = 2.13 (1 Tailed Value, P=0.05, df=4,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	420	0.409	0.173	7.849	*

2 Sample t table value = 6.31 (1 Tailed Value, P=0.05, df=1,1)

TN-98-448 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\448SURB.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	420	3	0.150	15.0	0.827

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	420	3	0.651	65.1	0.827

TITLE: TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
FILE: F:\LS\448GRO.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 3

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.1768	0.1768
1	CONTROL	2	0.1964	0.1964
1	CONTROL	3	0.1747	0.1747
2	80	1	0.0819	0.0819
2	80	2	0.0978	0.0978
2	80	3	0.1034	0.1034
3	180	1	0.0239	0.0239
3	180	2	0.0277	0.0277
3	180	3	0.0146	0.0146

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.175	0.196	0.183
2	80	3	0.082	0.103	0.094
3	180	3	0.015	0.028	0.022

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.012	0.007	6.55
2	80	0.000	0.011	0.006	11.86
3	180	0.000	0.007	0.004	30.52

```
TN-98-448  ARMSTRONG  LETTUCE-SAND  DRY WEIGHT
File: F:\LS\448GRO.ARM       Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D =    0.001

W =    0.952

Critical W (P = 0.05) (n =  9) = 0.829
Critical W (P = 0.01) (n =  9) = 0.764
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-448  ARMSTRONG  LETTUCE-SAND  DRY WEIGHT
File: F:\LS\448GRO.ARM       Transform: NO TRANSFORMATION

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    0.56

-------------------------------------------------------------------------------
Table Chi-square value =    9.21  (alpha = 0.01, df =   2)
Table Chi-square value =    5.99  (alpha = 0.05, df =   2)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GRO.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	2	0.039	0.019	185.612
Within (Error)	6	0.001	0.000	
Total	8	0.039		

Critical F value = 5.14 (0.05,2,6)
Since F > Critical F REJECT Ho: All equal

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.183	0.183		
2	80	0.094	0.094	10.574	*
3	180	0.022	0.022	19.236	*

Dunnett table value = 2.34 (1 Tailed Value, P=0.05, df=6,2)

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	80	3	0.020	10.7	0.088
3	180	3	0.020	10.7	0.161

TITLE: TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
FILE: F:\LS\448GROA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.1768	0.1768
1	CONTROL	2	0.1964	0.1964
1	CONTROL	3	0.1747	0.1747
2	Na CONTROL	1	0.1436	0.1436
2	Na CONTROL	2	0.1196	0.1196
2	Na CONTROL	3	0.1396	0.1396

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GROA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.175	0.196	0.183
2	Na CONTROL	3	0.120	0.144	0.134

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GROA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.012	0.007	6.55
2	Na CONTROL	0.000	0.013	0.007	9.59

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GROA.ARM Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality

D = 0.001

W = 0.941

Critical W (P = 0.05) (n = 6) = 0.788
Critical W (P = 0.01) (n = 6) = 0.713

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GROA.ARM Transform: NO TRANSFORMATION

F-Test for equality of two variances

GROUP	IDENTIFICATION	VARIANCE	F
1	CONTROL	0.000	
2	Na CONTROL	0.000	1.160

Critical F = 199.00 (P=0.01, 2, 2)

Since F <= Critical F, FAIL TO REJECT Ho: Equal Variances.

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GROA.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	0.004	0.004	22.744
Within (Error)	4	0.001	0.000	
Total	5	0.004		

Critical F value = 7.71 (0.05,1,4)
Since F > Critical F REJECT Ho: All equal

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GROA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.183	0.183		
2	Na CONTROL	0.134	0.134	4.769	*

2 Sample t table value = 2.13 (1 Tailed Value, P=0.05, df=4,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.183	0.183		
2	Na CONTROL	0.134	0.134	4.769	*

2 Sample t table value = 2.35 (1 Tailed Value, P=0.05, df=3,1)

TN-98-448 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\448GROA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.022	11.8	0.048

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.024	13.1	0.048

Conc. ID	1	2	3	4
Conc. Tested	0	80	180	420
Response 1	.17680	.08186	.02392	.13610
Response 2	.19640	.09782	.02768	.00350
Response 3	.17474	.10344	.01460	

*** Inhibition Concentration Percentage Estimate ***
Toxicant/Effluent: TN-98-448 ARMSTRONG
Test Start Date: Test Ending Date:
Test Species: L.SATIVA
Test Duration: 28-DAYS
DATA FILE: 448LSARM.icp
OUTPUT FILE: 448LSARM.i25

Conc. ID	Number Replicates	Concentration	Response Means	Std. Dev.	Pooled Response Means
1	3	0.000	0.183	0.012	0.183
2	3	80.000	0.094	0.011	0.094
3	3	180.000	0.022	0.007	0.041
4	2	420.000	0.070	0.094	0.041

The Linear Interpolation Estimate: 41.3821 Entered P Value: 25

Number of Resamplings: 200
The Bootstrap Estimates Mean: 41.5709 Standard Deviation: 2.7810
Original Confidence Limits: Lower: 36.3556 Upper: 47.5025
Expanded Confidence Limits: Lower: 30.8266 Upper: 54.2349
Resampling time in Seconds: 0.00 Random_Seed: -524096748

TN-98-472 ARMSTRONG LAB D.MAGNA-DEFINITIVE SODIUM PERCHLORATE

****

CONC.	NUMBER EXPOSED	NUMBER DEAD	PERCENT DEAD	BINOMIAL PROB.(PERCENT)
1550	20	20	100	LESS THAN 0.001
870	20	17	85	.1288414
490	20	9	45	41.19011
280	20	4	20	.5908965
155	20	0	0	LESS THAN 0.001

THE BINOMIAL TEST SHOWS THAT 280 AND 870 CAN BE
USED AS STATISTICALLY SOUND CONSERVATIVE 95 PERCENT
CONFIDENCE LIMITS BECAUSE THE ACTUAL CONFIDENCE LEVEL
ASSOCIATED WITH THESE LIMITS IS GREATER THAN 95 PERCENT.

AN APPROXIMATE LC50 OF 523.5796 IS OBTAINED BY
NONLINEAR INTERPOLATION BETWEEN 490 AND 870

RESULTS CALCULATED USING THE MOVING AVERAGE METHOD

SPAN	G	LC50	95 PERCENT CONFIDENCE LIMITS	
4	5.158859E-02	489.0357	409.5643	583.8597
3	8.728594E-02	488.7158	403.6999	623.8274
2	.2084207	498.983	389.3062	644.4774
1	.5479226	523.5793	247.8932	647.5853

RESULTS CALCULATED USING THE PROBIT METHOD

ITERATIONS	G	H	CHI-SQUARE	PROBABILITY
3	.1041884	1	1.372818	.7119184

SLOPE = 4.44224
95 PERCENT CONFIDENCE LIMITS = 3.008364 AND 5.876117

LC50 = 489.8448
95 PERCENT CONFIDENCE LIMITS = 405.811 AND 591.2504

****

TN-98-481 ARMSTRONG P.PROMELAS-DEFINITIVE 96-HR LC50

****

CONC.	NUMBER EXPOSED	NUMBER DEAD	PERCENT DEAD	BINOMIAL PROB.(PERCENT)
870	40	29	72.5	.3213202
490	40	16	40	13.40936
280	40	1	2.5	LESS THAN 0.001
155	40	0	0	LESS THAN 0.001
87	40	0	0	LESS THAN 0.001

THE BINOMIAL TEST SHOWS THAT 280 AND 870 CAN BE
USED AS STATISTICALLY SOUND CONSERVATIVE 95 PERCENT
CONFIDENCE LIMITS BECAUSE THE ACTUAL CONFIDENCE LEVEL
ASSOCIATED WITH THESE LIMITS IS GREATER THAN 95 PERCENT.

AN APPROXIMATE LC50 OF 582.6597 IS OBTAINED BY
NONLINEAR INTERPOLATION BETWEEN 490 AND 870

RESULTS CALCULATED USING THE MOVING AVERAGE METHOD

SPAN	G	LC50	95 PERCENT CONFIDENCE LIMITS	
2	.0700228	597.3543	524.0175	701.1934
1	.4474483	582.66	396.4859	712.0773

RESULTS CALCULATED USING THE PROBIT METHOD

ITERATIONS	G	H	CHI-SQUARE	PROBABILITY
5	8.645757E-02	1	2.214703	.529058

SLOPE = 4.785845
95 PERCENT CONFIDENCE LIMITS = 3.378631 AND 6.193058

LC50 = 614.1983
95 PERCENT CONFIDENCE LIMITS = 540.4935 AND 713.5048

****

TITLE: TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
FILE: F:\LS\481PPSUR.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 5

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
1	CONTROL	4	1.0000	1.0000
2	87	1	1.0000	1.0000
2	87	2	1.0000	1.0000
2	87	3	1.0000	1.0000
2	87	4	1.0000	1.0000
3	155	1	1.0000	1.0000
3	155	2	1.0000	1.0000
3	155	3	1.0000	1.0000
3	155	4	1.0000	1.0000
4	280	1	0.8000	0.8000
4	280	2	0.7000	0.7000
4	280	3	0.7000	0.7000
4	280	4	0.5000	0.5000
5	490	1	0.0000	0.0000
5	490	2	0.0000	0.0000
5	490	3	0.1000	0.1000
5	490	4	0.3000	0.3000

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	4	1.000	1.000	1.000
2	87	4	1.000	1.000	1.000
3	155	4	1.000	1.000	1.000
4	280	4	0.500	0.800	0.675
5	490	4	0.000	0.300	0.100

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.000	0.000	0.00
2	87	0.000	0.000	0.000	0.00
3	155	0.000	0.000	0.000	0.00
4	280	0.016	0.126	0.063	18.64
5	490	0.020	0.141	0.071	141.42

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.172

W = 0.748

Critical W (P = 0.05) (n = 20) = 0.905
Critical W (P = 0.01) (n = 20) = 0.868

Data FAIL normality test. Try another transformation.

Warning - The first three homogeneity tests are sensitive to non-normal data and should not be performed.

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Hartley's test for homogeneity of variance
Bartlett's test for homogeneity of variance

These two tests can not be performed because at least one group has zero variance.

Data FAIL to meet homogeneity of variance assumption.
Additional transformations are useless.

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

STEEL'S MANY-ONE RANK TEST - Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	RANK SUM	CRIT. VALUE	df	SIG
1	CONTROL	1.412				
2	87	1.412	18.00	10.00	4.00	
3	155	1.412	18.00	10.00	4.00	
4	280	0.969	10.00	10.00	4.00	*
5	490	0.305	10.00	10.00	4.00	*

Critical values use k = 4, are 1 tailed, and alpha = 0.05

TITLE: TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
FILE: F:\LS\481PPSUA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
1	CONTROL	4	1.0000	1.0000
2	Na CONTROL	1	0.1000	0.1000
2	Na CONTROL	2	0.0000	0.0000
2	Na CONTROL	3	0.1000	0.1000
2	Na CONTROL	4	0.3000	0.3000

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	4	1.000	1.000	1.000
2	Na CONTROL	4	0.000	0.300	0.125

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.000	0.000	0.00
2	Na CONTROL	0.016	0.126	0.063	100.66

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.091

W = 0.781

Critical W (P = 0.05) (n = 8) = 0.818
Critical W (P = 0.01) (n = 8) = 0.749

Data PASS normality test at P=0.01 level. Continue analysis.

BARTLETT□S TEST ABORTED (DIVISION BY ZERO)

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	2.275	2.275	150.308
Within (Error)	6	0.091	0.015	
Total	7	2.366		

Critical F value = 5.99 (0.05,1,6)
Since F > Critical F REJECT Ho: All equal

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	Na CONTROL	0.345	0.125	12.260	*

2 Sample t table value = 1.94 (1 Tailed Value, P=0.05, df=6,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	Na CONTROL	0.345	0.125	12.260	*

2 Sample t table value = 2.92 (1 Tailed Value, P=0.05, df=2,1)

TN-98-481 ARMSTRONG P.PROMELAS SURVIVAL
File: F:\LS\481PPSUA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	4			
2	Na CONTROL	4	0.079	7.9	0.875

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	4			
2	Na CONTROL	4	0.136	13.6	0.875

TITLE: TN-98-481 ARMSTRONG P.PROMELAS BIOMASS
FILE: F:\LS\481PPGRO.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 3

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.6800	0.6800
1	CONTROL	2	0.6590	0.6590
1	CONTROL	3	0.7390	0.7390
1	CONTROL	4	0.6680	0.6680
2	87	1	0.5720	0.5720
2	87	2	0.6510	0.6510
2	87	3	0.7030	0.7030
2	87	4	0.6660	0.6660
3	155	1	0.7090	0.7090
3	155	2	0.6180	0.6180
3	155	3	0.5570	0.5570
3	155	4	0.7010	0.7010

TN-98-481 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\481PPGRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	4	0.659	0.739	0.687
2	87	4	0.572	0.703	0.648
3	155	4	0.557	0.709	0.646

TN-98-481 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\481PPGRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.001	0.036	0.018	5.25
2	87	0.003	0.055	0.028	8.52
3	155	0.005	0.072	0.036	11.19

```
TN-98-481  ARMSTRONG  P.PROMELAS  BIOMASS
File: F:\LS\481PPGRO.ARM       Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D =    0.029

W =    0.920

Critical W (P = 0.05) (n = 12) = 0.859
Critical W (P = 0.01) (n = 12) = 0.805
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-481  ARMSTRONG  P.PROMELAS  BIOMASS
File: F:\LS\481PPGRO.ARM       Transform: NO TRANSFORMATION

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    1.18

-------------------------------------------------------------------------------
Table Chi-square value =    9.21  (alpha = 0.01, df =   2)
Table Chi-square value =    5.99  (alpha = 0.05, df =   2)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-481 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\481PPGRO.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	2	0.004	0.002	0.649
Within (Error)	9	0.029	0.003	
Total	11	0.033		

Critical F value = 4.26 (0.05,2,9)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-481 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\481PPGRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.687	0.687		
2	87	0.648	0.648	0.964	
3	155	0.646	0.646	1.007	

Dunnett table value = 2.18 (1 Tailed Value, P=0.05, df=9,2)

TN-98-481 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\481PPGRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	4			
2	87	4	0.087	12.7	0.039
3	155	4	0.087	12.7	0.040

TITLE: TN-98-481 ARMSTRONG P.PROMELAS BIOMASS
FILE: F:\LS\481PPGRA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.6800	0.6800
1	CONTROL	2	0.6590	0.6590
1	CONTROL	3	0.7390	0.7390
1	CONTROL	4	0.6680	0.6680
2	Na CONTROL	1	0.0120	0.0120
2	Na CONTROL	2	0.0270	0.0270
2	Na CONTROL	3	0.0730	0.0730

TN-98-481 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\481PPGRA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	4	0.659	0.739	0.687
2	Na CONTROL	3	0.012	0.073	0.037

TN-98-481 ARMSTRONG P.PROMELAS BIOMASS
File: F:\LS\481PPGRA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.001	0.036	0.018	5.25
2	Na CONTROL	0.001	0.032	0.018	85.14

Conc. ID	1	2	3	4	5	6
Conc. Tested	0	87	155	280	490	870
Response 1	.680	.572	.709	.389	0	0
Response 2	.659	.651	.618	.354	0	0
Response 3	.739	.703	.557	.385	.035	0
Response 4	.668	.666	.701	.306	.096	0

*** Inhibition Concentration Percentage Estimate ***
Toxicant/Effluent: TN-98-481 ARMSTRONG BIOMASS
Test Start Date: Test Ending Date:
Test Species: P.PROMELAS
Test Duration: 7 DAYS
DATA FILE: 481PPARM.icp
OUTPUT FILE: 481PPARM.i25

Conc. ID	Number Replicates	Concentration	Response Means	Std. Dev.	Pooled Response Means
1	4	0.000	0.687	0.036	0.687
2	4	87.000	0.648	0.055	0.648
3	4	155.000	0.646	0.072	0.646
4	4	280.000	0.359	0.038	0.359
5	4	490.000	0.033	0.045	0.033
6	4	870.000	0.000	0.000	0.000

The Linear Interpolation Estimate: 212.0699 Entered P Value: 25

Number of Resamplings: 200
The Bootstrap Estimates Mean: 209.7836 Standard Deviation: 9.0958
Original Confidence Limits: Lower: 188.6040 Upper: 223.8719
Expanded Confidence Limits: Lower: 174.5244 Upper: 230.9530
Resampling time in Seconds: 0.05 Random_Seed: -433777728

TN-98-480 ARMSTRONG C.DUBIA-RANGEFINDER 48-HR LC50

****

CONC.	NUMBER EXPOSED	NUMBER DEAD	PERCENT DEAD	BINOMIAL PROB.(PERCENT)
1000	10	9	90	1.074219
100	10	3	30	17.1875
10	10	0	0	9.765626E-02
1	10	0	0	9.765626E-02
.1	10	0	0	9.765626E-02

THE BINOMIAL TEST SHOWS THAT 10 AND 1000 CAN BE
USED AS STATISTICALLY SOUND CONSERVATIVE 95 PERCENT
CONFIDENCE LIMITS BECAUSE THE ACTUAL CONFIDENCE LEVEL
ASSOCIATED WITH THESE LIMITS IS GREATER THAN 95 PERCENT.

AN APPROXIMATE LC50 OF 205.2153 IS OBTAINED BY
NONLINEAR INTERPOLATION BETWEEN 100 AND 1000

RESULTS CALCULATED USING THE MOVING AVERAGE METHOD

SPAN	G	LC50	95 PERCENT CONFIDENCE LIMITS	
2	.1677535	192.5543	84.84911	569.0792
1	.5098044	205.2148	34.53573	496.0685

RESULTS CALCULATED USING THE PROBIT METHOD

ITERATIONS	G	H	CHI-SQUARE	PROBABILITY
6	.3556227	1	9.284668E-02	.9926818

SLOPE = 1.919137
95 PERCENT CONFIDENCE LIMITS = .7746766 AND 3.063596

LC50 = 201.8866
95 PERCENT CONFIDENCE LIMITS = 78.54169 AND 533.8308

****

TN-98-480 ARMSTRONG C.DUBIA SURVIVAL

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF ALIVE	NUMBER OF DEAD	TOTAL ANIMALS
CONTROL	8	2	10
0.1	7	3	10
TOTAL	15	5	20

CRITICAL FISHER'S VALUE (10,10,8) (p=0.05) IS 3. b VALUE IS 7.
Since b is greater than 3 there is no significant difference between CONTROL and TREATMENT at the 0.05 level.

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF ALIVE	NUMBER OF DEAD	TOTAL ANIMALS
CONTROL	8	2	10
1	8	2	10
TOTAL	16	4	20

CRITICAL FISHER'S VALUE (10,10,8) (p=0.05) IS 3. b VALUE IS 8.
Since b is greater than 3 there is no significant difference between CONTROL and TREATMENT at the 0.05 level.

TN-98-480

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF ALIVE	NUMBER OF DEAD	NUMBER OF TOTAL ANIMALS
CONTROL	8	2	10
10	6	4	10
TOTAL	14	6	20

CRITICAL FISHER'S VALUE (10,10,8) (p=0.05) IS 3. b VALUE IS 6.
Since b is greater than 3 there is no significant difference between CONTROL and TREATMENT at the 0.05 level.

SUMMARY OF FISHER'S EXACT TESTS

GROUP	IDENTIFICATION	NUMBER EXPOSED	NUMBER DEAD	SIG (P=.05)
	CONTROL	10	2	
1	0.1	10	3	
2	1	10	2	
3	10	10	4	

TN-98-480 ARMSTRONG C.DUBIA SURVIVAL

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF ALIVE	NUMBER OF DEAD	TOTAL ANIMALS
CONTROL	8	2	10
Na CONTROL	7	3	10
TOTAL	15	5	20

CRITICAL FISHER'S VALUE (10,10,8) (p=0.05) IS 3. b VALUE IS 7.
Since b is greater than 3 there is no significant difference between CONTROL and TREATMENT at the 0.05 level.

SUMMARY OF FISHER'S EXACT TESTS

GROUP	IDENTIFICATION	NUMBER EXPOSED	NUMBER DEAD	SIG (P=.05)
	CONTROL	10	2	
1	Na CONTROL	10	3	

TITLE: TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
FILE: F:\LS\480CDREP.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 4

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	31.0000	31.0000
1	CONTROL	2	16.0000	16.0000
1	CONTROL	3	39.0000	39.0000
1	CONTROL	4	0.0000	0.0000
1	CONTROL	5	0.0000	0.0000
1	CONTROL	6	31.0000	31.0000
1	CONTROL	7	19.0000	19.0000
1	CONTROL	8	28.0000	28.0000
1	CONTROL	9	15.0000	15.0000
1	CONTROL	10	10.0000	10.0000
2	0.1	1	14.0000	14.0000
2	0.1	2	13.0000	13.0000
2	0.1	3	26.0000	26.0000
2	0.1	4	27.0000	27.0000
2	0.1	5	10.0000	10.0000
2	0.1	6	17.0000	17.0000
2	0.1	7	28.0000	28.0000
2	0.1	8	0.0000	0.0000
2	0.1	9	0.0000	0.0000
2	0.1	10	10.0000	10.0000
3	1	1	20.0000	20.0000
3	1	2	0.0000	0.0000
3	1	3	49.0000	49.0000
3	1	4	25.0000	25.0000
3	1	5	11.0000	11.0000
3	1	6	1.0000	1.0000
3	1	7	8.0000	8.0000
3	1	8	6.0000	6.0000
3	1	9	11.0000	11.0000
3	1	10	22.0000	22.0000
4	10	1	1.0000	1.0000
4	10	2	0.0000	0.0000
4	10	3	26.0000	26.0000
4	10	4	24.0000	24.0000
4	10	5	15.0000	15.0000
4	10	6	19.0000	19.0000
4	10	7	11.0000	11.0000
4	10	8	0.0000	0.0000
4	10	9	0.0000	0.0000
4	10	10	0.0000	0.0000

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREP.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	10	0.000	39.000	18.900
2	0.1	10	0.000	28.000	14.500
3	1	10	0.000	49.000	15.300
4	10	10	0.000	26.000	9.600

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREP.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	177.433	13.320	4.212	70.48
2	0.1	104.500	10.223	3.233	70.50
3	1	212.456	14.576	4.609	95.27
4	10	115.378	10.741	3.397	111.89

```
TN-98-480  ARMSTRONG  C.DUBIA  REPRODUCTION
File: F:\LS\480CDREP.ARM       Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D = 5487.900

W =    0.958

Critical W (P = 0.05) (n = 40) = 0.940
Critical W (P = 0.01) (n = 40) = 0.919
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-480  ARMSTRONG  C.DUBIA  REPRODUCTION
File: F:\LS\480CDREP.ARM       Transform: NO TRANSFORMATION

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    1.48

-------------------------------------------------------------------------------
Table Chi-square value =   11.34  (alpha = 0.01, df =   3)
Table Chi-square value =    7.81  (alpha = 0.05, df =   3)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREP.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	3	439.875	146.625	0.962
Within (Error)	36	5487.900	152.442	
Total	39	5927.775		

Critical F value = 2.92 (0.05,3,30)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREP.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	18.900	18.900		
2	0.1	14.500	14.500	0.797	
3	1	15.300	15.300	0.652	
4	10	9.600	9.600	1.684	

Dunnett table value = 2.15 (1 Tailed Value, P=0.05, df=30,3)

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREP.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	10			
2	0.1	10	11.871	62.8	4.400
3	1	10	11.871	62.8	3.600
4	10	10	11.871	62.8	9.300

TITLE: TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
FILE: F:\LS\480CDREA.ARM
TRANSFORM: NO TRANSFORMATION NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	31.0000	31.0000
1	CONTROL	2	16.0000	16.0000
1	CONTROL	3	39.0000	39.0000
1	CONTROL	4	0.0000	0.0000
1	CONTROL	5	0.0000	0.0000
1	CONTROL	6	31.0000	31.0000
1	CONTROL	7	19.0000	19.0000
1	CONTROL	8	28.0000	28.0000
1	CONTROL	9	15.0000	15.0000
1	CONTROL	10	10.0000	10.0000
2	Na CONTROL	1	0.0000	0.0000
2	Na CONTROL	2	24.0000	24.0000
2	Na CONTROL	3	47.0000	47.0000
2	Na CONTROL	4	25.0000	25.0000
2	Na CONTROL	5	0.0000	0.0000
2	Na CONTROL	6	3.0000	3.0000
2	Na CONTROL	7	15.0000	15.0000
2	Na CONTROL	8	23.0000	23.0000
2	Na CONTROL	9	15.0000	15.0000
2	Na CONTROL	10	0.0000	0.0000

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREA.ARM Transform: NO TRANSFORMATION

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	10	0.000	39.000	18.900
2	Na CONTROL	10	0.000	47.000	15.200

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREA.ARM Transform: NO TRANSFORMATION

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	177.433	13.320	4.212	70.48
2	Na CONTROL	231.956	15.230	4.816	100.20

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREA.ARM Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality

D = 3684.500

W = 0.946

Critical W (P = 0.05) (n = 20) = 0.905
Critical W (P = 0.01) (n = 20) = 0.868

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREA.ARM Transform: NO TRANSFORMATION

F-Test for equality of two variances

GROUP	IDENTIFICATION	VARIANCE	F
1	CONTROL	177.433	
2	Na CONTROL	231.956	1.307

Critical F = 6.54 (P=0.01, 9, 9)

Since F <= Critical F, FAIL TO REJECT Ho: Equal Variances.

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREA.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	68.450	68.450	0.334
Within (Error)	18	3684.500	204.694	
Total	19	3752.950		

Critical F value = 4.41 (0.05,1,18)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	18.900	18.900		
2	Na CONTROL	15.200	15.200	0.578	

2 Sample t table value = 1.73 (1 Tailed Value, P=0.05, df=18,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	18.900	18.900		
2	Na CONTROL	15.200	15.200	0.578	

2 Sample t table value = 1.74 (1 Tailed Value, P=0.05, df=17,1)

TN-98-480 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\480CDREA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	10			
2	Na CONTROL	10	11.095	58.7	3.700

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	10			
2	Na CONTROL	10	11.131	58.9	3.700

Conc. ID	1	2	3	4	5	6
Conc. Tested	0	0.1	1	10	100	1000
Response 1	31	14	20	1	0	0
Response 2	16	13	0	0	0	0
Response 3	39	26	49	26	0	0
Response 4	0	27	25	24	0	0
Response 5	0	10	11	15	0	0
Response 6	31	17	1	19	0	0
Response 7	19	28	8	11	0	0
Response 8	28	0	6	0	0	0
Response 9	15	0	11	0	0	0
Response 10	10	10	22	0	0	0

*** Inhibition Concentration Percentage Estimate ***
Toxicant/Effluent: TN-98-480 ARMSTRONG
Test Start Date: Test Ending Date:
Test Species: C.DUBIA
Test Duration: 8 DAYS
DATA FILE: 480CDARM.icp
OUTPUT FILE: 480CDARM.i25

Conc. ID	Number Replicates	Concentration	Response Means	Std. Dev.	Pooled Response Means
1	10	0.000	18.900	13.320	18.900
2	10	0.100	14.500	10.223	14.900
3	10	1.000	15.300	14.576	14.900
4	10	10.000	9.600	10.741	9.600
5	10	100.000	0.000	0.000	0.000
6	10	1000.000	0.000	0.000	0.000

The Linear Interpolation Estimate: 2.2311 Entered P Value: 25

Number of Resamplings: 200
The Bootstrap Estimates Mean: 3.5586 Standard Deviation: 5.2972
Original Confidence Limits: Lower: 0.0520 Upper: 17.1140
Resampling time in Seconds: 0.11 Random_Seed: -556177812

TITLE: TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
FILE: F:\LS\490GERM.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 6

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	0.5000	0.5000
1	CONTROL	3	0.9000	0.9000
2	10	1	0.6000	0.6000
2	10	2	0.4000	0.4000
2	10	3	0.8000	0.8000
3	20	1	0.6000	0.6000
3	20	2	0.7000	0.7000
3	20	3	1.0000	1.0000
4	40	1	1.0000	1.0000
4	40	2	0.8000	0.8000
4	40	3	0.6000	0.6000
5	80	1	0.6000	0.6000
5	80	2	1.0000	1.0000
5	80	3	0.7000	0.7000
6	160	1	0.7000	0.7000
6	160	2	0.9000	0.9000
6	160	3	0.9000	0.9000

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERM.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.500	1.000	0.800
2	10	3	0.400	0.800	0.600
3	20	3	0.600	1.000	0.767
4	40	3	0.600	1.000	0.800
5	80	3	0.600	1.000	0.767
6	160	3	0.700	0.900	0.833

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERM.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.070	0.265	0.153	33.07
2	10	0.040	0.200	0.115	33.33
3	20	0.043	0.208	0.120	27.15
4	40	0.040	0.200	0.115	25.00
5	80	0.043	0.208	0.120	27.15
6	160	0.013	0.115	0.067	13.86

```
TN-98-490  ARMSTRONG  LETTUCE-SOIL  GERMINATION
File: F:\LS\490GERM.ARM       Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D =    0.794

W =    0.934

Critical W (P = 0.05) (n = 18) = 0.897
Critical W (P = 0.01) (n = 18) = 0.858
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-490  ARMSTRONG  LETTUCE-SOIL  GERMINATION
File: F:\LS\490GERM.ARM       Transform: ARC SINE(SQUARE ROOT(Y))

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    1.09

-------------------------------------------------------------------------------
Table Chi-square value =   15.09  (alpha = 0.01, df =   5)
Table Chi-square value =   11.07  (alpha = 0.05, df =   5)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	5	0.150	0.030	0.452
Within (Error)	12	0.794	0.066	
Total	17	0.944		

Critical F value = 3.11 (0.05,5,12)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.149	0.800		
2	10	0.893	0.600	1.219	
3	20	1.096	0.767	0.249	
4	40	1.135	0.800	0.065	
5	80	1.096	0.767	0.249	
6	160	1.163	0.833	-0.068	

Dunnett table value = 2.50 (1 Tailed Value, P=0.05, df=12,5)

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS.	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	10	3	0.491	61.4	0.200
3	20	3	0.491	61.4	0.033
4	40	3	0.491	61.4	0.000
5	80	3	0.491	61.4	0.033
6	160	3	0.491	61.4	-0.033

TITLE: TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
FILE: F:\LS\490GERMA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	0.5000	0.5000
1	CONTROL	3	0.9000	0.9000
2	Na CONTROL	1	0.6000	0.6000
2	Na CONTROL	2	0.5000	0.5000
2	Na CONTROL	3	0.2000	0.2000

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERMA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.500	1.000	0.800
2	Na CONTROL	3	0.200	0.600	0.433

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERMA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.070	0.265	0.153	33.07
2	Na CONTROL	0.043	0.208	0.120	48.04

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.309

W = 0.889

Critical W (P = 0.05) (n = 6) = 0.788
Critical W (P = 0.01) (n = 6) = 0.713

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

F-Test for equality of two variances

GROUP	IDENTIFICATION	VARIANCE	F
1	CONTROL	0.106	
2	Na CONTROL	0.049	2.171

Critical F = 199.00 (P=0.01, 2, 2)

Since F <= Critical F, FAIL TO REJECT Ho: Equal Variances.

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Bartlett's test for homogeneity of variance
Calculated B1 statistic = 0.23

Table Chi-square value = 6.63 (alpha = 0.01, df = 1)
Table Chi-square value = 3.84 (alpha = 0.05, df = 1)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	0.287	0.287	3.713
Within (Error)	4	0.309	0.077	
Total	5	0.595		

Critical F value = 7.71 (0.05,1,4)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.149	0.800		
2	Na CONTROL	0.712	0.433	1.927	

2 Sample t table value = 2.13 (1 Tailed Value, P=0.05, df=4,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.149	0.800		
2	Na CONTROL	0.712	0.433	1.927	

2 Sample t table value = 2.35 (1 Tailed Value, P=0.05, df=3,1)

TN-98-490 ARMSTRONG LETTUCE-SOIL GERMINATION
File: F:\LS\490GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.451	56.4	0.367

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.499	62.4	0.367

TITLE: TN-98-490 ARMSTRONG LETTUCE-SOIL SURVIVAL
FILE: F:\LS\490SUR.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 6

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
2	10	1	1.0000	1.0000
2	10	2	1.0000	1.0000
2	10	3	1.0000	1.0000
3	20	1	1.0000	1.0000
3	20	2	1.0000	1.0000
3	20	3	0.9000	0.9000
4	40	1	1.0000	1.0000
4	40	2	1.0000	1.0000
4	40	3	1.0000	1.0000
5	80	1	0.8300	0.8300
5	80	2	1.0000	1.0000
5	80	3	1.0000	1.0000
6	160	1	0.4300	0.4300
6	160	2	0.3300	0.3300
6	160	3	0.3300	0.3300

TN-98-490 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\490SUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	1.000	1.000	1.000
2	10	3	1.000	1.000	1.000
3	20	3	0.900	1.000	0.967
4	40	3	1.000	1.000	1.000
5	80	3	0.830	1.000	0.943
6	160	3	0.330	0.430	0.363

TN-98-490 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\490SUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.000	0.000	0.00
2	10	0.000	0.000	0.000	0.00
3	20	0.003	0.058	0.033	5.97
4	40	0.000	0.000	0.000	0.00
5	80	0.010	0.098	0.057	10.40
6	160	0.003	0.058	0.033	15.89

TN-98-490 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\490SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.072

W = 0.848

Critical W (P = 0.05) (n = 18) = 0.897
Critical W (P = 0.01) (n = 18) = 0.858

Data FAIL normality test. Try another transformation.

Warning - The first three homogeneity tests are sensitive to non-normal data and should not be performed.

TN-98-490 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: F:\LS\490SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Hartley's test for homogeneity of variance
Bartlett's test for homogeneity of variance

These two tests can not be performed because at least one group has zero variance.

Data FAIL to meet homogeneity of variance assumption.
Additional transformations are useless.

TN-98-490 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: f:\ls\490sur.arm Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	5	1.378	0.276	45.908
Within (Error)	12	0.072	0.006	
Total	17	1.450		

Critical F value = 3.11 (0.05,5,12)
Since F > Critical F REJECT Ho: All equal

TN-98-490 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: f:\ls\490sur.arm Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.412	1.000		
2	10	1.412	1.000	0.000	
3	20	1.358	0.967	0.859	
4	40	1.412	1.000	0.000	
5	80	1.323	0.943	1.403	
6	160	0.646	0.363	12.102	*

Dunnett table value = 2.50 (1 Tailed Value, P=0.05, df=12,5)

TN-98-490 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: f:\ls\490sur.arm Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	10	3	0.072	7.2	0.000
3	20	3	0.072	7.2	0.033
4	40	3	0.072	7.2	0.000
5	80	3	0.072	7.2	0.057
6	160	3	0.072	7.2	0.637

TN-98-490 ARMSTRONG LETTUCE-SOIL SURVIVAL
File: f:\ls\490sur.arm Transform: ARC SINE(SQUARE ROOT(Y))

WILCOXON'S RANK SUM TEST W/ BONFERRONI ADJUSTMENT - Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	RANK SUM	CRIT. VALUE	REPS	SIG
1	CONTROL	1.412	--	-	-	
2	10	1.412	10.50	None	3	
3	20	1.358	9.00	None	3	
4	40	1.412	10.50	None	3	
5	80	1.323	9.00	None	3	
6	160	0.646	6.00	None	3	

Critical values use k = 5, are 1 tailed, and alpha = 0.05

STEEL□S MANY-ONE RANK TEST ABORTED

TITLE: TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
FILE: F:\LS\490GRO.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 5

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.3225	0.3225
1	CONTROL	2	0.3551	0.3551
1	CONTROL	3	0.4677	0.4677
2	10	1	0.2896	0.2896
2	10	2	0.5014	0.5014
2	10	3	0.4023	0.4023
3	20	1	0.4111	0.4111
3	20	2	0.3534	0.3534
3	20	3	0.2781	0.2781
4	40	1	0.2271	0.2271
4	40	2	0.3469	0.3469
4	40	3	0.1390	0.1390
5	80	1	0.0771	0.0771
5	80	2	0.1734	0.1734
5	80	3	0.1044	0.1044

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.323	0.468	0.382
2	10	3	0.290	0.501	0.398
3	20	3	0.278	0.411	0.348
4	40	3	0.139	0.347	0.238
5	80	3	0.077	0.173	0.118

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.006	0.076	0.044	19.95
2	10	0.011	0.106	0.061	26.64
3	20	0.004	0.067	0.039	19.20
4	40	0.011	0.104	0.060	43.90
5	80	0.002	0.050	0.029	41.95

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GRO.ARM Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality

D = 0.070

W = 0.951

Critical W (P = 0.05) (n = 15) = 0.881
Critical W (P = 0.01) (n = 15) = 0.835

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GRO.ARM Transform: NO TRANSFORMATION

Bartlett's test for homogeneity of variance
Calculated B1 statistic = 1.24

Table Chi-square value = 13.28 (alpha = 0.01, df = 4)
Table Chi-square value = 9.49 (alpha = 0.05, df = 4)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GRO.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	4	0.166	0.042	5.960
Within (Error)	10	0.070	0.007	
Total	14	0.236		

Critical F value = 3.48 (0.05,4,10)
Since F > Critical F REJECT Ho: All equal

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.382	0.382		
2	10	0.398	0.398	-0.235	
3	20	0.348	0.348	0.503	
4	40	0.238	0.238	2.115	
5	80	0.118	0.118	3.867	*

Dunnett table value = 2.47 (1 Tailed Value, P=0.05, df=10,4)

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	10	3	0.168	44.1	-0.016
3	20	3	0.168	44.1	0.034
4	40	3	0.168	44.1	0.144
5	80	3	0.168	44.1	0.264

TITLE: TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
FILE: F:\LS\490GROA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.3225	0.3225
1	CONTROL	2	0.3551	0.3551
1	CONTROL	3	0.4677	0.4677
2	Na CONTROL	1	0.3659	0.3659
2	Na CONTROL	2	0.0662	0.0662
2	Na CONTROL	3	0.1759	0.1759

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GROA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.323	0.468	0.382
2	Na CONTROL	3	0.066	0.366	0.203

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GROA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.006	0.076	0.044	19.95
2	Na CONTROL	0.023	0.152	0.088	74.82

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GROA.ARM Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality

D = 0.058

W = 0.947

Critical W (P = 0.05) (n = 6) = 0.788
Critical W (P = 0.01) (n = 6) = 0.713

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GROA.ARM Transform: NO TRANSFORMATION

F-Test for equality of two variances

GROUP	IDENTIFICATION	VARIANCE	F
1	CONTROL	0.006	
2	Na CONTROL	0.023	3.963

Critical F = 199.00 (P=0.01, 2, 2)

Since F <= Critical F, FAIL TO REJECT Ho: Equal Variances.

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GROA.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	0.048	0.048	3.342
Within (Error)	4	0.058	0.014	
Total	5	0.106		

Critical F value = 7.71 (0.05,1,4)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GROA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.382	0.382		
2	Na CONTROL	0.203	0.203	1.828	

2 Sample t table value = 2.13 (1 Tailed Value, P=0.05, df=4,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.382	0.382		
2	Na CONTROL	0.203	0.203	1.828	

2 Sample t table value = 2.92 (1 Tailed Value, P=0.05, df=2,1)

TN-98-490 ARMSTRONG LETTUCE-SOIL DRY WEIGHT
File: F:\LS\490GROA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.209	54.7	0.179

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.286	74.9	0.179

Conc. ID	1	2	3	4	5	6
Conc. Tested	0	10	20	40	80	160
Response 1	.32254	.28964	.41114	.22712	.07710	.01910
Response 2	.35512	.50142	.35336	.34688	.17338	.01190
Response 3	.46772	.40228	.27806	.13902	.10438	.03070

*** Inhibition Concentration Percentage Estimate ***
Toxicant/Effluent: TN-98-490 ARMSTRONG LETTUCE-SOIL
Test Start Date: Test Ending Date:
Test Species: L.SATIVA
Test Duration: 28 DAYS
DATA FILE: 490ARMLS.icp
OUTPUT FILE: 490ARMLS.i25

Conc. ID	Number Replicates	Concentration	Response Means	Std. Dev.	Pooled Response Means
1	3	0.000	0.382	0.076	0.390
2	3	10.000	0.398	0.106	0.390
3	3	20.000	0.348	0.067	0.348
4	3	40.000	0.238	0.104	0.238
5	3	80.000	0.118	0.050	0.118
6	3	160.000	0.021	0.009	0.021

The Linear Interpolation Estimate: 30.0467 Entered P Value: 25

Number of Resamplings: 200
The Bootstrap Estimates Mean: 29.5916 Standard Deviation: 7.3089
Original Confidence Limits: Lower: 18.1044 Upper: 46.4061
Expanded Confidence Limits: Lower: 4.9678 Upper: 64.4013
Resampling time in Seconds: 0.06 Random_Seed: 509646156

TN-98-512 ARMSTRONG C.DUBIA-DEFINITIVE 48-HR LC50

****

CONC.	NUMBER EXPOSED	NUMBER DEAD	PERCENT DEAD	BINOMIAL PROB.(PERCENT)
100	10	7	70	17.1875
33	10	2	20	5.46875
10	10	0	0	9.765626E-02
3	10	0	0	9.765626E-02
1	10	0	0	9.765626E-02

AT A CONFIDENCE LEVEL OF 95 PERCENT THE BINOMIAL TEST
SHOWS THAT THE LC50 IS ABOVE 10

AN APPROXIMATE LC50 OF 64.77235 IS OBTAINED BY
NONLINEAR INTERPOLATION BETWEEN 33 AND 100

RESULTS CALCULATED USING THE MOVING AVERAGE METHOD

SPAN	G	LC50	95 PERCENT CONFIDENCE LIMITS	
1	.8025548	64.77245	30.43414	365.7897

RESULTS CALCULATED USING THE PROBIT METHOD

ITERATIONS	G	H	CHI-SQUARE	PROBABILITY
6	.4614222	1	9.654921E-02	.9922483

SLOPE = 3.062653
95 PERCENT CONFIDENCE LIMITS = .9822521 AND 5.143053

LC50 = 65.76475
95 PERCENT CONFIDENCE LIMITS = 39.73449 AND 144.0119

****

TN-98-512 ARMSTRONG C.DUBIA SURVIVAL

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF ALIVE	NUMBER OF DEAD	TOTAL ANIMALS
CONTROL	8	2	10
1	8	2	10
TOTAL	16	4	20

CRITICAL FISHER'S VALUE (10,10,8) (p=0.05) IS 3. b VALUE IS 8.
Since b is greater than 3 there is no significant difference between CONTROL and TREATMENT at the 0.05 level.

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF DEAD	NUMBER OF ALIVE	TOTAL ANIMALS
CONTROL	2	8	10
3	1	9	10
TOTAL	3	17	20

CRITICAL FISHER'S VALUE (10,10,2) (p=0.05) IS LESS THAN 0. b VALUE IS 1.
NO SIGNIFICANT DIFFERENCE

TN-98-512

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF ALIVE	NUMBER OF DEAD	NUMBER OF TOTAL ANIMALS
CONTROL	8	2	10
10	7	3	10
TOTAL	15	5	20

CRITICAL FISHER'S VALUE (10,10,8) (p=0.05) IS 3. b VALUE IS 7.
Since b is greater than 3 there is no significant difference between CONTROL and TREATMENT at the 0.05 level.

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF ALIVE	NUMBER OF DEAD	NUMBER OF TOTAL ANIMALS
CONTROL	8	2	10
33	3	7	10
TOTAL	11	9	20

CRITICAL FISHER'S VALUE (10,10,8) (p=0.05) IS 3. b VALUE IS 3.
Since b is less than or equal to 3 there is a significant difference between CONTROL and TREATMENT at the 0.05 level.

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF ALIVE	NUMBER OF DEAD	NUMBER OF TOTAL ANIMALS
CONTROL	8	2	10
100	1	9	10
TOTAL	9	11	20

CRITICAL FISHER'S VALUE (10,10,8) (p=0.05) IS 3. b VALUE IS 1.
Since b is less than or equal to 3 there is a significant difference between CONTROL and TREATMENT at the 0.05 level.

SUMMARY OF FISHER'S EXACT TESTS

GROUP	IDENTIFICATION	NUMBER EXPOSED	NUMBER DEAD	SIG (P=.05)
	CONTROL	10	2	
1	1	10	2	
2	3	10	1	
3	10	10	3	
4	33	10	7	*
5	100	10	9	*

TN-98-512 ARMSTRONG C.DUBIA SURVIVAL

FISHER'S EXACT TEST

IDENTIFICATION	NUMBER OF ALIVE	NUMBER OF DEAD	TOTAL ANIMALS
CONTROL	8	2	10
Na CONTROL	7	3	10
TOTAL	15	5	20

CRITICAL FISHER'S VALUE (10,10,8) (p=0.05) IS 3. b VALUE IS 7.
Since b is greater than 3 there is no significant difference between CONTROL and TREATMENT at the 0.05 level.

SUMMARY OF FISHER'S EXACT TESTS

GROUP	IDENTIFICATION	NUMBER EXPOSED	NUMBER DEAD	SIG (P=.05)
	CONTROL	10	2	
1	Na CONTROL	10	3	

TITLE: TN-98-512 ARMSTRONG C.DUBIA REPRODUCTION
FILE: F:\LS\512CDREP.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 4

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	14.0000	14.0000
1	CONTROL	2	18.0000	18.0000
1	CONTROL	3	23.0000	23.0000
1	CONTROL	4	32.0000	32.0000
1	CONTROL	5	20.0000	20.0000
1	CONTROL	6	31.0000	31.0000
1	CONTROL	7	27.0000	27.0000
1	CONTROL	8	28.0000	28.0000
1	CONTROL	9	27.0000	27.0000
1	CONTROL	10	8.0000	8.0000
2	1	1	29.0000	29.0000
2	1	2	26.0000	26.0000
2	1	3	19.0000	19.0000
2	1	4	14.0000	14.0000
2	1	5	23.0000	23.0000
2	1	6	23.0000	23.0000
2	1	7	13.0000	13.0000
2	1	8	24.0000	24.0000
2	1	9	20.0000	20.0000
2	1	10	31.0000	31.0000
3	3	1	28.0000	28.0000
3	3	2	18.0000	18.0000
3	3	3	36.0000	36.0000
3	3	4	39.0000	39.0000
3	3	5	20.0000	20.0000
3	3	6	23.0000	23.0000
3	3	7	20.0000	20.0000
3	3	8	22.0000	22.0000
3	3	9	21.0000	21.0000
3	3	10	36.0000	36.0000
4	10	1	13.0000	13.0000
4	10	2	23.0000	23.0000
4	10	3	35.0000	35.0000
4	10	4	24.0000	24.0000
4	10	5	21.0000	21.0000
4	10	6	24.0000	24.0000
4	10	7	24.0000	24.0000
4	10	8	4.0000	4.0000
4	10	9	34.0000	34.0000
4	10	10	20.0000	20.0000

TN-98-512 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\512CDREP.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	10	8.000	32.000	22.800
2	1	10	13.000	31.000	22.200
3	3	10	18.000	39.000	26.300
4	10	10	4.000	35.000	22.200

TN-98-512 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\512CDREP.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	60.178	7.757	2.453	34.02
2	1	34.400	5.865	1.855	26.42
3	3	62.011	7.875	2.490	29.94
4	10	81.733	9.041	2.859	40.72

```
TN-98-512  ARMSTRONG  C.DUBIA  REPRODUCTION
File: F:\LS\512CDREP.ARM       Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D = 2144.900

W =    0.974

Critical W (P = 0.05) (n = 40) = 0.940
Critical W (P = 0.01) (n = 40) = 0.919
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-512  ARMSTRONG  C.DUBIA  REPRODUCTION
File: F:\LS\512CDREP.ARM       Transform: NO TRANSFORMATION

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    1.58

-------------------------------------------------------------------------------
Table Chi-square value =   11.34  (alpha = 0.01, df =   3)
Table Chi-square value =    7.81  (alpha = 0.05, df =   3)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-512 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\512CDREP.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	3	116.475	38.825	0.652
Within (Error)	36	2144.900	59.581	
Total	39	2261.375		

Critical F value = 2.92 (0.05,3,30)
Since F < Critical F FAIL TO REJECT Ho: All equal.

TN-98-512 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\512CDREP.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	22.800	22.800		
2	1	22.200	22.200	0.174	
3	3	26.300	26.300	-1.014	
4	10	22.200	22.200	0.174	

Dunnett table value = 2.15 (1 Tailed Value, P=0.05, df=30,3)

TN-98-512 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\512CDREP.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	10			
2	1	10	7.422	32.6	0.600
3	3	10	7.422	32.6	-3.500
4	10	10	7.422	32.6	0.600

TITLE: TN-98-512 ARMSTRONG C.DUBIA REPRODUCTION
FILE: F:\LS\512CDREA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	14.0000	14.0000
1	CONTROL	2	18.0000	18.0000
1	CONTROL	3	23.0000	23.0000
1	CONTROL	4	32.0000	32.0000
1	CONTROL	5	20.0000	20.0000
1	CONTROL	6	31.0000	31.0000
1	CONTROL	7	27.0000	27.0000
1	CONTROL	8	28.0000	28.0000
1	CONTROL	9	27.0000	27.0000
1	CONTROL	10	8.0000	8.0000
2	Na CONTROL	1	26.0000	26.0000
2	Na CONTROL	2	25.0000	25.0000
2	Na CONTROL	3	36.0000	36.0000
2	Na CONTROL	4	34.0000	34.0000
2	Na CONTROL	5	13.0000	13.0000
2	Na CONTROL	6	14.0000	14.0000
2	Na CONTROL	7	40.0000	40.0000
2	Na CONTROL	8	20.0000	20.0000
2	Na CONTROL	9	19.0000	19.0000
2	Na CONTROL	10	30.0000	30.0000

TN-98-512 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\512CDREA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	10	8.000	32.000	22.800
2	Na CONTROL	10	13.000	40.000	25.700

TN-98-512 ARMSTRONG C.DUBIA REPRODUCTION
File: F:\LS\512CDREA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	60.178	7.757	2.453	34.02
2	Na CONTROL	86.011	9.274	2.933	36.09

Conc. ID	1	2	3	4	5	6
Conc. Tested	0	1	3	10	33	100
Response 1	14	29	28	13	0	0
Response 2	18	26	18	23	13	0
Response 3	23	19	36	35	6	0
Response 4	32	14	39	24	7	0
Response 5	20	23	20	21	0	0
Response 6	31	23	23	24	12	0
Response 7	27	13	20	24	17	0
Response 8	28	24	22	4	0	0
Response 9	27	20	21	34	16	0
Response 10	8	31	36	20	8	0

*** Inhibition Concentration Percentage Estimate ***
Toxicant/Effluent: TN-98-512 ARMSTRONG
Test Start Date: Test Ending Date:
Test Species: C.DUBIA
Test Duration: 7 DAYS
DATA FILE: 512CDARM.icp
OUTPUT FILE: 512CDARM.i25

Conc. ID	Number Replicates	Concentration	Response Means	Std. Dev.	Pooled Response Means
1	10	0.000	22.800	7.757	23.767
2	10	1.000	22.200	5.865	23.767
3	10	3.000	26.300	7.875	23.767
4	10	10.000	22.200	9.041	22.200
5	10	33.000	7.900	6.523	7.900
6	10	100.000	0.000	0.000	0.000

The Linear Interpolation Estimate: 17.0367 Entered P Value: 25

Number of Resamplings: 200
The Bootstrap Estimates Mean: 15.7881 Standard Deviation: 3.2837
Original Confidence Limits: Lower: 8.1411 Upper: 20.4715
Resampling time in Seconds: 0.05 Random_Seed: 851905800

TITLE: TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
FILE: F:\LS\491GERM.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 6

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.8000	0.8000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
2	10	1	0.6000	0.6000
2	10	2	0.7000	0.7000
2	10	3	0.7000	0.7000
3	20	1	0.7000	0.7000
3	20	2	0.6000	0.6000
3	20	3	0.9000	0.9000
4	40	1	0.8000	0.8000
4	40	2	0.6000	0.6000
4	40	3	0.7000	0.7000
5	80	1	0.5000	0.5000
5	80	2	0.7000	0.7000
5	80	3	0.7000	0.7000
6	160	1	0.7000	0.7000
6	160	2	0.4000	0.4000
6	160	3	0.5000	0.5000

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERM.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.800	1.000	0.933
2	10	3	0.600	0.700	0.667
3	20	3	0.600	0.900	0.733
4	40	3	0.600	0.800	0.700
5	80	3	0.500	0.700	0.633
6	160	3	0.400	0.700	0.533

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERM.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.013	0.115	0.067	12.37
2	10	0.003	0.058	0.033	8.66
3	20	0.023	0.153	0.088	20.83
4	40	0.010	0.100	0.058	14.29
5	80	0.013	0.115	0.067	18.23
6	160	0.023	0.153	0.088	28.64

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.241

W = 0.968

Critical W (P = 0.05) (n = 18) = 0.897
Critical W (P = 0.01) (n = 18) = 0.858

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Bartlett's test for homogeneity of variance
Calculated B1 statistic = 2.27

Table Chi-square value = 15.09 (alpha = 0.01, df = 5)
Table Chi-square value = 11.07 (alpha = 0.05, df = 5)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	5	0.414	0.083	4.129
Within (Error)	12	0.241	0.020	
Total	17	0.654		

Critical F value = 3.11 (0.05,5,12)
Since F > Critical F REJECT Ho: All equal

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.310	0.933		
2	10	0.956	0.667	3.064	*
3	20	1.042	0.733	2.321	
4	40	0.995	0.700	2.730	*
5	80	0.923	0.633	3.355	*
6	160	0.820	0.533	4.238	*

Dunnett table value = 2.50 (1 Tailed Value, P=0.05, df=12,5)

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERM.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	10	3	0.206	22.1	0.267
3	20	3	0.206	22.1	0.200
4	40	3	0.206	22.1	0.233
5	80	3	0.206	22.1	0.300
6	160	3	0.206	22.1	0.400

TITLE: TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
FILE: F:\LS\491GERMA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.8000	0.8000
1	CONTROL	2	1.0000	1.0000
1	CONTROL	3	1.0000	1.0000
2	Na CONTROL	1	0.9000	0.9000
2	Na CONTROL	2	0.8000	0.8000
2	Na CONTROL	3	0.8000	0.8000

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERMA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.800	1.000	0.933
2	Na CONTROL	3	0.800	0.900	0.833

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERMA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.013	0.115	0.067	12.37
2	Na CONTROL	0.003	0.058	0.033	6.93

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.075

W = 0.831

Critical W (P = 0.05) (n = 6) = 0.788
Critical W (P = 0.01) (n = 6) = 0.713

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

F-Test for equality of two variances

GROUP	IDENTIFICATION	VARIANCE	F
1	CONTROL	0.031	
2	Na CONTROL	0.007	4.616

Critical F = 199.00 (P=0.01, 2, 2)

Since F <= Critical F, FAIL TO REJECT Ho: Equal Variances.

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Bartlett's test for homogeneity of variance
Calculated B1 statistic = 0.86

Table Chi-square value = 6.63 (alpha = 0.01, df = 1)
Table Chi-square value = 3.84 (alpha = 0.05, df = 1)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	0.036	0.036	1.936
Within (Error)	4	0.075	0.019	
Total	5	0.112		

Critical F value = 7.71 (0.05,1,4)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.310	0.933		
2	Na CONTROL	1.154	0.833	1.391	

2 Sample t table value = 2.13 (1 Tailed Value, P=0.05, df=4,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.310	0.933		
2	Na CONTROL	1.154	0.833	1.391	

2 Sample t table value = 2.92 (1 Tailed Value, P=0.05, df=2,1)

TN-98-491 ARMSTRONG LETTUCE-SAND GERMINATION
File: F:\LS\491GERMA.ARM Transform: ARC SINE(SQUARE ROOT(Y))

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.163	17.5	0.100

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.241	25.8	0.100

TITLE: TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
FILE: F:\LS\491SUR.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 6

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	0.9000	0.9000
1	CONTROL	3	1.0000	1.0000
2	10	1	1.0000	1.0000
2	10	2	1.0000	1.0000
2	10	3	1.0000	1.0000
3	20	1	1.0000	1.0000
3	20	2	1.0000	1.0000
3	20	3	1.0000	1.0000
4	40	1	1.0000	1.0000
4	40	2	1.0000	1.0000
4	40	3	1.0000	1.0000
5	80	1	0.6000	0.6000
5	80	2	0.7100	0.7100
5	80	3	0.5700	0.5700
6	160	1	0.1400	0.1400
6	160	2	0.0000	0.0000
6	160	3	0.0000	0.0000

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.900	1.000	0.967
2	10	3	1.000	1.000	1.000
3	20	3	1.000	1.000	1.000
4	40	3	1.000	1.000	1.000
5	80	3	0.570	0.710	0.627
6	160	3	0.000	0.140	0.047

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SUR.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.003	0.058	0.033	5.97
2	10	0.000	0.000	0.000	0.00
3	20	0.000	0.000	0.000	0.00
4	40	0.000	0.000	0.000	0.00
5	80	0.005	0.074	0.043	11.76
6	160	0.007	0.081	0.047	173.21

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Shapiro - Wilk's test for normality

D = 0.063

W = 0.907

Critical W (P = 0.05) (n = 18) = 0.897
Critical W (P = 0.01) (n = 18) = 0.858

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

Hartley's test for homogeneity of variance
Bartlett's test for homogeneity of variance

These two tests can not be performed because at least one group has zero variance.

Data FAIL to meet homogeneity of variance assumption.
Additional transformations are useless.

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	5	3.420	0.684	129.619
Within (Error)	12	0.063	0.005	
Total	17	3.483		

Critical F value = 3.11 (0.05,5,12)
Since F > Critical F REJECT Ho: All equal

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	1.358	0.967		
2	10	1.412	1.000	-0.916	
3	20	1.412	1.000	-0.916	
4	40	1.412	1.000	-0.916	
5	80	0.915	0.627	7.470	*
6	160	0.234	0.047	18.951	*

Dunnett table value = 2.50 (1 Tailed Value, P=0.05, df=12,5)

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	10	3	0.080	8.3	-0.033
3	20	3	0.080	8.3	-0.033
4	40	3	0.080	8.3	-0.033
5	80	3	0.080	8.3	0.340
6	160	3	0.080	8.3	0.920

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SUR.ARM Transform: ARC SINE(SQUARE ROOT(Y))

WILCOXON'S RANK SUM TEST W/ BONFERRONI ADJUSTMENT - Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	RANK SUM	CRIT. VALUE	REPS	SIG
1	CONTROL	1.358				
2	10	1.412	12.00	None	3	
3	20	1.412	12.00	None	3	
4	40	1.412	12.00	None	3	
5	80	0.915	6.00	None	3	
6	160	0.234	6.00	None	3	

Critical values use k = 5, are 1 tailed, and alpha = 0.05

STEEL□S MANY-ONE RANK TEST ABORTED

TITLE: TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
FILE: F:\LS\491SURA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	1.0000	1.0000
1	CONTROL	2	0.9000	0.9000
1	CONTROL	3	1.0000	1.0000
2	Na CONTROL	1	1.0000	1.0000
2	Na CONTROL	2	1.0000	1.0000
2	Na CONTROL	3	1.0000	1.0000

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SURA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.900	1.000	0.967
2	Na CONTROL	3	1.000	1.000	1.000

TN-98-491 ARMSTRONG LETTUCE-SAND SURVIVAL
File: F:\LS\491SURA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.003	0.058	0.033	5.97
2	Na CONTROL	0.000	0.000	0.000	0.00

TITLE: TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
FILE: F:\LS\491GRO.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 4

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.0660	0.0660
1	CONTROL	2	0.0796	0.0796
1	CONTROL	3	0.0743	0.0743
2	10	1	0.0556	0.0556
2	10	2	0.0618	0.0618
2	10	3	0.0700	0.0700
3	20	1	0.0585	0.0585
3	20	2	0.0624	0.0624
3	20	3	0.0631	0.0631
4	40	1	0.0555	0.0555
4	40	2	0.0606	0.0606
4	40	3	0.0413	0.0413

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.066	0.080	0.073
2	10	3	0.056	0.070	0.062
3	20	3	0.059	0.063	0.061
4	40	3	0.041	0.061	0.052

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GRO.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.007	0.004	9.38
2	10	0.000	0.007	0.004	11.61
3	20	0.000	0.002	0.001	4.01
4	40	0.000	0.010	0.006	19.11

```
TN-98-491  ARMSTRONG  LETTUCE-SAND  DRY WEIGHT
File: F:\LS\491GRO.ARM       Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality
-------------------------------------------------------------------------------

D =    0.000

W =    0.949

Critical W (P = 0.05) (n = 12) = 0.859
Critical W (P = 0.01) (n = 12) = 0.805
-------------------------------------------------------------------------------

Data PASS normality test at P=0.01 level. Continue analysis.


TN-98-491  ARMSTRONG  LETTUCE-SAND  DRY WEIGHT
File: F:\LS\491GRO.ARM       Transform: NO TRANSFORMATION

-------------------------------------------------------------------------------
Bartlett's test for homogeneity of variance
Calculated B1 statistic =    2.56

-------------------------------------------------------------------------------
Table Chi-square value =   11.34  (alpha = 0.01, df =   3)
Table Chi-square value =    7.81  (alpha = 0.05, df =   3)

Data PASS B1 homogeneity test at 0.01 level. Continue analysis.
```

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GRO.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	3	0.001	0.000	4.242
Within (Error)	8	0.000	0.000	
Total	11	0.001		

Critical F value = 4.07 (0.05,3,8)
Since F > Critical F REJECT Ho: All equal

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.073	0.073		
2	10	0.062	0.062	1.851	
3	20	0.061	0.061	2.042	
4	40	0.052	0.052	3.554	*

Dunnett table value = 2.42 (1 Tailed Value, P=0.05, df=8,3)

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GRO.ARM Transform: NO TRANSFORMATION

DUNNETT'S TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	10	3	0.014	19.4	0.011
3	20	3	0.014	19.4	0.012
4	40	3	0.014	19.4	0.021

TITLE: TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
FILE: F:\LS\491GROA.ARM
TRANSFORM: NO TRANSFORM NUMBER OF GROUPS: 2

GRP	IDENTIFICATION	REP	VALUE	TRANS VALUE
1	CONTROL	1	0.0660	0.0660
1	CONTROL	2	0.0796	0.0796
1	CONTROL	3	0.0743	0.0743
2	Na CONTROL	1	0.0614	0.0614
2	Na CONTROL	2	0.0776	0.0776
2	Na CONTROL	3	0.0694	0.0694

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GROA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 1 of 2

GRP	IDENTIFICATION	N	MIN	MAX	MEAN
1	CONTROL	3	0.066	0.080	0.073
2	Na CONTROL	3	0.061	0.078	0.069

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GROA.ARM Transform: NO TRANSFORM

SUMMARY STATISTICS ON TRANSFORMED DATA TABLE 2 of 2

GRP	IDENTIFICATION	VARIANCE	SD	SEM	C.V. %
1	CONTROL	0.000	0.007	0.004	9.38
2	Na CONTROL	0.000	0.008	0.005	11.70

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GROA.ARM Transform: NO TRANSFORMATION

Shapiro - Wilk's test for normality

D = 0.000

W = 0.912

Critical W (P = 0.05) (n = 6) = 0.788
Critical W (P = 0.01) (n = 6) = 0.713

Data PASS normality test at P=0.01 level. Continue analysis.

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GROA.ARM Transform: NO TRANSFORMATION

F-Test for equality of two variances

GROUP	IDENTIFICATION	VARIANCE	F
1	CONTROL	0.000	
2	Na CONTROL	0.000	1.398

Critical F = 199.00 (P=0.01, 2, 2)

Since F <= Critical F, FAIL TO REJECT Ho: Equal Variances.

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GROA.ARM Transform: NO TRANSFORMATION

ANOVA TABLE

SOURCE	DF	SS	MS	F
Between	1	0.000	0.000	0.394
Within (Error)	4	0.000	0.000	
Total	5	0.000		

Critical F value = 7.71 (0.05,1,4)
Since F < Critical F FAIL TO REJECT Ho: All equal

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GROA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 1 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.073	0.073		
2	Na CONTROL	0.069	0.069	0.628	

2 Sample t table value = 2.13 (1 Tailed Value, P=0.05, df=4,1)

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	TRANSFORMED MEAN	MEAN CALCULATED IN ORIGINAL UNITS	T STAT	SIG
1	CONTROL	0.073	0.073		
2	Na CONTROL	0.069	0.069	0.628	

2 Sample t table value = 2.35 (1 Tailed Value, P=0.05, df=3,1)

TN-98-491 ARMSTRONG LETTUCE-SAND DRY WEIGHT
File: F:\LS\491GROA.ARM Transform: NO TRANSFORMATION

EQUAL VARIANCE t-TEST - TABLE 2 OF 2 Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.013	17.9	0.004

UNEQUAL VARIANCE t-TEST Ho:Control<Treatment

GROUP	IDENTIFICATION	NUM OF REPS	Minimum Sig Diff (IN ORIG. UNITS)	% of CONTROL	DIFFERENCE FROM CONTROL
1	CONTROL	3			
2	Na CONTROL	3	0.014	19.7	0.004

Conc. ID	1	2	3	4	5
Conc. Tested	0	10	20	40	80
Response 1	.06600	.05556	.05854	.05554	.00633
Response 2	.07964	.06182	.06238	.06062	.01880
Response 3	.07434	.07002	.06312	.04128	.01563

*** Inhibition Concentration Percentage Estimate ***
Toxicant/Effluent: TN-98-491 ARMSTRONG LETTUCE-SAND
Test Start Date: Test Ending Date:
Test Species: L.SATIVA
Test Duration: 28 DAYS
DATA FILE: 491ARMLS.icp
OUTPUT FILE: 491ARMLS.i25

Conc. ID	Number Replicates	Concentration	Response Means	Std. Dev.	Pooled Response Means
1	3	0.000	0.073	0.007	0.073
2	3	10.000	0.062	0.007	0.062
3	3	20.000	0.061	0.002	0.061
4	3	40.000	0.052	0.010	0.052
5	3	80.000	0.014	0.006	0.014

The Linear Interpolation Estimate: 34.3271 Entered P Value: 25

Number of Resamplings: 200
The Bootstrap Estimates Mean: 34.5431 Standard Deviation: 7.1117
Original Confidence Limits: Lower: 22.3348 Upper: 45.9265
Expanded Confidence Limits: Lower: 9.1432 Upper: 58.6859
Resampling time in Seconds: 0.05 Random_Seed: 680413150