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CHARACTERIZATION OF NEUTRON AND PROTON EXPOSURE ON THE RADIATION RESISTANT BACTERIUM, *DEINOCOCCUS RADIODURANS*

THESIS

Ronald C. Lenker, Major, USA

AFIT-ENP-MS-17-M-100

DEPARTMENT OF THE AIR FORCE AIR UNIVERSITY

AIR FORCE INSTITUTE OF TECHNOLOGY

Wright-Patterson Air Force Base, Ohio

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CHARACTERIZATION OF NEUTRON AND PROTON EXPOSURE ON THE RADIATION RESISTANT BACTERIUM, *DEINOCOCCUS RADIODURANS*

THESIS

Presented to the Faculty

Department of Engineering Physics

Graduate School of Engineering and Management

Air Force Institute of Technology

Air University

Air Education and Training Command

In Partial Fulfillment of the Requirements for the

Degree of Master of Science in Nuclear Engineering

Ronald C. Lenker, MS

Major, USA

March 2017

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AFIT-ENP-MS-17-M-100

Abstract

Deinococcus radiodurans is a robust bacterium that is known for its extraordinary resistance to ionizing radiation. In general, many of the investigations of this bacterium's resistance have revolved around low linear energy transfer radiation, such as gamma and electron radiation. This study explored *Deinococcus radiodurans*'s ability to survive high linear energy transfer radiation, specifically proton and neutron radiation. *Deinococcus radiodurans* was dehydrated to reduce the effects of low linear energy transfer radiation of varying amounts and rehydrated. The resulting colonies were counted and compared to colonies of non-irradiated control samples using a two population, t-statistic test. With few, non-trend forming exceptions, the results of these comparisons showed, with 95% certainty, that there was no statistical difference between the non-irradiated controls and the irradiated samples.



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I would like to express my sincere appreciation to my faculty advisor, the faculty of ENP, and the scientists and researchers of USAFSAM and the Sandia Ion Beam Laboratory.

Ronald C. Lenker



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CHARACTERIZATION OF NEUTRON AND PROTON EXPOSURE ON THE RADIATION RESISTANT BACTERIUM, *DEINOCOCCUS RADIODURANS*

I. Introduction

General Issue

Successfully surviving and navigating an irradiated battlefield, searching for survivors at the location of a nuclear reactor meltdown, or continuing to explore our solar system all involve exposure to ionizing radiation. As such, there continues to be a need within the United States Department of Defense and other governmental organizations to develop medical capabilities to either prevent or neutralize the biological damage caused by ionizing radiation. The Defense Threat Reduction Agency has a multiyear BAA for Basic Research for Combating Weapons of Mass Destruction (HDTRA-11-12-BRCWMD-BAA) to include "advancing knowledge to protect life."[1] The National Institute of Health also has research goals aligned to this endeavor, with "Determining mechanisms for radiation protection, mitigation and treatment."[1]

By investigating the mechanisms behind *Deinococcus radiodurans*'s (Dr) remarkable ability to resist ionizing radiation, we may further the understanding of how to protect human cells from the dangers of ionizing radiation. Specifically, investigations will be made into Dr's survivability in a neutron and proton environment, experiencing high linear energy transfer (LET) radiation.



Problem Statement

The purpose of this research is to develop an understanding of Dr's ability to deal with varying levels of heavy charged particle (HCP) and neutron radiation measured in Grays (Gy). In SI units, the Gy is a Joule per kilogram (J/kg). Specifically, the type of HCP radiation to be researched is proton radiation. The overarching goal of this research is to test Dr's survivability in both neutron and proton environments. Populations exposed to varying levels of both neutron and proton radiation will be compared with non-irradiated control groups.

Hypothesis

The objective of these series of experiments is to test Dr's resistance to both neutron and proton radiation, at varying doses. The hypothesis: Dr demonstrates resistance to gamma induced ionizing radiation (low LET), but will not show similar resistance to neutron nor proton radiation (high LET). The null hypothesis: The populations of the experimental group (neutron or proton irradiated) and control group (no radiation) will not be statistically different.

Research Objectives

The research objectives are as follows:

- 1. Compare untreated samples of wild type Dr to samples with varying irradiation treatments of neutrons and protons.
- 2. Compare untreated samples of Dr mutants to samples with varying irradiation treatments of neutrons and protons.



Assumptions/Limitations

There is no specifically known Relative Biological Effectiveness (RBE) for Dr, however the International Commission on Radiological Protection (ICRP) created a standard RBE based on the type of radiation and in some cases, such as neutrons, the particles' energy. Another way to measure radiation in addition to the Gy is the Sievert (Sv), which is also J/kg. However, Sieverts include a RBE. This RBE contains different weights depending on the type of radiation. For photons and electrons, a weighting factor of 1 is used. This means for low LET radiation, there is no difference between Gy and Sv.

However, there is a weight factor for both HCP and neutrons. In the case of HCP, such as the protons used in this experiment, the weighting factor is 20. This means that unlike radiations involving electrons and photons, where Gy and Sv are the same, the equivalent dose of proton radiation in Sv will be twenty times that of the absorbed dose in Gy. The weighting factor is slightly different for neutrons because it is based on their energy. For this experiment, a weighting factor of 10 corresponds to the neutrons of energy 2.45 MeV.[2]

For the experiments conducted on Dr, the intent is to look at how Dr reacts to high linear energy transfer (LET) as a result of the bombardment of protons and neutrons. In order to minimize the effects of low LET and radicals created in water, the samples are desiccated. In previous experiments it has been shown Dr is fairly impervious to desiccation and can be revived with few losses even after several weeks. All samples are expected to be desiccated for around two weeks or less. Further, they will be shipped in



sterile containers to prevent contamination. However, they will be subjected to slight jarring and temperature fluctuations associated with shipping.

During the proton experiment, samples will need to be exposed to the environment of the ion beam laboratory while shifting their holder plate onto the stage of the ion beam. There is some risk of contamination during these periods, but will be mediated by as short as possible exposures and the samples will be covered following the end of proton irradiation.

Finally, there are only a limited number of samples that will be able to be radiated due time constraints of neutron generator / particle beam use. This will affect the depth of statistical data that can be gleaned from the experiments.

II. Literature Review

Chapter Overview

The purpose of this chapter is to enlighten the reader on the basic biology of Dr and its ability to repair itself following radiation treatment. The discussion will also delve into radiation itself by describing the differences of high and low LET. Finally, it will explain some of the Dr mutants used in the experiments.

A Brief Description of *Deinococcus radiodurans*

Deinococcus radiodurans is a robust bacterium that is known for its extraordinary resistance to ionizing radiation in the form of gamma radiation. In fact, this biological adaptation led to its discovery as a contaminant in radiation-sterilized corned beef cans in the mid-20th Century. This organism has the capacity to withstand massive DNA



damage inflicted by ionizing radiation. For example, Bruch, et al. tested a Mn(II) speciation of Dr with doses up to 10 kGy of gamma rays with only a two log kill lethality.[3] "Well-aerated, exponential-phase cultures...will survive 5000 Gy of gamma radiation without loss of viability, and survivors are routinely recovered from cultures exposed to as much as 20 kGy".[4] The mechanisms for this biological adaptation are still being investigated, though they are suspected to be related to its DNA, its protective proteins, or as a by-product of its ability to overcome severe desiccation.[5]

Some of the features of this particular bacteria include two large chromosomes, and two smaller plasmids.[5] This genetic material is toroid in form. Dr is gram-positive, pigmented, and non-motile. Additionally, it is a non-spore forming, spherical bacterium whose size ranges of 1.5 to 3.5 microns in diameter, and exists in tetrads. It is capable of growing with a doubling time of about 80 minutes in a rich nutrient environment. [6]

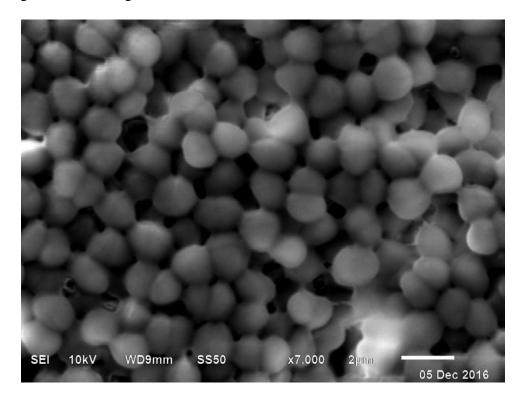


Figure 1. Deinococcus radiodurans taken by SEM at USAFSAM.



High LET and Low LET

Linear energy transfer can be described as the "average energy locally imparted to the medium by a charged particle of specific energy traversing a distance."[7] In low LET, "the average spacing between energy transfer events along the track of the charged particle will be on the order of hundreds of nanometers." This means for low LET, you may only see an order of magnitude of 10 energy transfer events per μ m. Examples of low LET radiation are gamma and electrons.

However, for high LET, "the formation of regions of ionization will be close together and will, in the limit, form a continuous chain, or column, of ionization damage."[7] Therefore, for high LET, one might see an order of magnitude of as high as 1000s of energy transfer events per µm. Examples of high LET radiation include alpha particles, protons, and neutrons.

Neutrons are not charged particles. However, neutrons will cause elastic, inelastic, non-elastic, neutron capture, and spallation events involving charged particles.[7] A charged particle has the intrinsic property of an electric charge and can be either positive or negative. An atom for example is made of protons which have a positive charge, electrons which have a negative charge, and neutrons which do not carry a charge. Atoms themselves are neutral as well, but may become ionized. This process happens when an electron is stripped off the atom and the resulting ion will have an overall positive charge.

Since we will be dealing with mono-energetic neutrons of 2.45 MeV, the events we will be concerned with include elastic, inelastic, and non-elastic scatter. A neutron elastic scatter is "the kinetic interaction of an energetic neutron with a nucleus of the



absorbing medium in which classical kinematics describes the energy transfer. The elastic scattering process is important for neutrons with energies up to 14 MeV or so."[7] For neutrons that undergo inelastic scatter, the process is slightly different. In this case, an initial neutron will be absorbed within a target nucleus, creating a short-lived compound nucleus which then re-emits a neutron. This reaction will only occur if the initial neutron's energy "is greater than the threshold energy necessary for conservation of energy and momentum."[7] Finally, a non-elastic scatter is similar to an inelastic scatter, but after the neutron is captured, the re-emitted particle is not another neutron.[7] At this time, there has been very little experimentation involving high LET radiation and Dr.

Direct and Indirect Action

Both high LET and low LET can result in either direct or indirect action. In the case of indirect damage, the ionization and excitation of water by beta (electrons), gamma (photons), and HCP radiation result in the creation of radical species. For example, energetic photons may cause water to enter an excited state, then dissociate in H· and OH· radicals. Likewise, ionization of water results in H₂0⁺ and e⁻. These products will go on to interact with other water molecules and hydrogen to form other radicals such as H₂0⁻, H·, and e_{aq}^{-} .[7] These radicals then attack cellular components including DNA.

In regards to direct damage, Alpen states, "Of greater importance with high LET radiations is the high likelihood that an ionizing event will occur directly in the important



target bioactive molecule."[7] In this study, the bioactive molecule of consideration is deoxyribonucleic acid (DNA).

DNA

DNA is the genetic code found in all living organisms. The complex molecule's shape is that of a double-helix whose spiral is made up of two strands of monomer nucleotides. These nucleotides consist of a deoxyribose sugar molecule that is covalently bonded to a phosphate molecule, forming a sort of phosphate-sugar backbone. Like the rungs on a twisted ladder, this backbone also has base pair steps. Each base pair is a combination of a purine and a pyrimidine bound through hydrogen bonding. The purine Adenine bonds with the pyrimidine Thymine. Likewise, the purine Guanine bonds with the pyrimidine Cytosine. The order of the bases pairs forms the genetic code which tells a cell how to form the proteins necessary for cellular functions.[8]

The bases and sugar molecules of the DNA present targets, which both can undergo chemical reactions from the radicals mentioned in the previous section. The more damaging attack however, is when these radicals break the covalent bond between the sugar and phosphate molecules on the backbone. If this type of damage occurs to the DNA, the result may be either a single strand break (SSB) or a double strand break (DSB). In the case of a SSB, one of the two strands of DNA are severed. For DSBs, both DNA strands are severed in proximity of each other, usually within 10 base pairs or less. If a cell is unable to repair either a SSB or a DSB, the genetic code may be unusable by the cell. Without this information, mutations may occur or the cell may be unable to produce proteins needed for survival, resulting in cell death. Specifically, "for simpler



organisms, such as bacteriophages and viruses...measurement of DSBs in organisms with double-stranded DNA precisely correlate with biological inactivation."[7]

DNA Damage from Direct and Indirect Actions

DNA damage may result from either direct or indirect damage. In general, a cell's DNA exposed to high LET often receives numerous DSBs, which completely sever the DNA. This is due to the more numerous events per distance as mentioned earlier. DSBs are "far more serious in the consequences for a cell…and repair of DSBs is an error-prone process that will frequently lead to mutation in the genome and/or loss of reproductive capacity."[7]

Indirect damage to DNA is the result of radicals created during indirect events. Low LET is usually the cause of the "indirect action of the products of radiolysis" which can result in SSBs.[7] SSBs are more readily repaired, though multiple SSBs in proximity can result in DSBs. Alpen further states, "it has been suggested that the high LET radiation...produces its damaging effect by production of double-strand breaks as single events, whereas low LET radiation is thought to produce a preponderance of damage through interaction of two sublethal events."[7]

Numerous studies involving low LET radiation (such as gamma and electrons) have led to further questions about Dr's radio-resistance. Is Dr able to survive due to having several copies of DNA available, the production of unique proteins which provide more protection to the DNA from radicals, a higher amount of scavengers which remove the radicals before they can attack its DNA, a higher functionality of repair enzymes



capable of high fidelity DSB repair, presence of Manganese which seems to provide resistance, or some combination of the above?

Deinococcus radiodurans DNA Damage and Repair

Both high LET and low LET radiation affect a cell's DNA, causing either SSBs or DSBs. In order to repair SSBs, Dr uses a method of repair called excision repair. In this method, "the nucleotide excision repair removes pyrimidine dimers and oxidatively damaged DNA."[9] This is accomplished when the UvrA-UvrB protein complex, found in bacteria, locates and verifies the damage. The damaged area is removed and is filled by polymerase I. The repair is completed when DNA ligase I "seals the nick."[10] Polymerase I and ligase are enzymes involved in DNA repair.

Dr exhibits a two phase reconstruction of its DNA following DSBs. The first phase involves "a process dubbed extended synthesis-dependent single-strand DNA annealing (ESDSA)."[11]. In this process, shown in Figure 2, "chromosomal fragments with overlapping homologies are used both as primers and as templates for massive synthesis of complementary strands" and "depends on DNA polymerase I and incorporates more nucleotides than does normal replication in intact cells." [12] These newly created strands, which are complementary, become high-precision extensions which are able "join together contiguous DNA fragments into long, linear, double stranded intermediates."

This then leads into the second phase, which "involves RecA protein-mediated double strand break repair."[11] At this point, "these intermediates require RecAdependent crossovers to mature into circular chromosomes that comprise double-stranded



patchworks of numerous DNA blocks synthesized before radiation, connected by DNA blocks synthesized after radiation."[12]

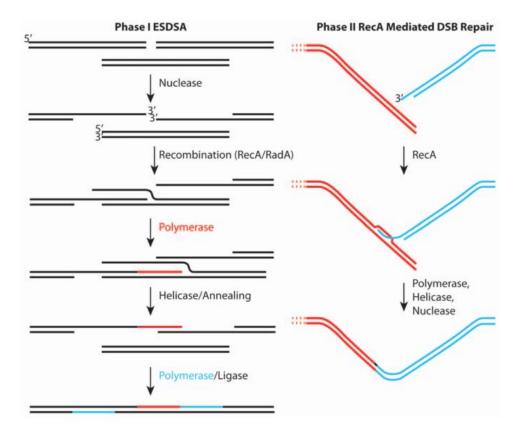


Figure 2. Two stages of genome reconstitution in Deinococcus radiodurans.[11]

Deinococcus radiodurans and Mutant Strains

The *Deinococcus radiodurans* R1 strain selected for this experiment was acquired from the American Type Culture Collection (ATCC) for use by United States Air Force School of Aerospace Medicine (USAFSAM). In addition to this wild-type (WT) strain, the laboratory staff, at USASAM, created 11 mutant strains. Three of these strains were selected for testing during both neutron and proton exposure and are listed in the Table 1.



#	Gene KO	Common Name	Proper Genotype
1	none	WT	
5	DR_1279	Mn SOD	$\Delta DR_{1279::mlox}$
8	DR_1546	Cu/Zn SOD	∆DR_1546::KAN
	DR_A0202	Cu/Zn SOD	∆ <i>DR_A0202::NAT</i>
11	BshA	Bacillithiol Biosynthesis	∆bshA::mlox

Table 1. Deinococcus radiodurans R1 Stain List

Each of the mutants in the study has one or two genes removed that are suspected to have a role in the radio-resistance of Dr. This resistance involves the radicals created from the interaction of ionizing, low LET radiation and water as previously mentioned. In the case of Mutants #5 and #8, a superoxide dismutase (SOD) was removed or "knocked out" (KO). A SOD is an antioxidant enzyme which can break down a superoxide radical to a chemical less damaging to a cell. For Mutants #5 and #8, the metal cofactors are manganese (Mn) and copper (Cu) / zinc (Zn).

For Mutant #11, the gene KO is not a SOD. Instead it is bacillithiol A (BshA), which is "responsible for the first committed step in bacillithiol biosynthesis."[13] This compound is found in many Gram-positive bacteria, such as Dr. "It is involved in maintaining cellular redox balance as well as the destruction of reactive oxygen species."[13]



Additionally, a laboratory strain of Escherichia coli (EC), common name DH5A, acquired from Protein Express, Inc. was used during the 3rd neutron irradiation experiment.

III. Methodology

Chapter Overview

The purpose of this chapter is to describe the methods used to conduct experimental procedures on Dr to test the hypothesis listed in the first chapter. This section begins with how Dr was prepared prior to irradiation. Next, a brief description of both neutron and proton generation is given. The next subsection looks at irradiation and rehydration of samples. Finally, an explanation on the methods of statistical analysis is given.

Deinococcus Radiodurans Sample Preparation

Initial Sample Growth

The bacteria preparation consisted of several steps, ultimately yielding a Dr sample that was 2-5 x 10^8 CFU/ml. These steps were conducted at USAFSAM. Initially, WT and the selected mutants were grown in a tryptone-glucose-yeast extract (TGY, with antibiotic selection of Nourseothricin (NAT) and Kanamycin (KAN) for mutant #8 only) culture medium (0.5 % tryptone, 0.3% yeast extract, 0.1% glucose). Colonies were streaked for isolation and incubated for 48 hours at 32 °C in unsealed plastic bags in order to prevent drying. After the 48 hours, a single colony per strain was inoculated into 5 ml of TGY culture medium using 14 ml round bottom tubes, again with antibiotics for



mutant #8. The inoculated colonies were incubated overnight at 32 °C and 220 RPM for aeration. The following day, the cultures were diluted 1:100 (200 μ l of overnight cell culture) into 20 ml of fresh TGY culture medium within a 150 ml flask with appropriate selection of antibiotics for mutant #8. The flasks were incubated overnight at 32 °C and 220 RPM.

After approximately 24 hours, the cultures were diluted to an optical density (OD_{600}) of 0.25 in 40 ml of TGY culture medium into 250 ml flasks. This was achieved using the Thermo Scientific NanoDrop 2000c Spectrophotometer and accompanying software. A 1:10 dilution sample of each Dr strain (100 µl of culture, 900 µl TGY) was added to a cuvette. The NanoDrop 2000c then took readings based on a 10mm pathlength of light. Below is a sample calculation showing how much culture needed to be added to achieve the OD₆₀₀ of 0.25. The initial OD₆₀₀ was multiplied by 10 to account for a 1:10 dilution. Tables of these measurements for each experiment appear in Appendix A.

$$40 \ ml * \frac{.25}{4.97} = 2.0 \ ml$$

The flasks were then incubated four hours at 32 °C and 220 RPM to achieve early log phase.

After the incubation period was completed, the cultures were concentrated 10x by centrifugation, with 30 ml of the cultures transferred into 50 ml conical tubes, set to 3500 RPM for 20 minutes in a table top centrifuge. During the spin, OD₆₀₀ readings were taken to determine the CFU/ml post four hour incubation. A calculation was done to



determine the amount of media to achieve an OD_{600} of 5. Tables of these calculations are found in Appendix A.

$$30 ml * \frac{.624}{5} = 3.7 ml$$

Next, the supernatant was poured off completely and the remaining pellets were resuspended into fresh TGY culture media to achieve an OD_{600} of 5, which corresponds to 2-5 x 10⁸ CFU/ml.

Sample Plate Preparation

In a biosafety cabinet, the samples were transferred to the wells of a 96 well plate column in order to easily deposit the samples onto the 96 well, flat bottom plate lids. The procedure was utilized for the first and second neutron experiments.

Using a multi-channel pipet, 60 µl of cells were transferred to the lid "wells" of three 96 well, flat bottom plate lids as shown in Figure 3. One plate lid was used as an untreated control, while the other two plate lids were irradiated. The lid wells were used instead of the actual wells because of the follow on experiments. Specifically, at Sandia National Lab using the QASPR-3 (Qualification Alternative to the Sandia Pulse Reactor 3) tandem ion beam, only a 96 well plate lid, not the plate, was initially thought to fit the sample stage in the QASPR-3's irradiation chamber, so all experimentation was completed using the lid wells.



	1	2	3	4	5	6	7	8	9	10	11	12
A	1	1	1	1	1	1	1	1	1	1	1	1
В												
С	5	5	5	5	5	5	5	5	5	5	5	5
D												
E	8	8	8	8	8	8	8	8	8	8	8	8
F												
G	11	11	11	11	11	11	11	11	11	11	11	11
Н												

Figure 3. This array depicts the location of each strain of Dr. Each strain (represented by number, i.e. 1 is WT, 5 is Mutant #5, etc.) was separated from the others by a row. This setup allowed for twelve samples per strain.

After reviewing several sample sizes, $60 \ \mu$ l drops were chosen as they provided the most level, even surface compared to other drop sizes. The plate lids were left within the BSL cabinet's laminar flow hood in order to dry overnight. After 24 hours of drying, the plate lids were placed on their respective plates and sealed with parafilm. They then sat desiccated for a day awaiting treatment. This was done in order to simulate shipping to Sandia National Laboratory for the proton experiment.



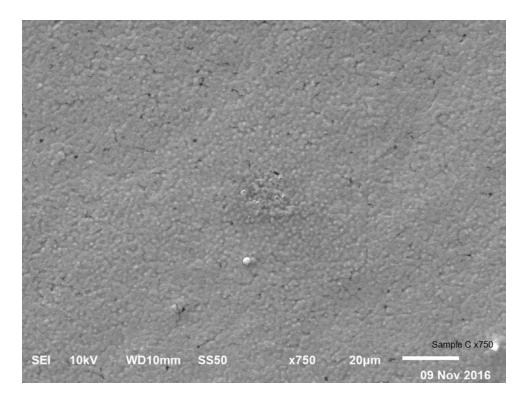


Figure 4. 60μ l drop of Deinococcus radiodurans at 2-5 x 10^8 CFUs / ml count taken by SEM at USAFSAM.

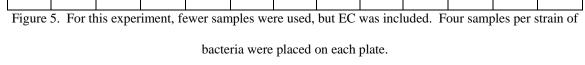
A remaining 96 well, flat bottom plate with 40 μ l of TGY in row A and 180 μ l of TGY culture media in rows B-H was next used as a control to determine an initial CFU baseline. This baseline, referred to as a CFU input, provides a control for un-desiccated, non-irradiated bacteria. 60 μ l drops of culture were added to row A, with the strains as follows: 1 1 1/5 5 5/8 8 8/11 11 11. The cells were then diluted 10 fold, seven times in series down the plate column by transferring 20 μ l into the 180 μ l of TGY media in rows B through H. Finally, 5 μ l spots were transferred to TGY agar trays, which were then incubated for 48 hours at 32 °C in unsealed plastic bags in order to prevent drying.



For the 3rd neutron experiment, EC was added. The cell culture media used for EC was LB broth (1.0 % tryptone, 0.5% yeast extract, and 0.5% sodium chloride) and EC was incubated in 37 °C. The procedures above were followed with the additional of EC.

A modification from the procedure occurred when placing the samples onto the plate. Instead of using a multi-channel pipette, a single channel pipette was used in order to gain more precision when placing the drops in the center of their wells. Figure 5 shows how the samples were arrayed for the 3rd neutron experiment. Four plates were created for irradiation, with a fifth plate as an un-irradiated control.

	1	2	3	4	5	6	7	8	9	10	11	12
A	1	1	1	1					EC	EC	EC	EC
В												
C	5	5	5	5								
D												
E	8	8	8	8								
F												
G	11	11	11	11								
Н												



The plate setup for the proton experiment was modified as well. Two sets of plates (A & B) were created in the event any plate was damaged during shipping. Each



set consisted of WT, and mutants 5, 8, and 11, with an untreated control plate. This time, each row of the samples were designated to receive varying amounts of proton irradiation. Another non-irradiated control was on the plate designated for irradiation that would also experience the same environmental condition inside the QASPR-3, minus irradiation. The untreated control plates of sets A and B had eight samples per strain. These setups are depicted in Figures 6 and 7, using WT as an example.

	1	2	3	4	5	6	7	8	9	10	11	12
А	1	1	1	1	1	1	1	1		100 Gy	/	1
В												
C	1	1	1	1	1	1	1	1		500 Gy	/	1
D												
E	1	1	1	1	1	1	1	1	1000 Gy			1
F												
G	1	1	1	1	1	1	1	1		2500 G	У	1
Н												

Figure 6. The samples in columns 1-8, rows A, C, E, and G were set to receive various amounts of irradiation. These rows set to receive 100, 500, 1000, 2500 Gy respectively. All samples in column 12 did not receive any radiation. The 1 in each box represents wild type, but plates with the other mutants were also constructed.

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	1	2	3	4	5	6	7	8	9	10	11	12
А	1	1	1	1	1	1	1	1				
В												
С	5	5	5	5	5	5	5	5				
D												
E	8	8	8	8	8	8	8	8				
F												
G	11	11	11	11	11	11	11	11				
Н												

Figure 7. Rows A, C, E, and G held WT, mutant 5, 8, and 11 respectively.

Neutron Generation

The Adelphi Technology, Inc. DD109.1 Neutron Generator was the source of neutrons for the irradiation of Dr. This neutron generator produces the neutrons via a Deuteron-Deuteron (D-D) reaction. It is capable of a neutron output of up to 1x10⁹ neutrons per second and can operate in a continuous or pulsed manner. The fast neutrons are produced mono-energetically at 2.45 MeV and the source size is approximately 16mm in diameter. This neutron generator operates with an ion beam supplied by a microwave plasma source. Microwave power is supplied by a magnetron. The ion source uses the electron cyclotron resonance effect to produce a high plasma density for the high current and high D+ content.[14]

The reaction of interest for neutron generation is the following:



$$2D + 2D \rightarrow 3He (0.87 \text{ MeV}) + n (2.45 \text{ MeV})$$

The generator is able to do this by using a titanium hydride target, which is impregnated with deuterium atoms. Deuterium gas is injected into the plasma chamber, which is ionized by the microwave source. A sufficient voltage, which overcomes the Coulomb barrier, is applied between the ion chamber and target. This accelerates the deuterium ions to the target, enabling them to fuse with the deuterons in the titanium. The products of this fusion are the 2.45 MeV neutrons and He. However, this reaction only occurs 50% of the time. The other 50% of the time the following reaction occurs [15]:

$$2D + 2D \rightarrow T + H$$

Neutron Dose Calculations

In order to calculate the dose of radiation via neutron exposures, the method as outlined by Cember in *Introduction to Health Physics* was followed. [16] Using N, the number of atoms/kg, f, the mean fractional energy transferred from neutron to scattered atom during collision with the neutron, and σ , the scattering cross section of the element for neutrons of energy E (2.45 MeV), the following value was found, as shown in Table 2.



	% Mass	Ν,				
Element		atoms/kg	f	σ, cm²	Nσf	
Oxygen	0.13	2.69E+25	0.111	8.45410E-25	2.524E+00	
Carbon	0.31	6.41E+24	0.142	1.58290E-24	1.441E+00	
Hydrogen	0.49	5.98E+25	0.5	2.59131E-24	7.748E+01	
Nitrogen	0.07	1.49E+24	0.124	1.30501E-24	2.411E-01	
				Σ Nσf	8.169E+01	cm²/kg

Table 2. Deinococcus radiodurans Cell Composition

The following references apply to the values on this table: % Mass[17], N [16], f[16], and σ [18]

Because the generator is able to produce a 1×10^9 neutrons per second and geometry of the neutron generator results in a solid angle ($\Omega/4\pi$) of 0.16, the result is a geometric attenuated source, S, of 1.60×10^8 neutrons per second. The next consideration was the area, A, of a flat bottom, 96 well plate lid, whose total area is 109.269 cm². The following is calculated:

$$\dot{D}(E) = S * \frac{1}{A} * E * \Sigma \operatorname{Nof}$$
$$\dot{D}(2.45 \ MeV) = \left(1.60x10^8 \frac{n}{s}\right) * \left(\frac{1}{109.269 \ cm^2}\right) * (2.45 \ MeV) * \left(81.69 \ \frac{cm^2}{kg}\right)$$
$$* 1.6x10^{-13} \frac{J}{Mev} = 4.689x10^{-5} \ \frac{Gy}{s}$$

However, the dose rate is per the entire plate lid and the samples are per well of the plate lid. Each well represents 1.35% of the surface area of the sample plate.



Therefore, the dose rate per well is reduced to 6.344×10^{-7} Gy/s. The following table depicts the dose per well based on the how the bacteria was irradiated.

	Hours	Dose (Gy)	Dose (Sv)
	5	1.1E-02	1.1E-01
Dose Per Well		2.3E-02	2.3E-01
(sample)	10		
	15	3.4E-02	3.4E-01
	20	4.6E-02	4.6E-01

Table 3. Neutron Dose per Well

Neutron Irradiation of Samples

For the 1st neutron experiment, three plates were taken to the neutron generator, located in Building 470 on Area B of Wright Patterson Air Force Base. The untreated plate was left outside of the neutron generator room, which is in the basement level of Building 470. The two treated plates were subjected to 5 hour and 10 hour neutron irradiation treatments, respectively. These plates were placed on the large cylinder of the neutron generator as close as possible to the source. The generator was run for five hours and the 5 hour treatment plate was removed and placed beside the untreated plate. The 10 hour treated plate received an additional 5 hours of neutron irradiation for a total of 10 hours. The same procedure was followed during the 2nd neutron experiment, only this time the first plate was removed at 15 hours and the second plate received a total of 20



hours of irradiation. After both iterations, all three plates (untreated plus the two treated plates) were taken back to USAFSAM.

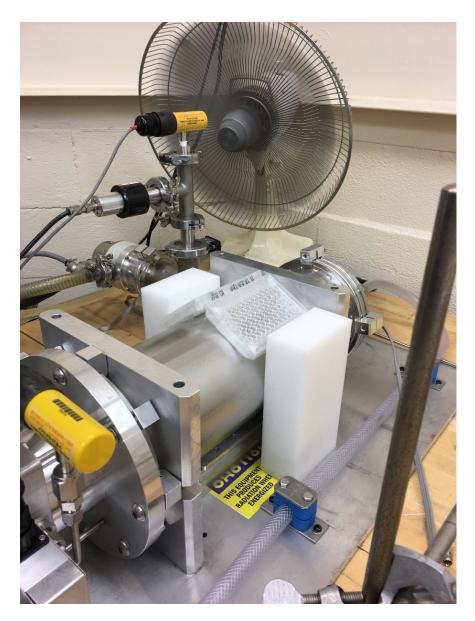


Figure 8. Two samples plates on the neutron generator.

For the 3rd neutron experiment, unlike the previous two neutron experiments, all four plates were irradiated during the same session. A specified plate was removed and



placed outside the neutron generator room when the proper time of irradiation was achieved.

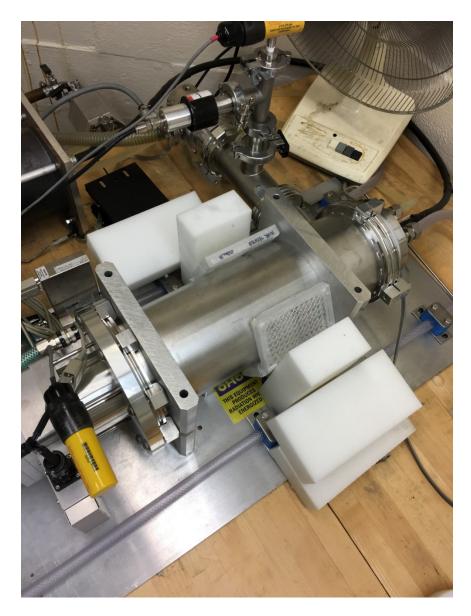


Figure 9. 4 treatment plates for irradiation by the neutron generator.



Rehydration of Samples and Spotting Post Neutron Irradiation

After an approximate 24 hour waiting period to again to simulate shipping conditions, all three sample plates for the first and second neutron experiments were rehydrated with 60 μ l of fresh TGY medium. The medium was pipetted up and down 20 times to re-suspend the cells. Next, the re-hydrated cells were pipetted up and down an additional 20 times to further re-suspend then transferred to a new 96 well, flat bottom plate. Another 40 μ l of fresh TGY culture medium was added for a total of 100 μ l of cell culture. The bacteria were then diluted 10 fold, seven times in series by transferring 20 μ l in the 180 μ l of TGY media. Finally, 5 μ l spots were transferred to TGY agar trays, which were then incubated for 48 hours at 32 °C in unsealed plastic bags in order to prevent drying. The resulting colonies were then counted. This was the same serial dilution procedure as previously mentioned for the CFU input control.

In the case of the 3^{rd} neutron experiment, a modification involved the re-hydration of the cells. The cells were diluted 10 fold, seven times in series down the plate column as previously mentioned. However, the additional 40 µl of TGY was not added to the 60 µl rehydrated spots in row A of the column well plate this time, resulting in all counts conducted at the 10^{-5} , not 10^{-4} dilution. Next, EC was spotted in 5 µl spots on LB agar, incubated for 24 hours, then the resulting colonies were counted. In addition to the 5 µl spots, 100 µl of Dr was spread on round TGY plates. This was done in order to decrease the variability of the experiment if possible. These trays were incubated for 48 hours.



Colony Counting Post Neutron Irradiation

After the 48 hour incubation period, cell colonies were counted at the 4th dilution of each sample tray for the first and second neutron experiment. The cells were counted via visual inspection. The number of colonies per each sample was then recorded. Following the 3rd neutron experiment, the 100 µl spread plates were counted and recorded.

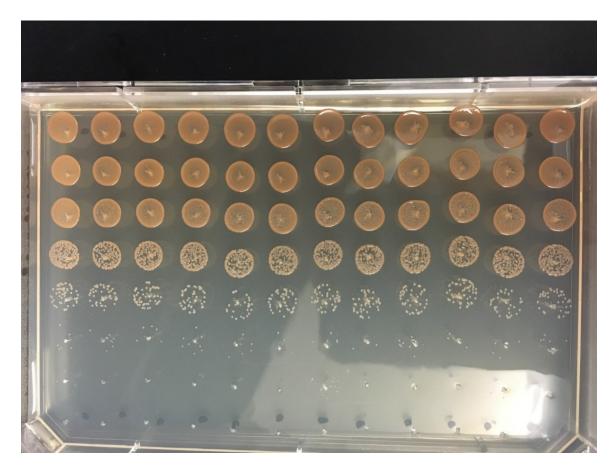


Figure 10. Wild Type *Deinococcus radiodurans* following a five hour neutron treatment in the 1st Neutron experiment.



Proton Generation

The protons used for irradiation of Dr samples were generated by one of the Sandia National Laboratory's ion beams, QASPR-3. This device is a located at the Sandia National Laboratory's Ion Beam Lab located on Kirtland Air Force Base, New Mexico. This lab was opened in 2010 and is a "state-of-the-art facility using ion and electron accelerators to study and modify materials."[19] The QASPR-3 is a HVE 6 MV Tandem ion accelerator which "can accelerate most elements from hydrogen to gold. It is used for in-situ electrical testing, optical testing, and mechanical testing to determine the response of materials to radiation damage at various temperatures from -230 °C to 1200 °C. There is also a microbeam with a spot size of approximately 1 µm." [19] In the case of this experiment, the ion beam was used as proton radiation source.

Proton Dose Calculations

As mentioned earlier, a 60 μ l drop, desiccated, is the target layer for the beam. Since the cells are spherical, ranging from 1.5 to 3.5 μ m in diameter, an average diameter of 2.5 μ m and an average radius is 1.25 μ m was used for calculations. The 60 μ l drop is taken from concentration of 2-5x10⁸ CFU/ml. Again, taking the average, the concentration is 3.5x10⁸ CFU/ml.

$$60 \ \mu l * \frac{1 \ m l}{1000 \ \mu l} * \ 3.5 \ x \ 10^8 \ \frac{CFU}{ml} = 2.1 \ x \ 10^7 CFU$$

So, in a 60 μ l drop, it is expected to have 2.1 x 10⁷ CFUs. Based on the average size and shape of Dr, the volume Dr in the drop is determined by the following:

Volume of
$$Dr = \frac{4}{3} * \pi * (1.25 \ x \ 10^{-6} m)^3 * 4 * 2.1 \ x \ 10^7 = 6.87 \ x \ 10^{-10} \ m^3$$



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Assuming, at most, the layer will take up the entire lid plate well, whose area is $3.165 \times 10^{-5} \text{ m}^2$, the layer depth is demonstrated via the follow equation:

Layer Depth of
$$Dr = \frac{Volume \ of \ Dr}{3.165 \ x \ 10^{-5} \ m^2} = 0.0000217 \ m$$

This means that the 60 μ l drop as a layer depth of 21.7 μ m. The polystyrene plate lid has a thickness of 1.27 mm. The density of Dr is 0.9392 g/cm³. [17]

Inputting the above layer measurements into SRIM and TRIM [20], it was

determined that 4.5 MeV protons would deposit .85 eV/Angstrom into the Dr layer.

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	styrene (ICRU-22	1.27		1.06	1.0034{	E	XF	_	Carbon			12.01		31.0		7.4
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Figure 11. Input screen for TRIM, with the first layer of Dr and the second layer the plate lid.



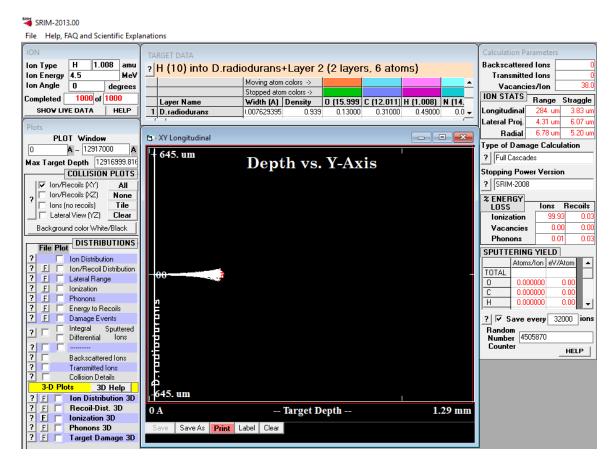


Figure 12. Based on the inputs in the previous figure, TRIM simulation of 4.5 MeV proton ions irradiating

the Dr sample.



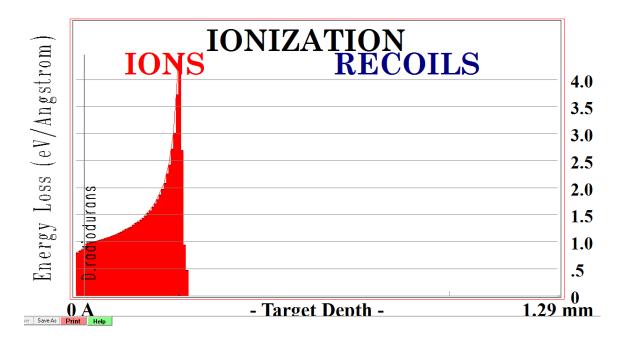


Figure 13. Chart created by TRIM showing the ionization in both Dr and the polystyrene lid. This shows the ionization in the Dr layer to be around 0.85 eV / Angstrom.

Knowing this ionization allows one to determine the fluence needed to achieve a certain dose of irradiation.

$$Dose = \frac{Ionization}{Density} * Fluence$$

 $0.85 \frac{eV}{Angstrom-Ion} * \frac{1.6022 \times 10^{-19} J}{1 \, eV} * \frac{1 \times 10^8 Angstrom}{1 \, cm} * \frac{cm^3}{0.9392 \, g} * \frac{7.2 \times 10^9 Ions}{1 \, cm^2} * \frac{1000 \, g}{1 \, kg} = 104 \, Gy \sim 100 \, Gy$



	Fluence (Ion/cm ²)	Dose (Gy)	Dose (Sv)
	7.20E+08	1.0E+01	2.1E+02
Dose Per Well			
(sample)	7.20E+09	1.0E+02	2.1E+03
	3.60E+10	5.2E+02	1.0E+04
	7.20E+10	1.0E+03	2.1E+04
	1.80E+11	2.6E+03	5.2E+04
	7.20E+11	1.0E+04	2.1E+05

Table 4. Proton Dose per Well

Proton Irradiation of Samples

The dehydrated samples were shipped to the Ion Beam Lab which took two days. The radiation experiment lasted three days, which took place five days after the samples arrived at the Ion Beam Lab. Wild type Dr and mutants #5 and #8 were both irradiated with protons as shown in Figure 10 below, however mutant #11 was not due to time constraints. On a second Wild Type plate, one row was irradiated for a dose of 10 Gy and another row was irradiated for a dose 10,000 Gy.

The three controls mentioned earlier were devised for this experiment because Dr would experience longer times in a dehydrated state than experienced for the previous experiments.



Each sample plate was adhered to the stage on the QASPR-3, which had limited mobility to move in the x and y directions, rotate, and move along the radius. Because of this, the ion beam's vacuum had to be evacuated and the plate repositioned for each row of irradiation.

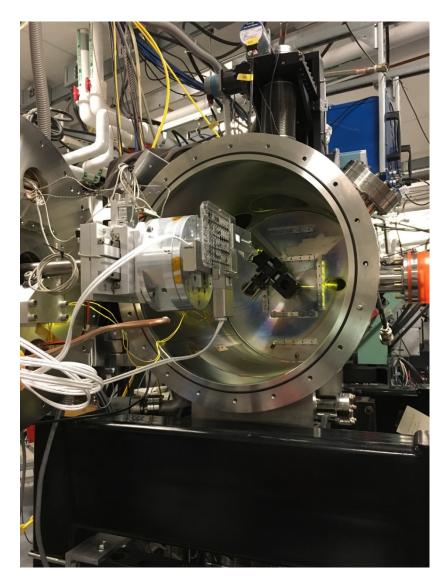


Figure 13. Dr sample plate attached to the stage of the QASPR-3.





Figure 14. The QASPR-3 proton beam was able to hit the total area each well by firing shots in a grid pattern based on the area of the beam. Top Row: Shots 1-4; Center Row: Shots 5-8; Bottom Row: Shots 9-12.

At the beginning of each day of experimentation the beams conditions such as the beam current and area were validated. The beam itself was calibrated using a phosphorus target situated on the stage above the sample lid as shown in Figure 13. This enabled the operator of the beam to both validate the fluence in ions/cm² and the beam's width, which would determine the grid pattern of shots, such in Figure 14. The ion beam's fluence was always within ten percent of the requested fluence. The QASPR-3 was able to accelerate the protons in a directed beam so that the entire well was evenly covered with no overlap, with an example of a well in Figure 14. The samples were shipped the next day following the end of the experiment and arrived back at USAFSAM two days later.



Rehydration of Samples and Spotting Post Proton Irradiation

After arriving back at USAFAM, the samples were rehydrated five days later. The process was similar to the rehydration of samples following the neutron experiments. All irradiated sample and control plates were rehydrated with 60 μ l of fresh TGY medium. The medium was pipetted up and down 20 times to re-suspend the cells. Next, the re-hydrated cells were pipetted up and down an additional 20 times to further resuspend then transferred to a new 96 well, flat bottom plate. The bacteria were then diluted 10 fold, seven times in series by transferring 20 μ l in the 180 μ l of TGY media. Finally, 5 μ l spots were transferred to TGY agar trays, which were then incubated for 48 hours at 32 °C in unsealed plastic bags in order to prevent drying. The resulting colonies were then counted.

Colony Counting Post Proton Irradiation

After a 72 hour incubation period, cell colonies were counted at the 5th dilution of each sample tray for the proton experiment. The cells were counted via visual inspection. The number of colonies per each sample was then recorded.



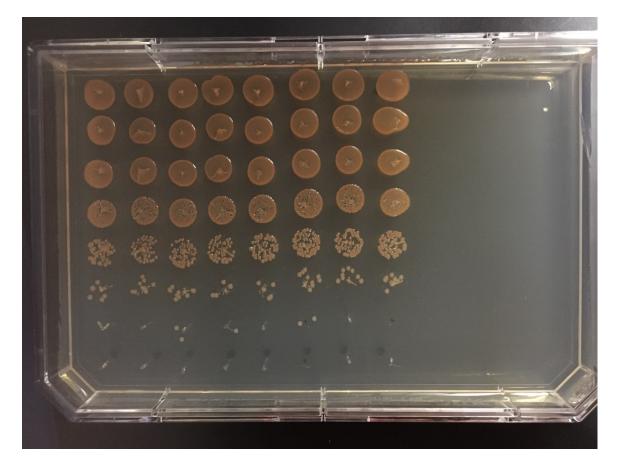


Figure 15. Wild Type Dr re-growth after 500 Gy irradiation. Colonies were counted at the 10⁻⁵ dilution.

Statistical Methods of Comparison

A statistical analysis was conducted between the following samples - CFU input control to non-irradiated control, and non-irradiated control to the irradiated sample populations. The statistical analysis consisted of a small, independent sample test of hypothesis for a population, μ_1 , to another population, μ_2 , using the Student's t-Statistic.[21] This method was chosen because of the small sample size (< 30 samples), with the following assumptions: 1 – the two samples are randomly selected in an independent manner from the two target populations, 2 – both samples' populations have



distributions that are approximately normal, and 3 – the population variances are equal. Due to this, a pooled sample estimator, s_p^2 , was used. This was calculated the following way:

$$s_p^2 = \frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}$$

where n is the number of samples per strain irradiation treatment and s₂ is the sample variance.

The populations were then compared using a one-tailed test, with the subsequent equations showing the null hypothesis, H₀, the alternate hypothesis, H_a, the test statistic, t, each samples mean colony counts, x-bar₁ and x-bar₂, and the rejection region, t_a, which is based on $(n_1 + n_2 - 2)$ degrees of freedom. The variable, a, was 0.05 to reflect a 95 % confidence.[21]

$$H_0: (\mu_1 - \mu_1) = 0$$
$$H_a: (\mu_1 - \mu_1) > 0$$
$$t = \frac{(\overline{x_1} - \overline{x_2})}{\sqrt{s_p^2(\frac{1}{n_1} + \frac{1}{n_2})}}$$

Rejection Region: $t > t_a$

IV. Analysis and Results

Chapter Overview

The purpose of this chapter is to review the statistical analysis conducted between the irradiated sample colonies and their controls. All populations were compared with 95% certainty. The comparisons are broken down by experiment, with only the cases of



statistical difference or close to statistical difference appearing the Tables 5 - 8. Close to statistical difference is defined as a difference of 0.1 or less between the t-statistics and the rejection region.

1st and 2nd Neutron Experiments

For the 1st and 2nd neutron experiments, the CFU input control and the nonirradiated sample control were compared. Then, the irradiated samples were compared to the non-irradiated controls for each strain. Figures 16 and 19 shows the total CFU count for each control and irradiated strain. Tables 5 and 6 depicts cases of statistical difference or cases that were close to statistical difference.

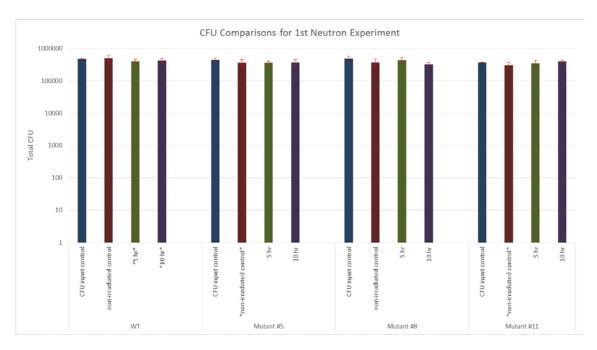


Figure 16. Total CFU comparison for the 1st Neutron Experiment.



Populations 1	Populations 2	Strain
Non-Irradiated Control	5 Hour Dose – 1.1 cGy	WT
Non-Irradiated Control	10 Hour Dose – 2.3 cGy	WT
CFU input Control	Non-Irradiated Control	5

Table 5. 1st Neutron Experiment Statistically Significant Population Comparisons

The populations for the 5 and 10 hour irradiations of WT showed statistical differences from the non-irradiated controls. In each case, the test statistics were greater than the rejection region. In the listed comparison for Mutant #5, the test statistic was close to the border of the rejection region, but did not go into the rejection region.



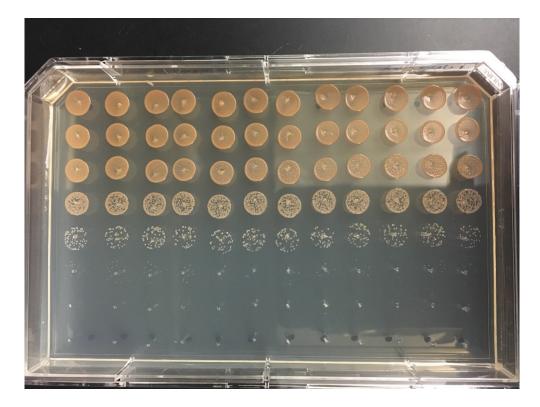


Figure 17. Dr Wild Type untreated with neutron radiation – 1st Neutron Experiment

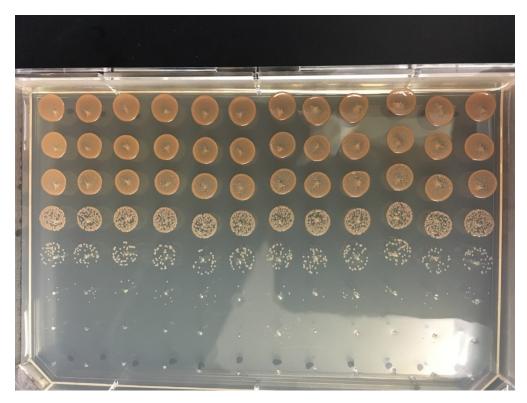


Figure 18. Dr Wild Type neutron irradiated for 5 hours – 1st Neutron Experiment



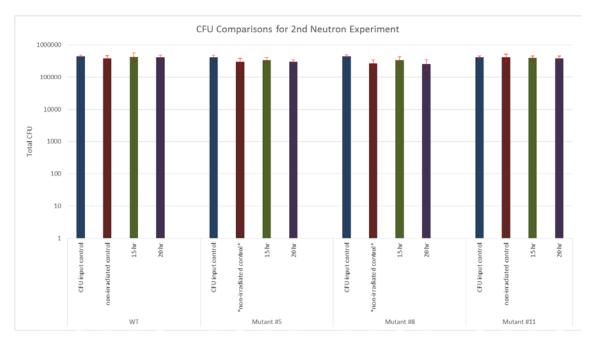


Figure 19. Total CFU comparison for the 2nd Neutron Experiment.

Table 6.	2 nd Neutro	n Experiment	t Statistically	Significant	Population	Comparisons
				0 0		

Populations 1	Populations 2	Strain
CFU input Control	Non-Irradiated Control	5
CFU input Control	Non-Irradiated Control	8

In regards to the control vs control comparison of Mutant #5, the test statistic was found to be in the rejection region. The control versus control comparison of Mutant #8 also demonstrated a difference in populations, where the test statistic was deep into the rejection region.

Upon reviewing the tables for the 1st and 2nd Neutron Experiments it can be seen that there does not seem to be any trends forming at these amounts of neutron radiation.



Of all comparisons that showed a statistical difference or close to a statistical difference populations for these first two experiments, the latter two did not involve radiation, only dehydration.

3rd Neutron Experiment

The results from the third neutron radiation experiment are depicted next. For these comparisons, the CFU input control was not compared as it completed with 5 μ l spots, not 100 μ l spreads. This set of input controls was countable at the expected dilution.

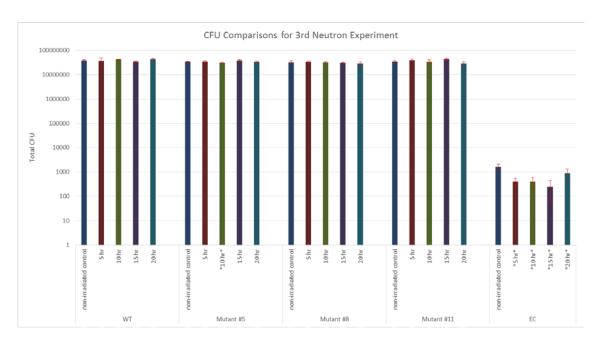


Figure 20. Total CFU comparison for the 3rd Neutron Experiment.



Populations 1	Populations 2	Strain
Non-Irradiated Control	10 Hour Dose – 2.3 cGy	5
Non-Irradiated Control	5 Hour Dose – 1.1 cGy	EC
Non-Irradiated Control	10 Hour Dose – 2.3 cGy	EC
Non-Irradiated Control	15 Hour Dose – 3.4 cGy	EC
Non-Irradiated Control	20 Hour Dose – 4.6 cGy	EC

Table 7. 3rd Neutron Experiment Statistically Significant Population Comparisons

In regards to Mutant #5's entry, the test statistic was deeply within the rejection region. Like the previous experiments, no trends are readily apparent. This time, the only the difference between populations occurred between the non-irradiated control and 10 hour dose to Mutant #5's samples. However, *E. coli* did show a sensitivity to both desiccation and neutron treatment. EC's CFU input controls showed countable colonies starting at a 10^{-5} dilution, but the untreated control only had countable colonies at the 10^{-2} dilution. Additionally, the neutron radiation also had an effect on EC, unlike Dr.



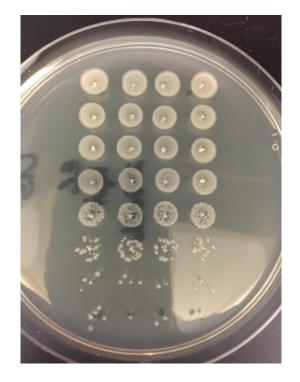


Figure 21. EC CFU input control, with countable colonies at the 10⁻⁵ dilution



Figure 22. EC untreated control, with countable colonies at the 10^{-2} dilution.



In every case of irradiation treatment, there was difference between that dose and the non-irradiated control. An interesting result in these comparisons is that while the test statistics for the 5, 10, and 15 hours irradiation treatments were extremely into the rejection region, the final dose, which was a higher irradiation, was not nearly as far in the rejection region as the others.

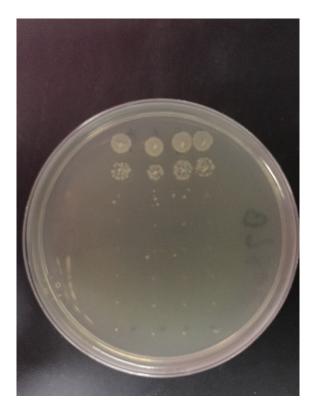


Figure 23. EC at 5 hours of neutron treatment.

1st, 2nd, 3rd Neutron Experiments Findings

For neutron radiation at this dose (cGy), it has been demonstrated that the hypothesis, which stated Dr would not resist neutron (high LET) radiation, was **not** upheld. Instead, in the vast majority of population comparisons, the null hypothesis,



which stated the populations of the experimental groups (neutron radiated) and control groups (no radiation) would not be statistically different, could not be disproved.

Proton Experiment

The proton experiment had a total of three controls that were compared to each other, and the 3rd control was then compared to all the irradiated samples. These controls consisted of a CFU input control (Control 1), a Non-Irradiated Control – No Vaccum (NV, Control 2), and a Non-Irradiated Control – Vacuum (V, Control 3). This third control was on the plate with the treated samples, but was not treated itself. It did experience the same conditions inside the chamber of the QASPR-3, minus proton radiation.

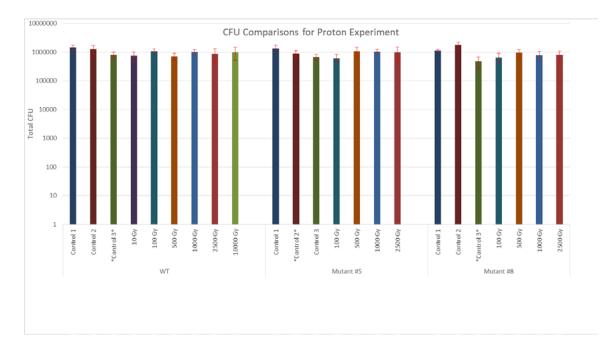


Figure 24. Total CFU comparison for the Proton Experiment.



Populations 1	Populations 2	Strain
Non-Irradiated Control (NV)	Non-Irradiated Control (V)	WT
CFU Input Control	Non-Irradiated Control (NV)	5
Non-Irradiated Control (NV)	Non-Irradiated Control (V)	8

Table 8. Proton Experiment Statistically Significant Population Comparisons

For the Wild Type, the comparison showed a difference between the controls. Likewise, Mutant #5 also showed a difference in a control versus control comparison. This time, it was between the CFU input control and the Non-Irradiated Control – (NV). Finally, for Mutant #8, the t-statistics was well within the rejection region. Interestingly, there were no statistical differences between radiated and non-irradiation populations.

Much like the neutron experiments, it has been demonstrated that the hypothesis, which stated Dr would not resist proton (high LET) radiation, was **not** upheld. Instead, all of the population comparisons between the irradiated samples and the non-irradiated control in the vacuum supported the null hypothesis, which stated the populations of the experimental groups (proton radiated) and control groups (no radiation) would not be statistically different, could not be disproved.



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V. Conclusions and Recommendations

Conclusions of Research

These experiments have shown that not only is Dr resistant low LET radiation, but high LET radiation as well. For the neutron experiments, the low amount of radiation (no greater than cGy), seems to account for the lack of consistent effect of neutron irradiation. It was already demonstrated that Dr can receive a dose of 5 kGy of ionizing radiation of low LET with no lethality. [11] Likewise, previous experiments have shown a gamma dose of 10 kGy will still result in survival close to only 10⁻² lethality.[3] It is reasonable to assume that the low amount of radiation is why the neutron irradiation resulted in no lethality.

However, at the surface, the proton experiment seems to be at odds with the findings of Paulino-Lima et al. In their study in regards to proton irradiation found in solar winds, the researchers used lower energy protons (200 keV protons, not 4.5 MeV protons) and had a greater LET (6.24 eV / Angstrom, compared to .86 eV / Angstrom). Taking this a step further, researchers found that dried plasmids exposed to 10 MeV protons, with 6.39 keV/ μ m LET resulted in 2.8 DSB/1000 Mbp-Gy.[22] The Mbp is the number of mega base pairs per plasmid. If you combine Dr's number of base pairs per DNA (3.06 Mbp) and plasmids (233 Kbp)[5], you get a total of 3.293 Mbp. Since both the energy and LET of the protons are on about the same order of magnitude (the LET for the proton experiment was .85 eV/Angstrom = 8.5 keV/ μ m, and the energy of the protons was 4.5 MeV), an estimate of the number of DSB based on the number of Dr's



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Mbp and the irradiation dosage it received. This estimate is an upper level estimate, as the plasmids presented no other biological targets, unlike the cells of Dr.

$$\frac{2.8 DSB}{1000 Mbp - Gy} * 3.293 Mbp * 10 Gy = .09 DSB$$

So, at 10 Gy, the Dr sample only incurred a faction of a DSB. Table 9 depicts the number of DSB estimated to have occurred based on the dose in Gy.

Table 9. Estimated Number of Deinococcus radiodurans DSBs at an LET of 8.5 keV/µm

Dose (Gy)	# of DSBs
10	.09
100	.90
500	4.6
1000	9.2
2500	23
10000	92

Minton and Daly have stated that "*D.radiodurans* exposed to 1.0 to 1.5 Mrad (1 rad = .01 Gy, so 1.0 to 1.5 Mrad = 10,000 to 15,000 Gy) gamma-irradiation sustains >120 DNA double strand per chromosome (In Minton and Daly's work, the term chromosome appears to equal the term genome); these double strand breaks are mended over a period of hours with 100% survival and virtually no mutagenesis.[23] At the maximum proton dose of 10000 Gy used for this experiment, only 92 DSBs are estimated to occur, so this



may be why there were no differences between the non-irradiated controls and the proton irradiated samples.

In the solar wind experiment, a LET of 6.24 eV/Angstrom (62.4 keV), from 200 keV protons, was used.[17] This is an order of magnitude above what was done in the plasmid experiment. Assuming a linear relationship between LET and number of DSBs, it may be estimated that the Dr of that experiment experienced DSBs at an order of magnitude greater as well. Using the previous computational frame work:

$$\frac{28 DSB}{1000 Mbp - Gy} * 3.293 Mbp * 10 Gy = .90 DSB$$

Dose (Gy)	# of DSBs
10	.90
100	9.2
1000	92
10000	920

Table 10. Estimated Number of *Deinococcus radiodurans* DSBs at an LET of 62.4

keV/µ	m
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This may explain why data from this experiment showed a reduced survival rate at 1000 Gy (less than 2 log kill) and 10000 Gy (about 3 log kill). So one possible explanation for Dr's survival is that even though more energetic protons were used, an order of magnitude less of LET may have resulted in less damage overall to Dr's DNA.



Interestingly, no single mutant stood out as being more sensitive to the proton irradiation. The mutant gene KOs were devised to disrupt pathways which protected against radicals resulting from indirect damage caused by low LET. This adds validity to the idea that indirect damage is more detrimental to Dr's ability to repair itself than direct damage.[22] Because of the ability to survive around a hundred DSBs, the protective mechanism at play seems to be Dr's capability to repair DNA DSBs.

Another major difference between the experiments was in the method used to create a sample. The researchers in *Survival of Deinococcus radiodurans Against Laboratory-Simulated Solar Wind Charged Particles* used a monolayer of cells. This was done to prevent irradiation shielding from dead cells. Because this experiment had more layers, there may have been some shielding. Likewise, some shielding may have occurred from the organic molecules of the TGY cell medium that did not evaporate while Dr was left to dehydrate under the biosafety cabinet.

Finally, the mechanisms normally associated with desiccation may have already been up-regulated during the de-hydration process. As such, this may have given Dr an advantage in repair during rehydration and re-growth.

Recommendations for Future Research

The results of these experiments certainly lead to more questions for future research. On such question is in regards to the neutron research. The neutron generator available at the Air Force Institute of Technology was somewhat limited in that it could only produce a 10⁹ neutrons per second, without consideration of geometric attenuation. If possible, subjecting Dr to greater neutron fluxes may result in greater lethality than



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demonstrated in this experiment. Possible neutron sources include the Ohio State University Research Reactor, which is capable of neutron fluxes in the order of magnitude of 10¹³ n/cm²/s, though these neutrons are thermal neutrons, not fast neutrons like those used in this experiment.[24] Another venue for greater neutron flux is the Spallation Neutron Source located at Oak Ridge National Laboratory.

Another interesting aspect of this research would be looking at another type of high LET radiation, such as alpha particles, which are essentially helium ions. The QASAR-3 is also able to produce this type of ion as well. If feasible, changing the sample preparation to a monolayer and washing of the cells to prevent shielding may also yield different results then were shown in the proton experiment during this research. Further researcher may also need to consider the LET, not the just the energy of the particles used for irradiation.



Appendix A: Optical Density Measurements

Table 11. Initial Dr Optical Densities and Required Culture for an OD₆₀₀ of 0.25 for 1st

Strain	Initial OD ₆₀₀	Amount of Culture to Add
		to 40 ml TGY to achieve
		OD ₆₀₀ of 0.25
WT (1)	.566	1.8 ml
Mutant #5	.382	2.6 ml
Mutant #8	.497	2.0 ml
Mutant #11	.527	1.9 ml

Neutron Experiment

Table 12. Initial Dr Optical Densities and Required Culture for an OD₆₀₀ of 0.25 for 2nd

Neutron Experiment

Strain	Initial OD ₆₀₀	Amount of Culture to Add
		to 40 ml TGY to achieve
		OD ₆₀₀ of 0.25
WT (1)	.497	2.0 ml
Mutant #5	.390	2.6 ml
Mutant #8	.463	2.2 ml
Mutant #11	.508	2.0 ml



Table 13. Initial Dr Optical Densities and Required Culture for an OD₆₀₀ of 0.25 for 3rd

Strain	Initial OD ₆₀₀	Amount of Culture to Add to 40 ml TGY / LB to achieve OD ₆₀₀ of .25
WT (1)	.542	1.9 ml
Mutant #5	.385	2.6 ml
Mutant #8	.342	2.9 ml
Mutant #11	.501	2.0 ml
EC	.424	2.4 ml

Neutron Experiment

Table 14. Initial Dr Optical Densities and Required Culture for an OD_{600} of 0.25 for

Proton Irradiation Experiment

Strain	Initial OD ₆₀₀	Amount of Culture to Add to 40 ml TGY / LB to achieve OD ₆₀₀ of .25
WT (1)	.510	2.0 ml
Mutant #5	.326	3.1 ml
Mutant #8	.349	2.9 ml
Mutant #11	.491	2.0 ml



Table 15. Post 4 Hour Incubation Optical Density and Amount of TGY required to

Strain	Post 4 Hour Incubation	Amount of TGY to Add to		
	OD ₆₀₀	pellet to achieve OD_{600} of		
		5		
WT (1)	.624	3.7 ml		
Mutant #5	.712	4.3 ml		
Mutant #8	.549	3.3 ml		
Mutant #11	.761	4.6 ml		

achieve an OD_{600} of 5 for 1^{st} Neutron Experiment

Table 16. Post 4 Hour Incubation Optical Density and Amount of TGY required to

Strain	Post 4 Hour Incubation	Amount of TGY to Add to		
	OD ₆₀₀	pellet to achieve OD ₆₀₀ of		
		5		
WT (1)	.569	3.4 ml		
Mutant #5	.574	3.4 ml		
Mutant #8	.503	3.0 ml		
Mutant #11	.681	4.1 ml		



Table 17. Post 4 Hour Incubation Optical Density and Amount of TGY required to

Strain	Post 4 Hour Incubation	Amount of TGY / LB to		
	OD ₆₀₀	Add to pellet to achieve		
		OD ₆₀₀ of 5		
WT (1)	.524	3.1 ml		
Mutant #5	.620	3.7 ml		
Mutant #8	.585	3.5 ml		
Mutant #11	.787	4.7 ml		
EC	2.133	12.8 ml		

achieve an OD₆₀₀ of 5 for 3rd Neutron Experiment

Table 18. Post 4 Hour Incubation Optical Density and Amount of TGY required to

Strain	Post 4 Hour Incubation	Amount of TGY to Add to		
	OD ₆₀₀	pellet to achieve OD ₆₀₀ of		
		5		
WT (1)	.636	3.8 ml		
Mutant #5	.773	4.6 ml		
Mutant #8	.630	3.8 ml		
Mutant #11	.765	4.6 ml		

achieve an OD_{600} of 5 for Proton Irradiation Experiment



Appendix B: Neutron Dose Calculations

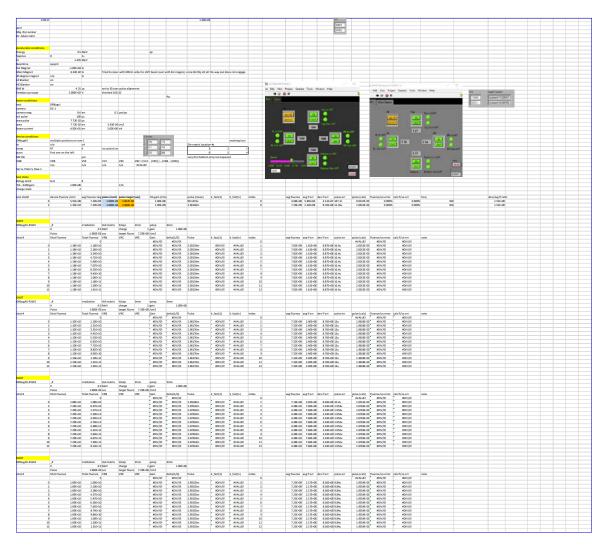
2.45 MeV Neutrons									
Element	% Mass	N, atoms/kg	f	σ, cm ²	Nơf		σ, cm	ENDF/B-VII.1	http://www.nndc.bnl.gov/exfor/endf00.jsp
0-16	0.13	2.69E+25	0.111	8.45410E-25	2.524E+00		% Mass	Dr and Solar Wind artic	le
C-0	0.31	6.41E+24	0.142	1.58290E-24	1.441E+00				
H-1	0.49	5.98E+25	0.5	2.59131E-24	7.748E+01		other	Intro to Health Physics	
N-14	0.07	1.49E+24	0.124	1.30501E-24	2.411E-01			Cember	
				ΣNσf	8.169E+01	cm²/kg			
E	2.45	Mev							
Ω/4π	0.16								
S(from Generator)	1.00E+09	neutrons/s							
S(geometric attenuation)	1.60E+08	neutrons/s							
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Plate Width	8.55	cm							
Plate Area	109.269	cm^2							
Well Top Diameter	0.686	cm							
Well Top Area	1.478421	cm^2							
Surface Area Per Well	0.0135								
Dose Rate Per Plate	4.689E-05	Gy/s							
Dose Rate Per Well (sample)	6.344E-07	Gy/s							
	Hours	Dose (Gy)	Dose(Sv)						
Dose Per Well (sample)	5	1.1E-02	1.1E-01						
	10	2.3E-02	2.3E-01						
	15	3.4E-02	3.4E-01						
	20	4.6E-02	4.6E-01						



Appendix C: Proton Dose Calculations

Ionization	0.85	eV/A-Ion			
ev to J	1.60E-19	J/eV	Fluence (lons / cm^2)	Dose (Gy)	Dose (Sv)
Angstrom to cm	1.00E+08	Angstrom / cm	7.20E+08	1.0E+01	2.1E+02
Dr density	0.9392	g/cm^3	7.20E+09	1.0E+02	2.1E+03
g to kg	1000	g/kg	3.60E+10	5.2E+02	1.0E+04
			7.20E+10	1.0E+03	2.1E+04
			1.80E+11	2.6E+03	5.2E+04
			7.20E+11	1.0E+04	2.1E+05



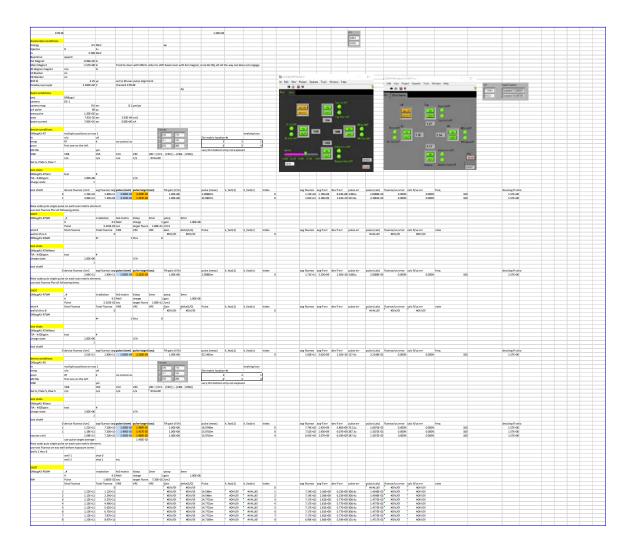


Appendix D: QASAR-3 Parameters



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	est shot#	desire fluence	(rm2 =	or fluence have	culte (com)	rules tares	t (sec)	TiA min (V/A		nuba (meas)	k fact(1)	k factial	index	net finance	nor flarr	dev filerr	vine err	cultura (craici)	fluerce/us error	cale film arr	fran	dev (see firstin	
	6	D	2.716+11	1.675+10	1.5905-0	1.5072-00	1	1.005+08		42.5654m	1,000(4)	A Jacoport	0	1.762+	1 5.655-09	6.945+09	135.Bu	4.25652-02	0.000%	0.000%	100	1.546+00	_
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			2.508+11	1.676+00	1.5908-0	1513-0		1001-08		42.7/06m				1.754+	1 5.726-09	6.946+09	10.74	4.27732-02	0.0055	0000		1.541+00	
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And the set of t	hot# wells1thru8	H Pulse Shot Fluence		6.300E-04 fotal Fluence 0	MeV Isec VRB	charge target fluer VRC	7.20E+05 VRE	1 gain 3 /om2 Gain #DEV/DE	1.00E+00 delta(1/G) #DIV/0I	S Pulse	k_fact(1)	k_fact(n)	index 0	agfuero	avgflerr	dev fil err	sulse err	pulse (calc) #VALUE1	fluence/us error #DIV/01	calcfl/us err #DIV/01	note		
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Matrix Matrix <td>hot # wells1 thru 8 well 2-3 pics not saved levice conditions</td> <td>Shot Fluence</td> <td></td> <td></td> <td>MeV sec VRB</td> <td>charge target fluer VRC</td> <td>1 7.20E+05 VRE</td> <td>a gain 9 /cm2 Gain #DIV/DI</td> <td>1.00E+00 delta(1/G) #DIV/01</td> <td>Pulse</td> <td></td> <td></td> <td>0</td> <td>agfuero</td> <td>avgflerr</td> <td>dev filerr</td> <td>sulse err</td> <td>pulse (calc) eVALLE1</td> <td>fluence/us error #Drv/01</td> <td>calcfi/us err #CitV/01</td> <td>ncte</td> <td></td> <td></td>	hot # wells1 thru 8 well 2-3 pics not saved levice conditions	Shot Fluence			MeV sec VRB	charge target fluer VRC	1 7.20E+05 VRE	a gain 9 /cm2 Gain #DIV/DI	1.00E+00 delta(1/G) #DIV/01	Pulse			0	agfuero	avgflerr	dev filerr	sulse err	pulse (calc) eVALLE1	fluence/us error #Drv/01	calcfi/us err #CitV/01	ncte		
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	test shot#	device fluence /cm2	avg fluence tag	pulse (nom) pulse target	t (sec)	TIA gain (V/A)	1	pulse (meas)	k_fact(1)	k_fact(n)	index	agfuerce	avgfierr	dev fil err	pulse err	pulse (calc)	fluence/us error	calc fl/us err	freq	dev/avg fi ratio 1.600+00	
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and the server and the		0 8.295+0	avg fluence tar	pulse (nom) 1.0000-0	V/A	:[sec]	TIA gain (V/A) 1.00E+38		pulse (meas) 99.1321u	k_fact(1)	k_fact(n)	index 0	avg fluence 5.362+0	avgflerr 8 1205-07	dev fil err 4.085+07	pulse err 152.8n	pulse (calc) 9.9132E-05	fluence/us error 0.000%	calc fl/us err 0.000%	freq 10	dev/avg fi ratio 1555+00	
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ceura pune in weil i in the centre, to poly, howards earnings	Intervent Scillon makely between time und Review manketer menso para Article La Patient S, Row 7 the L	A Anti- Partial Control of a with S A A A A A A A A A A A A A A A A A A	Production 4.4 1.3000-04 7.000 Total Flammer 0 0 0	4c3 XMV VIS VIS VIS VIS VIS VIS VIS VIS VIS VI	X08pp Usget Tuere V8c V8c r/s r/s V8c r/s 1,005-00 1,005-00 1,005-00 1,005-00 1,005-00 1,005-00	2.35 7.23C-00 Wet-IVCC- WALLET	5 votre p apin 8 (m2) c scov/p0 c c (V/RC) - (VRC) - (VRC)) - (VRC) 100 gen (V/A) 100 c - 00 100 c - 00	3.1 1.025-05 603/03 8. (VR8))	Pate Pate De matte location 2 cery thin bitters a pate (meas) 13.300m 14.570m	k.fact(1)	k facin)		ag fuerce	aug fi err	dev fi err	pulse err	pulse (cafc) evALUET	Sueco/us error scrv/si	aleti/us err Brit/DI	158	MART OF	
ceura pune in weni i in tra conteri, to poz, no vuene earnage	Intervent Scillon makely between time und Review manketer menso para Article La Patient S, Row 7 the L	A Anti- Partial Control of a with S A A A A A A A A A A A A A A A A A A	readiation 44 1.3265-04 7.456 7.456 7.45	4c3 XMV VIS VIS VIS VIS VIS VIS VIS VIS VIS VI	X08pp Usget Tuere V8c V8c r/s r/s V8c r/s 1,005-00 1,005-00 1,005-00 1,005-00 1,005-00 1,005-00	2.35 7.23C-00 Wet-IVCC- WALLET	5 votre p apin 8 (m2) c scov/p0 c c (V/RC) - (VRC) - (VRC)) - (VRC) 100 gen (V/A) 100 c - 00 100 c - 00	3.1 1.025-05 603/03 8. (VR8))	Pate Pate De matte location 2 cery thin bitters a pate (meas) 13.300m 14.570m	k.fact(1)	k facin)		aq funce 1386-0 1386-0 1386-1 2380-1	<pre>agter agter a</pre>	dev fl er Sev fl er S 552-07-05 S 582-07-07	pile er	pine (zić) #04.00 pine (zić) 1.1887 © 1.1887 ©	Buerce/us error scry/si Buerce/us error score 0.000%	oft fifue err einnyfet oft fifue err 0 0000 0 0000	158	MART OF	
Set Net Assist function Set Turns Set Turns Assist function Set Turns	Interest Products of Pro- line and Pro- ter and Pro- responses of Pro- page 2014 and Pro- page 2014 and Pro- Parks of Parks of Pro- Parks of Parks	A Anti- Partial Control of a with S A A A A A A A A A A A A A A A A A A	readiation 44 1.3265-04 7.456 7.456 7.45	4c3 XMV VIS VIS VIS VIS VIS VIS VIS VIS VIS VI	X08pp Usget Tuere V8c V8c r/s r/s V8c r/s 1,005-00 1,005-00 1,005-00 1,005-00 1,005-00 1,005-00	2.35 7.23C-00 Wet-IVCC- WALLET	5 votre p apin 8 (m2) c scov/p0 c c (V/RC) - (VRC) - (VRC)) - (VRC) 100 gen (V/A) 100 c - 00 100 c - 00	3.1 1.025-05 603/03 8. (VR8))	Pate Pate De matte location 2 cery thin bitters a pate (meas) 13.300m 14.570m	k.fact(1)	k facin)		aq funce 1386-0 1386-0 1386-1 2380-1	<pre>agter augter augte</pre>	dev fl er Sev fl er S 552-07-05 S 582-07-07	pile er	pine (zić) #04.00 pine (zić) 1.1887 © 1.1887 ©	Buerce/us error scry/si Buerce/us error score 0.000%	oft fifue err einnyfet oft fifue err 0 0000 0 0000	158	MART OF	
v serve (struggeneration) 100-00 (struggeneration) v (server) 100-00 (struggeneration) 200 (st	Interest Products of Pro- line and Pro- ter and Pro- responses of Pro- page 2014 and Pro- page 2014 and Pro- Parks of Parks of Pro- Parks of Parks	A Anti- Partial Control of a with S A A A A A A A A A A A A A A A A A A	readiation 44 1.3265-04 7.456 7.456 7.45	4c3 XMV Vision Vision Vision Vicini V	X08pp Usget Tuere V8c V8c r/s r/s V8c r/s 1,005-00 1,005-00 1,005-00 1,005-00 1,005-00 1,005-00	2.35 7.23C-00 Wet-IVCC- WALLET	5 votre p apin 8 (m2) c scov/p0 c c (V/RC) - (VRC) - (VRC)) - (VRC) 100 gen (V/A) 100 c - 00 100 c - 00	3.1 1.025-05 603/03 8. (VR8))	Pate Pate De matte location 2 cery thin bitters a pate (meas) 13.300m 14.570m	k.fact(1)	k facin)		aq funce 1386-0 1386-0 1386-1 2380-1	<pre>agter augter augte</pre>	dev fl er Sev fl er S 552-07-05 S 582-07-07	pile er	pine (zić) #04.00 pine (zić) 1.1887 © 1.1887 ©	Buerce/us error scry/si Buerce/us error score 0.000%	oft fifue err einnyfet oft fifue err 0 0000 0 0000	158	MART OF	
	Hand Fig. 2014 Fig. 2	y y y h h h h h h h h h h h h h h h h h	Indiana 4 (1) 1020 Annua 5 (1) 6 (1) 6 (1) 6 (1) 7 (1)	And	Mategoria Mategoria Anage Canage Urage Tales A A A	2353 N 728-08 WRE WRE WRE WRE WRE WRE WRE WRE	S ymps 1 (m2) 1 (m2)	111 10006 400(10) 100/0 100/0 100/0 100/0 100/0	Pater Da matici location 3 cory film bitters a cory film bitters a 11 MBP/n 12 MBP/n 13 MBP/n 13 MBP/n 14 MBP/n 14 MBP/n	 X, fact(1) X, fact(1) X, fact(1) X, fact(1) 	 Ref(s) Ref(s)		ng floros 1 316-0 1 560-0 1 560-0 100-0 100-0 100-0 100-0 100-0 100-0 100-0 100-0 100-0 100-0 100-0 100-0 100-0 100-0 100-0 10	<pre>segter l 1784-00 l 1784-00 l 1784-00 l 1864-00 l 18</pre>	dev flar dev flar 557-05 558-00 dev flar	pilut err	phat (cdd) #VALR1 phat (cdd) 1.1382 C0 1.4376 Q	Bueros/us error sovy(b) Bueros/us error 0.000x 0.000x 0.000x	ok 5/us er 601/01 000 000 000 000 000 000 000 000 00	50 50 50 50 50 50 50 50 50 50 50 50 50 5	Pr(rs) 1-00	



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Appendix E: Deinococcus Radiodurans Statistical Analysis

Protocol 4 Analysis															
Data															
Strain			-		1 (\	wт	1		-	·					
CFU Input	44	49	48		- (/								
Untreated Samples	63		65		44	56	5 45	40	46	53	62	34			
5 Hr Treated Samples	46		47			41			37						
10 Hr Treated Samples	46		48			48			40						
All colony counts at 10 ^{-4 dilution}															
Statistics															
	n _{1 -CFU input}	3		n _{1-Untreated}	12		n _{1 -Treated 5 Hr}	12		n _{1 -Treated 10 Hr}	12				
	x-bar _{1-CFU input}	47.0		x-bar _{1-Untreated}	49.8		x-bar _{1-Treated 5 Hr}	39.7		x-bar _{1-Treated 10 Hr}	41.8	1			
		2.6	-		10.1			7.1			6.9	1			
	S1-CFU input	2.0		S _{1-Untreated}	10.1		S _{1-Treated} 5 Hr	7.1		S _{1-Treated} 10 Hr	6.9				
Population Compariso	ons														
Comparison Set 1 - Strain 1(WT)															
u .		NUT	L	nothoris - The	ro in m		difforance hat	or th		Ellipput sonul-t	ior -	000 +1	o Untract	od Benul-	tion
H ₀ :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} = 0$									CFU input populat					
H _a :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} > 0$	Alte	rna	te Hypothesis :	= The	re i	is a difference be	twee	en t	he CFU input pop	ulati	on ar	nd the Untr	reated Pop	pulation
s _p ²	86.8974														
t, test statistic	-0.4709		-						-						
rejection region	t > t _a														
α	0.05														
df	13														
t _α	1.771														
p-value	0.519558773														
Since4709 < 1.771, I do not reject t	he null hypothesis, there is	no d	iffe	erence betwee	n the	CF	U Input populati	on ar	nd t	he Untreated Pop	oulat	ion			
Н₀:	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0$	Null	Ну	pothesis = Thei	re is r	10 0	difference betwe	en th	ne l	Jntreated popula	tion	and t	he Treated	populatio	on
H _a :	$\mu_{1-untreated}$ - $\mu_{1-treated 5 Hr}$ >0	Alte	rna	te Hypothesis :	= The	re i	s a difference be	twee	en t	he CFU input pop	ulati	on ar	nd the Untr	reated Po	pulation
s _n ²	75.8333											-			
t, test statistic	2.8597														
rejection region	t > t _a		-			-			-			-			
α	0.05		1												
df	22		1												
t	1.717	1													
p-value	0.519713215	1	-					-				-			
Since 2.8597 > 1.717, I do reject the r		iffere	enc	e between the	Untr	eat	ted and the 5 Hr	Freat	ed I	Populations					
H _o :	μ _{1-untreated} - μ _{1-treated 10 Hr} = 0	Null	Hyp	pothesis = The	re is n	10 0	difference betwe	en th	ne l	Intreated popula	tion	and t	he Treated	l populatio	on
H _a :	$\mu_{1-untreated}$ - $\mu_{1-treated 10 Hr} > 0$	Alte	rna	te Hypothesis :	= The	re i	s a difference be	twee	en t	he CFU input pop	ulati	on ar	nd the Untr	reated Po	pulation
s _p ²	74.2424														
t, test statistic	2.2743														
rejection region	t > t _α														
α	0.05														
df	22														
t _α	1.717														
p-value	0.519713215	1													
	null hypothesis, there is a d	ifford	-	o hotwoon the	Untr	oat	ad and the 10 Hr	Troa	tod	Populations					



Drotocol 4 Analysis															
Protocol 4 Analysis			-			-			-						
Data															
Strain					Muta	ant	#5								
CFU Input	E1	42	42		Iviuta	ant	#5		_	1					
	51			24	20	24	24	22	24	20	42	24			
Untreated Samples	57		40	31		34			24			_			
5 Hr Treated Samples	32		41	30		42			32			_	1		
10 Hr Treated Samples	46	30	37	40	37	18	41	41	47	33	34	43			
All colony counts at 10 ^{-4 dilution}															
Statistics									-						
Statistics			_			-			-			-			
	n _{5-CFU input}	3		n _{5-Untreated}	12		n _{5-Treated 5 Hr}	12		n _{5-Treated 10 Hr}	12				
	x-bar _{5-CFU input}	45.0		x-bar _{5-Untreated}	35.7		x-bar _{5-Treated 5 Hr}	35.7		x-bar _{5-Treated 10 Hr}	37.3				
		5.2			9.0	-		4.8			7.9				
	S5-CFU input	5.2		S _{5-Untreated}	5.0		S _{5-Treated 5 Hr}	4.0		S _{5-Treated} 10 Hr	7.5				
Population Compariso	ons														
Comparison Set 2 - Strain 5															
						<u> </u>								10 .	
H ₀ :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} = 0$									FU input populat					
Н":	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} > 0$	Alte	rnat	e Hypothesis :	= The	re i	s a difference be	twee	en t	he CFU input pop	ulati	on ar	nd the Untr	eated Pop	ulation
2			-			-			-						
s _p ²	72.2051														
t, test statistic	1.7016								_						
rejection region	t>t _a											-			
α	0.05														
df	13					-									
						-			-						
τ _α	1.771		-			-			-						
p-value	0.519558773														
Since 1.7016 < 1.771, I do not reject t	he null hypothesis, there i	s no c	liffe	rence betwee	n the	e CF	U Input populati	on ai	nd t	he Untreated Po	pulat	ion			
H _o :	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0$	Null	Hvp	othesis = The	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a	and t	he Treated	populatio	n
на:	$\mu_{1-\text{untreated}} = \mu_{1-\text{treated 5 Hr}} > 0$														
n _a .		Aite	mau	e nypotriesis.	- me	ie i	s a uniference be	twee	:11 L	lie cro input pop	uiatii	JII al	iu the onti-	eateu Pop	ulation
	Pre-undeated Pre-ueated Shi			7.											
c ²															
s _p	51.9697														
s _p ² t, test statistic)													
s _p t, test statistic	51.9697)													
s _p	51.9697														
s _p t, test statistic	51.9697														
s _p t, test statistic	51.9697 0.0000 t > t _α														
³ p t, test statistic rejection region α	51.9697 0.0000 t>t _α 0.05 22														
Pp t, test statistic rejection region α df t _a	51.9697 0.0000 t>t _α 0.05 22 1.717														
Pp t, test statistic rejection region α df t _a p-value	51.9697 0.0000 t > t _α 0.05 22 1.717 0.519713215		liffe		n the	e Ur	treated and the	5 Hr	Tre	ated Populations					
P _p t, test statistic rejection region α df t _a p-value Since 0.0000 > 1.717, I do not reject t	51.9697 0.0000 t > t _α 0.05 22 1.717 0.519713215 he null hypothesis, there i	s no c		rence betwee											
P _p t, test statistic rejection region α df t _a p-value Since 0.0000 > 1.717, I do not reject tl	$\begin{array}{c} 51.9697\\ 0.0000\\ t>t_{\alpha}\\ 0.05\\ 22\\ 1.717\\ 0.519713215\\ \textbf{he null hypothesis, there i}\\ \mu_{1-untreated} \ \ -\mu_{1-treated 10Hr} = 0 \end{array}$	s no c	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				
P _p t, test statistic rejection region α df t _a p-value Since 0.0000 > 1.717, I do not reject tl	51.9697 0.0000 t > t _α 0.05 22 1.717 0.519713215 he null hypothesis, there i	s no c	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				
Pp t, test statistic rejection region α df t _a p-value Since 0.0000 > 1.717, I do not reject tl H ₀ : H _a :	$\begin{array}{c} 51.9697\\ 0.0000\\ t>t_{\alpha}\\ 0.05\\ 22\\ 1.717\\ 0.519713215\\ he null hypothesis, there i\\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0\\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0 \end{array}$	s no c Null Alte	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				
² p t, test statistic rejection region α df t _a p-value Since 0.0000 > 1.717, I do not reject tl H ₀ : H ₁ :	$\begin{array}{c} 51.9697\\ 0.0000\\ t>t_{\alpha}\\ 0.05\\ 22\\ 1.717\\ 0.519713215\\ he null hypothesis, there i\\ \mu_{1-untreated} \ \ -\mu_{1-treated \ 10Hr} = 0 \end{array}$	s no c Null Alte	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				
² p t, test statistic rejection region α df t _a p-value Since 0.0000 > 1.717, I do not reject th H ₀ : H ₀ : S_p^2 t, test statistic	51.9697 0.0000 t > t _α 0.05 22 1.717 0.519713215 he null hypothesis, there i μ _{1-untreated} ~ μ _{1-treated} 10 Hr = 0 μ _{1-untreated} ~ μ _{1-treated} 10 Hr > 0 71.6780 -0.4581	s no c Null Alte	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				
² p t, test statistic rejection region α df t _a p-value Since 0.0000 > 1.717, I do not reject th H ₀ : H ₀ : S_p^2 t, test statistic	$\begin{array}{c} 51.9697\\ 0.0000\\ t>t_{\alpha}\\ 0.051\\ 22\\ 1.717\\ 0.519713215\\ \textbf{he null hypothesis, there i}\\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ 71.6780\\ -0.4581\\ t>t_{\alpha}\\ \end{array}$	Null Alte	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				
P_p t, test statistic rejection region α df t_a p-value Since 0.0000 > 1.717, I do not reject th H ₀ : H ₀ : H _a : s_p^2 t, test statistic rejection region α	$\begin{array}{c} 51.9697\\ 0.0000\\ t>t_{\alpha}\\ 0.05\\ 22\\ 1.717\\ 0.519713215\\ he null hypothesis, there i\\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0\\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0\\ 71.6780\\ -0.4581\\ t>t_{\alpha}\\ 0.05\end{array}$	Null Alte	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				
P_p t, test statistic rejection region α df t_a p-value Since 0.0000 > 1.717, I do not reject th H ₀ : H ₀ : H _a : s_p^2 t, test statistic rejection region α	$\begin{array}{c} 51.9697\\ 0.0000\\ t>t_{\alpha}\\ 0.051\\ 22\\ 1.717\\ 0.519713215\\ \textbf{he null hypothesis, there i}\\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ 71.6780\\ -0.4581\\ t>t_{\alpha}\\ \end{array}$	Null Alte	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				
P _p t, test statistic rejection region α df t _a p-value Since 0.0000 > 1.717, I do not reject tl H ₀ : H ₀ : H ₁ : S _p ² t, test statistic rejection region α df	$\begin{array}{c} 51.9697\\ 0.0000\\ t>t_{\alpha}\\ 0.05\\ 22\\ 1.717\\ 0.519713215\\ he null hypothesis, there i\\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0\\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0\\ 71.6780\\ -0.4581\\ t>t_{\alpha}\\ 0.05\end{array}$	Null Alte	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				
P_p t, test statistic rejection region α df t_a p-value Since 0.0000 > 1.717, I do not reject th H ₀ : H ₀ : H ₁ : s_p^2 t, test statistic rejection region α	$\begin{array}{c} 51.9697\\ 0.0000\\ t > t_{\alpha}\\ 0.05\\ 22\\ 1.717\\ 0.519713215\\ he null hypothesis, there i\\ \mu_{1-untreated} - \mu_{1-treated 10 \ Hr} = 0\\ \mu_{1-untreated} - \mu_{1-treated 10 \ Hr} > 0\\ 71.6780\\ -0.4581\\ t > t_{\alpha}\\ 0.05\\ 22\\ \end{array}$	s no c Null Alte	Hyp	rence betwee	re is r	no d	lifference betwe	en th	ne L	Intreated popula	tion a				





Protocol 4 Analysi	s													
Data														
itrain					Muta	ant	#8							
CFU Input	43	58	42											
Intreated Samples	58	43	42	38	25	28	26	26	41	33	45	44		
Hr Treated Samples	48	46	39	37	39	37	45	54	41	67	35	34		
10 Hr Treated Samples	26	26	31	30	43	28	37	33	31	26	39	36		
All colony counts at 10 ^{-4 dilution}			_											
Statistics			_											
	n _{8 -CFU input}	3		n _{8-Untreated}	12	1	n _{8 -Treated 5 Hr}	12	İ	n _{8 -Treated 10 Hr}	12			
					_				-					
	x-bar _{8-CFU input}	47.7		x-bar _{8-Untreated}	37.4		x-bar _{8-Treated 5 Hr}	43.5	-	x-bar _{8-Treated 10 Hr}	32.2			
	S8-CFU input	9.0		S _{8-Untreated}	10.1		S _{8-Treated 5 Hr}	9.5		S _{8-Treated 10 Hr}	5.6			
Population Comparis	sons		_											
Comparison Set 3 - Strain 8														
		:												
H ₀ :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} = 0$												ne Untreated Populat	
H _a :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} > 0$	Alter	nat	e Hypothesis =	= The	re is	s a difference be	twee	en t	he CFU input pop	ulati	on ar	nd the Untreated Pop	ulatior
2 0	97.9679													
, test statistic	1.6043													
			_						-					
ejection region	t>t _a		_			_			_					
1	0.05		_						_					
df	13		_											
α	1.771													
o-value	0.519558773													
Since 1.6043 < 1.771, I do not rejec	ct the null hypothesis, there i	s no di	iffe	rence betwee	n the	CF	U Input populati	on ai	nd t	he Untreated Po	pulat	ion		
H ₀ :	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0$	Null	Нур	othesis = Ther	e is n	no d	ifference betwe	en th	ne L	Intreated popula	tion a	and t	he Treated populatio	n
ч Н _а :	μ _{1-untreated} - μ _{1-treated 5 Hr} >0													
										ne ei o input pop				
2 p	95.3598													
2 p														
, test statistic	95.3598													
, test statistic	95.3598 -1.5259 t > t _a													
,2 , test statistic ejection region	95.3598 -1.5259 t > t _α 0.05													
ρ , test statistic rejection region α	95.3598 -1.5259 t>t _α 0.05 22													
ς, test statistic rejection region α df	95.3598 -1.5259 t>t _α 0.05 22 1.717													
; p ² ;, test statistic ;ejection region x ff ;a p-value	t > t _a 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.007 0.005 0.007 0.005 0005 0005 005													
; p ² ;, test statistic ;ejection region x ff ;a p-value	t > t _a 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.005 0.007 0.005 0.007 0.005 0005 0005 005		liffe				ntreated and the							
s _p ² ;, test statistic rejection region α ff α value since -1.5259 > 1.717, I do not reje	95.3598 -1.5259 t > t _α 0.05 22 1.717 0.519713215 ect the null hypothesis, there	is no c		erence betwee	en th	eU		2 5 Hr	· Tre	ated Population				
; p ² ;, test statistic rejection region α ff :a value Since -1.5259 > 1.717, I do not reje	95.3598 -1.5259 t > t _α 0.05 22 1.717 0.519713215 ect the null hypothesis, there μ _{1-untreated} ⁻ μ _{1-treated 10 μ_f = 0}	is no c	Нур	erence betwee	en the	e U	ifference betwe	e 5 Hr	· Tre	eated Population	s tion a			
; p ² ;, test statistic rejection region α ff :a value Since -1.5259 > 1.717, I do not reje	95.3598 -1.5259 t > t _α 0.05 22 1.717 0.519713215 ect the null hypothesis, there	is no c	Нур	erence betwee	en the	e U	ifference betwe	e 5 Hr	· Tre	eated Population	s tion a			
² _p ² , test statistic rejection region α ff 	95.3598 -1.5259 t > t _a 0.05 22 1.717 0.519713215 ect the null hypothesis, there µ1-untreated ⁻ µ1-treated 10 Hr ⁻ O µ1-untreated ⁻ µ1-treated 10 Hr ⁻ O	is no c Null I Alter	Нур	erence betwee	en the	e U	ifference betwe	e 5 Hr	· Tre	eated Population	s tion a			
; _p ² ;, test statistic rejection region x df :a -value since -1.5259 > 1.717, I do not reje 4 ₀ : 4 _p :	95.3598 -1.5259 t > t _α 0.05 22 1.717 0.519713215 ect the null hypothesis, there μ _{1-untreated} ⁻ μ _{1-treated 10 μ_f = 0}	is no c Null I Alter	Нур	erence betwee	en the	e U	ifference betwe	e 5 Hr	· Tre	eated Population	s tion a			
r_p^2 , test statistic rejection region x ff r_a D-value Since -1.5259> 1.717, I do not reje H_0 : H_a : r_p^2 r_p^2 , test statistic	95.3598 -1.5259 t > t _a 0.05 22 1.717 0.519713215 ext the null hypothesis, there µ1-untreated - µ3-treated 10 Hr = 0 µ1-untreated - µ3-treated 10 Hr > 0 66.1174 1.5815	is no c Null I Alter	Нур	erence betwee	en the	e U	ifference betwe	e 5 Hr	· Tre	eated Population	s tion a			
r_p^2 , test statistic rejection region x ff r_a D-value Since -1.5259> 1.717, I do not reje H_0 : H_a : r_p^2 r_p^2 , test statistic	95.3598 -1.5259 t>t_a 0.05 22 1.717 0.519713215 ext he null hypothesis, there µ1-untreated - µ1-treated 10 Hr > 0 66.1174 1.5815 t>t_a	is no c Null I Alter	Нур	erence betwee	en the	e U	ifference betwe	e 5 Hr	· Tre	eated Population	s tion a			
² _p ² ² , test statistic ² , test statistic ³ , a ⁴ , a ³ , b ⁴ , test statistic ¹ , test test statistic ¹ ,	95.3598 -1.5259 t>t _α 0.05 22 1.717 0.519713215 ect the null hypothesis, there µ1-untreated ~ µ1-treated 10 Hr = 0 µ1-untreated ~ µ1-treated 10 Hr > 0 66.1174 1.5815 t>t _α 0.05	Null I Alter	Нур	erence betwee	en the	e U	ifference betwe	e 5 Hr	· Tre	eated Population	s tion a			
s _p ² t, test statistic α df t _a p-value Since -1.5259> 1.717, I do not reje H ₀ : H ₀ :	95.3598 -1.5259 t > t _a 0.05 22 1.717 0.519713215 ect the null hypothesis, there µ _{1-untreated} - µ _{1-treated} 10 µr = 0 µ _{1-untreated} - µ _{1-treated} 10 µr > 0 66.1174 1.5815 t > t _a 0.05 2	is no c Null I Alter	Нур	erence betwee	en the	e U	ifference betwe	e 5 Hr	· Tre	eated Population	s tion a			
s_p^2 s	95.3598 -1.5259 t>t _α 0.05 22 1.717 0.519713215 ect the null hypothesis, there µ1-untreated ~ µ1-treated 10 Hr = 0 µ1-untreated ~ µ1-treated 10 Hr > 0 66.1174 1.5815 t>t _α 0.05	is no c Null I Alter	Нур	erence betwee	en the	e U	ifference betwe	e 5 Hr	· Tre	eated Population	s tion a			



Protocol 4 Analysis															
,,												_			
Data															
itrain					Muta	nt #	<u>‡11</u>								
CFU Input	37		38												
Intreated Samples	43	30	32	42	21	32	30	25	21	32	20	33			
Hr Treated Samples	31	31	26	28	42	44	38	37	29	47	40	21			
0 Hr Treated Samples	44	36	34	38	42	44	39	46	38	42	40	33			
All colony counts at 10 ^{-4 dilution}															
Statistics						-			-			-			
		3			12	1		12	i -		12				
	n _{11-CFU input}			n _{11-Untreated}			n _{11 -Treated 5 Hr}		-	N _{11 -Treated 10 Hr}					
	x-bar _{11-CFU input}	37.3		x-bar _{11-Untreated}	30.1		x-bar _{11-Treated 5 Hr}	34.5		x-bar _{11-Treated 10 Hr}	39.7				
	S _{11-CFU} input	0.6		S _{11-Untreated}	7.5		S _{11-Treated 5 Hr}	8.0		S _{11-Treated 10 Hr}	4.1				
Population Compariso	ons					-			-						
Comparison Set 4 - Strain 11									-						
H ₀ :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} = 0$	Null	Hvr	othesis = The	re is r	10 r	lifference betwe	en ti	ne (FU input populat	ion a	nd th	ne Untreate	d Populati	on
┨。:	$\mu_{1-CFU input} - \mu_{1-Untreated} > 0$	Alte	rnat	e Hypothesis	= Ine	re i	s a difference be	twee	en t	he CFU input pop	ulatio	on ar	nd the Untre	eated Popu	llatio
2 p	47.8141														
, test statistic	1.6243														
ejection region	t>t _a					-			-			-			
x	0.05														
lf	13														
	1.771														
α						-			-			<u> </u>			
p-value	0.519558773														
Since 1.6243 < 1.771, I do not reject	the null hypothesis, there is	no d	liffe	rence betwee	n the	CF	U Input populati	ion a	nd t	he Untreated Po	pulat	ion			
H ₀ :	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0$	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a	nd t	he Treated	populatio	۱
	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} > 0$														
-d -	Fit-dutieated Fit-treated 2 Hr +														
. 2	60.1780					-			-						
	60.1780														
	60.1780														
	-1.3946														
, test statistic															
, test statistic	-1.3946														
:, test statistic ejection region x	$t > t_{\alpha}$ 0.05														
:, test statistic ejection region x	-1.3946 t>t _a 0.05 22														
, test statistic ejection region x tf	-1.3946 t>t _α 0.05 22 1.717														
r, test statistic rejection region x ff 	-1.3946 t>t _a 0.05 22 1.717 0.519713215	s no	diff	erence betwe	en th	eU	ntreated and the		· Tre	ated Population:	5				
rejection region ¤ ff • • • value Since -1.3946 > 1.717, I do not reject	-1.3946 t > t _a 0.05 22 1.717 0.519713215 t the null hypothesis, there														
;, test statistic rejection region α ff - -value Since -1.3946 > 1.717, I do not reject	-1.3946 t > t _α 0.05 22 1.717 0.519713215 the null hypothesis, there μ _{1-treated} - μ _{1-treated 10 Hr} = 0	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				
, test statistic ejection region x ff -value since -1.3946 > 1.717, I do not reject 4 ₀ :	-1.3946 t > t _a 0.05 22 1.717 0.519713215 t the null hypothesis, there	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				
;, test statistic rejection region α ff ·	$\begin{array}{c} -1.3946 \\ \\ t > t_{\alpha} \\ 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline 0.519713215 \\ \hline the null hypothesis, there \\ \\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0 \\ \\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0 \\ \end{array}$	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				
, test statistic ejection region x ff 	-1.3946 t > t _α 0.05 22 1.717 0.519713215 the null hypothesis, there μ _{1-treated} - μ _{1-treated 10 Hr} = 0	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				
, test statistic rejection region x ff α b-value bince -1.3946 > 1.717, I do not reject H ₀ : H _a : p p p test statistic	-1.3946 t > t _α 0.05 22 1.717 0.519713215 the null hypothesis, there μ _{1-untreated} - μ _{1-treated} 10 Hr = 0 μ _{1-untreated} - μ _{1-treated} 10 Hr > 0 36.6174 -3.8793	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				
, test statistic rejection region x ff α b-value bince -1.3946 > 1.717, I do not reject H ₀ : H _a : p p p test statistic	-1.3946 t > t _α 0.05 22 1.717 0.519713215 tthe null hypothesis, there μ1-untreated - μ1-treated 10 Hr = 0 μ1-untreated - μ1-treated 10 Hr > 0 36.6174 -3.8793 t > t _α	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				
, test statistic ejection region x if 	$\begin{array}{c} -1.3946\\ t > t_{\alpha}\\ 0.05\\ 22\\ 1.717\\ 0.519713215\\ the null hypothesis, there\\ \mu_{1-untreated} - \mu_{1-treated 10 H} = 0\\ \mu_{1-untreated} - \mu_{1-treated 10 H} > 0\\ 36.6174\\ -3.8793\\ t > t_{\alpha}\\ 0.05\\ \end{array}$	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				
; test statistic rejection region α df iα -value since -1.3946 > 1.717, I do not reject d ₀ : d ₀ : d ₁ : s ² p ² , test statistic rejection region α	$\begin{array}{c c} & -1.3946 \\ \hline & & \\ t > t_{\alpha} & \\ & 0.05 \\ 22 \\ \hline & 1.717 \\ \hline & 0.519713215 \\ \hline \\ the null hypothesis, there \\ \hline \\ \mu_{1-untreated} - \mu_{1-treated 10 H} = 0 \\ \hline \\ \mu_{1-untreated} - \mu_{1-treated 10 H} > 0 \\ \hline \\ \hline \\ & 36.6174 \\ \hline \\ & -3.8793 \\ \hline \\ t > t_{\alpha} & \\ \hline \\ & 0.05 \\ 22 \\ \end{array}$	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				
s_p^2 t, test statistic rejection region α df t_{α} p-value Since - 1.3946 > 1.717, I do not reject H_0 : H_0 : H_0 : t_{α}^2 t, test statistic rejection region α df t_{α}	$\begin{array}{c} -1.3946\\ t > t_{\alpha}\\ 0.05\\ 22\\ 1.717\\ 0.519713215\\ the null hypothesis, there\\ \mu_{1-untreated} - \mu_{1-treated 10 H} = 0\\ \mu_{1-untreated} - \mu_{1-treated 10 H} > 0\\ 36.6174\\ -3.8793\\ t > t_{\alpha}\\ 0.05\\ \end{array}$	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				
, test statistic ejection region x ff a -value since -1.3946 > 1.717, I do not reject 4 ₀ : 4 ₀ : 4 ₁ : p 2 , test statistic ejection region x ff	$\begin{array}{c c} & -1.3946 \\ \hline & & \\ t > t_{\alpha} & \\ & 0.05 \\ 22 \\ \hline & 1.717 \\ \hline & 0.519713215 \\ \hline \\ the null hypothesis, there \\ \hline \\ \mu_{1-untreated} - \mu_{1-treated 10 H} = 0 \\ \hline \\ \mu_{1-untreated} - \mu_{1-treated 10 H} > 0 \\ \hline \\ \hline \\ & 36.6174 \\ \hline \\ & -3.8793 \\ \hline \\ t > t_{\alpha} & \\ \hline \\ & 0.05 \\ 22 \\ \end{array}$	Null	Нур	othesis = The	re is r	no d	lifference betwe	en ti	ne l	Intreated popula	tion a				





										CFU S	td. Dev.
VT								WT	CFU input control	470000	26457.513
1 -CFU input	3	n1 -Untreated	12	n1-Treated 5 Hr	12	n1 - Treated 10 Hr	12		non-irradiated control	498333.3	100709.6
bar1-CFU input		x-bar1-Untreated	49.83333333	x-bar1-Treated 5 Hr		x-bar1-Treated 10 Hr	41.83333333		*5 hr*	396666.7	70881.89
-CFU input	2.645751311	s1-Untreated	10.07096035	s1-Treated 5 Hr	7.088189066	s1-Treated 10 Hr	6.860073328		*10 hr*	418333.3	68600.73
lutant #5								Mutant #5	CFU input control	450000	51961.52
5 - CFU input	3	n5 - Untreated	12	n5 - Treated 5 Hr	12	n5 - Treated 10 Hr	12		*non-irradiated control*	356666.7	89679.56
bar5-CFU input	45	x-bar5-Untreated	35.66666667	x-bar5-Treated 5 Hr	35.66666667	x-bar5-Treated 10 Hr	37.25		5 hr	356666.7	48492.42
5-CFU input	5.196152423	s5-Untreated	8.967956424	s5-Treated 5 Hr	4.849242365	s5-Treated 10 Hr	7.93295772		10 hr	372500	79329.5
lutant #8								Mutant #8	CFU input control	476666.7	89628.8
8 - CFU input	3	n8-Untreated	12	n8 -Treated 5 Hr	12	n8 - Treated 10 Hr	12		non-irradiated control	374166.7	100585.4
bar8-CFU input	47.66666667	x-bar8-Untreated	37.41666667	x-bar8-Treated 5 Hr	43.5	x-bar8-Treated 10 Hr	32.16666667		5 hr	435000	94628.46
B-CFU input	8.96288644	s8-Untreated	10.05854077	s8-Treated 5 Hr	9.462846007	s8-Treated 10 Hr	5.57320429		10 hr	321666.7	55732.0
lutant #11								Mutant #11	CFU input control	373333.3	5773.502
11 - CFU input	3	n11-Untreated	12	n11 - Treated 5 Hr	12	n11 -Treated 10 Hr	12		*non-irradiated control*	300833.3	75131.19
-bar11-CFU inpu	37.33333333	x-bar11-Untreated	30.08333333	x-bar11-Treated 5 H	r 34.5	x-bar11-Treated 10 Hr	39.66666667		5 hr	345000	79943.16
11-CFU input	0.577350269	s11-Untreated	7.513119838	s11-Treated 5 Hr	7.994316163	s11-Treated 10 Hr	4.097301403		10 hr	396666.7	40973.01
	0000		CFU Co	omparisons for 1st	Neutron Exp	periment		i i			
	0000	İİİ	CFU Co	omparisons for 1st	Neutron Exp	periment	11	11			
10		İİİ	CFU Co	omparisons for 1st	Neutron Exp	periment		İİ			
10	0000		CFU Co	omparisons for 1st	Neutron Exp	periment					
10	0000 — —		CFU Co	omparisons for 1st	Neutron Exp	eeriment					
10	0000		CFU Co	mparisons for 1st	Neutron Exp						
10	0000		CFU Co	omparisons for 1st	Neutron Exp	periment					
10	0000		CFU Co	mparisons for 1st	Neutron Exp						
10	00000	ottol					etrol field*	5 hr			
10	00000	and other of basis					input control technology in the control *	5 hr			
10	00000	*1 miles do nirol internationa					50 liquid control adlated control*	5 hr			
10	00000	The radius dominod control and the radius dominod and the radius dom	CFU Co		Neutron Exp		GU liquit control méradiated control*	5 hr 10 hr			
10	00000	*5 hr *10					CEU liquat control a from the co	5 hr 10 hr			
10	00000	• • • • • • • • • • • • • • • • • • •					*non-ir	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2			



Protocol 5 Analysis															
PIOLOCOLO S Allalysis			-					-	-		-	-			_
Data															
Strain					1 ()	WT)			-						_
CFU Input	46	41	47	1	10										
Untreated Samples			36		22	28	40	40	36	20	47	59		_	_
	36							_	-					_	_
15 Hr Treated Samples	23		48			49	42	_	61					_	_
20 Hr Treated Samples	35	46	42	41	31	27	42	46	46	39	54	40	9	_	
All colony counts at 10 ^{-4 dilution}															
Statistics												_			
Statistics			-					· · ·	-					_	
	n _{1 -CFU input}	3		n _{1-Untreated}	12		n _{1 -Treated 15 Hr}	12		n _{1 -Treated 20 Hr}	12				
	x-bar _{1-CFU input}	44.7		x-bar _{1-Untreated}	37.9		x-bar _{1-Treated 15 H}	42.5		x-bar _{1-Treated 20 Hr}	40.8				
		3.2			8.7			12.7	-		7.3				_
	S _{1-CFU} input	3.2		S _{1-Untreated}	0.7		S _{1-Treated} 15 Hr	12.7		S _{1-Treated} 20 Hr	7.5				
Population Comparise	ons														
Comparison Set 1 - Strain 1(WT)															
		NL-1P	1100	athosic T			fforons- h-s	0.015.41		Cillinguit a secol d	Le:		ha Urtin	tod D-	ulatia
H ₀ :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} = 0$									CFU input populat					
H _a :	μ _{1-CFU input} - μ _{1-Untreated} > 0	Alte	rnat	e Hypothesis :	= The	re is	a difference b	etwee	en t	he CFU input pop	oulati	on ai	nd the Un	treated	Population
s_ ²	65.9679														
t, test statistic	1.2875														
rejection region	t>t _a		-					-	-		-	-		_	_
			-						-						_
α	0.05	_	-					-	-			-		_	
df	13		-			_								_	
dt t _a	1.771	1													
tα	1.771	1										_			
df t _a p-value Since 1.2875 < 1.771, I do not reject	1.771 0.519558773		liffe	rence betwee	n the	e CFI	U Input populat	ion a	nd t	he Untreated Po	pulat	ion			
t _a p-value Since 1.2875 < 1.771, I do not reject	1.771 0.519558773 the null hypothesis, there i	s no c											he Treate		ation
t <u>a</u> p-value Since 1.2875 < 1.771, I do not reject H _o :	1.771 0.519558773 the null hypothesis, there is μ _{1-untreated} - μ _{1-treated 5 Hr} = 0	s no c Null	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t _a p-value Since 1.2875 < 1.771, I do not reject	1.771 0.519558773 the null hypothesis, there i	s no c Null	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t <u>a</u> p-value Since 1.2875 < 1.771, I do not reject H _o :	1.771 0.519558773 the null hypothesis, there is μ1-untreated - μ1-treated 5 Hr = 0 μ1-untreated - μ1-treated 5 Hr > 0	s no c Null Alte	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H _a : s _p ²	1.771 0.519558773 the null hypothesis, there is μ1-untreated - μ1-treated 5 Hr = 0 μ1-untreated - μ1-treated 5 Hr > 0 118.2689	s no c Null Alte	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H ₂ :	1.771 0.519558773 the null hypothesis, there is μ1-untreated - μ1-treated 5 Hr = 0 μ1-untreated - μ1-treated 5 Hr > 0	s no c Null Alte	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H _a : s _p ² t, test statistic	1.771 0.519558773 the null hypothesis, there is µ1-untreated - µ1-treated 5 Hr = 0 µ1-untreated - µ1-treated 5 Hr > 0 118.2689 -1.0323	s no c Null Alte	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H _a : s _p ²	$\begin{tabular}{ c c c c c } \hline 1.771 & 0.519558773 & $the null hypothesis, there is $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$	s no c Null Alte	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t_{α} p-value Since 1.2875 < 1.771, I do not reject H_0 : H_1 : s_p^2 t, test statistic rejection region α	$\begin{array}{c c} 1.771 \\ \hline 0.519558773 \\ \mbox{the null hypothesis, there is} \\ \hline \mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0 \\ \hline \mu_{1-untreated} - \mu_{1-treated 5 Hr} > 0 \\ \hline 118.2689 \\ \hline -1.0323 \\ \mbox{t} > t \\ \mbox{t} \\ \mbox{t} > t_{\alpha} \\ \hline 0.05 \end{array}$	s no c Null Alte	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H _a : s _p ² t, test statistic	$\begin{tabular}{ c c c c c } \hline 1.771 & 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.5100000000000000000000000000000000000$	Null Alte	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t_{α} p-value Since 1.2875 < 1.771, I do not reject H_0 : H_1 : s_p^2 t, test statistic rejection region α	$\begin{array}{c c} 1.771 \\ \hline 0.519558773 \\ \mbox{the null hypothesis, there is} \\ \hline \mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0 \\ \hline \mu_{1-untreated} - \mu_{1-treated 5 Hr} > 0 \\ \hline 118.2689 \\ \hline -1.0323 \\ \mbox{t} > t \\ \mbox{t} \\ \mbox{t} > t_{\alpha} \\ \hline 0.05 \end{array}$	Null Alte	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t_{α} p-value Since 1.2875 < 1.771, I do not reject H_0 : H_1 : s_p^2 t, test statistic rejection region α	$\begin{tabular}{ c c c c c } \hline 1.771 & 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.5100000000000000000000000000000000000$	Null Alte	Нур	oothesis = The	re is r	no d	ifference betw	een ti	he l	Jntreated popula	ition a	and t			
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H _a : s _p ² t, test statistic rejection region α df t _a p-value	1.771 0.519558773 the null hypothesis, there is µi-untreated - µi-treated 5 Hr = 0 µi-untreated - µi-treated 5 Hr > 0 118.2689 -1.0323 t > t_a 0.005 22 1.717 0.519713215	s no c Null Alte	Hyp rnat	oothesis = Thei e Hypothesis =	re is n	no d re is	ifference betw	een th	he l	Intreated popula	oulation a	and t			
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H ₃ : Sp ² t, test statistic rejection region α df t _a	1.771 0.519558773 the null hypothesis, there is µi-untreated - µi-treated 5 Hr = 0 µi-untreated - µi-treated 5 Hr > 0 118.2689 -1.0323 t > t_a 0.005 22 1.717 0.519713215	s no c Null Alte	Hyp rnat	oothesis = Thei e Hypothesis = erence betwee	re is n = Then 	re is	ifference betw a difference b	een the	he l en t	Intreated popula he CFU input pop	ns	and t	nd the Un	treated	Population
t_a p-value Since 1.2875 < 1.771, I do not reject $H_0:$ $H_0:$ s_p^2 t, test statistic rejection region α df t_a p-value Since -1.0323 < 1.717, I do not reject $H_0:$	$\begin{array}{c c} 1.771\\ 0.519558773\\ \mbox{the null hypothesis, there is}\\ \mu_{1-untreated} - \mu_{1-treated 5 \mbox{ Hr}} = 0\\ \mu_{1-untreated} - \mu_{1-treated 5 \mbox{ Hr}} > 0\\ 118.2689\\ -1.0323\\ \mbox{t} > t_{\alpha}\\ t > t_{\alpha}\\ 0.05\\ 22\\ 1.717\\ 0.519713215\\ \mbox{the null hypothesis, there}\\ \end{array}$	s no c Null Alte	Hyr rnat diff	oothesis = Thei e Hypothesis = erence betwee pothesis = Thei	re is n = The en the	e Un	ifference betw a difference b ntreated and th ifference betw	een the	he l en t	Intreated popula he CFU input pop	ns	and t	he Treate	ed popul:	Population
t _a <u>p-value</u> Since 1.2875 < 1.771, I do not reject H ₀ : H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0323 < 1.717, I do not reject H ₀ : H _a :	$\begin{array}{c c} 1.771\\ 0.519558773\\ \hline the null hypothesis, there is \\ \mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0\\ \mu_{1-untreated} - \mu_{1-treated 5 Hr} > 0\\ \hline 118.2689\\ - 1.0323\\ \hline t > t_{\alpha}\\ \hline t > t_{\alpha}\\ \hline t > t_{\alpha}\\ \hline 10.055\\ - 1.0323\\ \hline t > t_{\alpha}\\ \hline 118.2689\\ - 1.0323\\ - 1.0323\\ -$	s no c Null Alte	Hyr rnat diff	oothesis = Thei e Hypothesis = erence betwee pothesis = Thei	re is n = The en the	e Un	ifference betw a difference b ntreated and th ifference betw	een the	he l en t	Intreated popula he CFU input pop	ns	and t	he Treate	ed popul:	Population
t_a p-value Since 1.2875 < 1.771, I do not reject H_0 : H_a : s_p^2 t, test statistic rejection region α df t_a p-value Since -1.0323 < 1.717, I do not reject H_0 : H_a :	$\begin{array}{c c} 1.771 \\ \hline 0.519558773 \\ \hline \textbf{H}_{2} \ \textbf{untreated} \ \textbf{-} \ \textbf{\mu}_{1-\text{treated 5 Hr}} = 0 \\ \hline \textbf{\mu}_{1-\text{untreated}} \ \textbf{-} \ \textbf{\mu}_{1-\text{treated 5 Hr}} = 0 \\ \hline \textbf{\mu}_{1-\text{untreated}} \ \textbf{-} \ \textbf{\mu}_{1-\text{treated 5 Hr}} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{118.2689} \\ \hline 118.2689 \\ \hline -1.0323 \\ \hline \textbf{t} \ \textbf{-} \ \textbf{t}_{\alpha} \\ \hline \textbf{0.05} \\ \hline 222 \\ \hline 1.717 \\ \hline 0.519713215 \\ \hline \textbf{tte null hypothesis, there} \\ \hline \textbf{\mu}_{1-\text{untreated}} \ \textbf{-} \ \textbf{\mu}_{1-\text{treated 10 Hr}} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{\mu}_{1-\text{untreated}} \ \textbf{-} \ \textbf{\mu}_{1-\text{treated 10 Hr}} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{\mu}_{1-\text{untreated}} \ \textbf{-} \ \textbf{\mu}_{1-\text{treated 10 Hr}} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-} \ \textbf{-} \ \textbf{0} \\ \hline \textbf{-} \ \textbf{-}$	Null Alte	Hyr rnat diff	oothesis = Thei e Hypothesis = erence betwee pothesis = Thei	re is n = The en the	e Un	ifference betw a difference b ntreated and th ifference betw	een the	he l en t	Intreated popula he CFU input pop	ns	and t	he Treate	ed popul:	Population
t_a p-value Since 1.2875 < 1.771, I do not reject H_0 : H_a : s_p^2 t, test statistic rejection region α df t_a p-value Since -1.0323 < 1.717, I do not reject H_0 : H_a :	$\begin{array}{c c} 1.771\\ 0.519558773\\ \hline the null hypothesis, there is \\ \mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0\\ \mu_{1-untreated} - \mu_{1-treated 5 Hr} > 0\\ \hline 118.2689\\ - 1.0323\\ \hline t > t_{\alpha}\\ \hline t > t_{\alpha}\\ \hline t > t_{\alpha}\\ \hline 10.519713215\\ \hline tthe null hypothesis, there\\ \hline \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0\\ \hline \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0\\ \hline \end{array}$	Null Alte	Hyr rnat diff	oothesis = Thei e Hypothesis = erence betwee pothesis = Thei	re is n = The en the	e Un	ifference betw a difference b ntreated and th ifference betw	een the	he l en t	Intreated popula he CFU input pop	ns	and t	he Treate	ed popul:	Population
t_a p-value Since 1.2875 < 1.771, I do not reject $H_0:$ $H_0:$ $H_a:$ s_p^2 t, test statistic rejection region α df t_a p-value Since -1.0323 < 1.717, I do not reject $H_0:$ $H_0:$ S_p^2 t, test statistic	$\begin{array}{c c} 1.771 \\ \hline 0.519558773 \\ \hline \textbf{H}_2 & \textbf{U}$	Null Alte	Hyr rnat diff	oothesis = Thei e Hypothesis = erence betwee pothesis = Thei	re is n = The en the	e Un	ifference betw a difference b ntreated and th ifference betw	een the	he l en t	Intreated popula he CFU input pop	ns	and t	he Treate	ed popul:	Population
t_a p-value Since 1.2875 < 1.771, I do not reject $H_0:$ $H_0:$ $H_a:$ s_p^2 t, test statistic rejection region α df t_a p-value Since -1.0323 < 1.717, I do not reject $H_0:$ $H_0:$ S_p^2 t, test statistic	1.771 0.519558773 the null hypothesis, there is μi-untrasted - μi-treated 5 Hr = 0 μi-untrasted - μi-treated 5 Hr > 0 118.2689 -1.0323 t > t _α 0.005 22 1.717 0.519713215 tthe null hypothesis, there μi-untreated - μi-treated 10 Hr = 0 μi-untreated - μi-treated 10 Hr = 0 μi-untreated - μi-treated 10 Hr > 0 64.5076 -0.8641	s no c Null Alte	Hyr rnat diff	oothesis = Thei e Hypothesis = erence betwee pothesis = Thei	re is n = The en the	e Un	ifference betw a difference b ntreated and th ifference betw	een the	he l en t	Intreated popula he CFU input pop	ns	and t	he Treate	ed popul:	Population
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H ₀ : Sp ² t, test statistic rejection region α df t _a p-value Since -1.0323 < 1.717, I do not reject H ₀ : H ₀ : H ₀ : Sp ² t, test statistic rejection region α	$\begin{tabular}{ c c c c c } \hline 1.771 & 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.5195873 \\ \hline 0.5195873 \\ \hline 0.519713215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.519715215 \\ \hline 0.519715$	s no c Null Alte	Hyr rnat diff	oothesis = Thei e Hypothesis = erence betwee pothesis = Thei	re is n = The en the	e Un	ifference betw a difference b ntreated and th ifference betw	een the	he l en t	Intreated popula he CFU input pop	ns	and t	he Treate	ed popul:	Population
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H ₃ : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0323 < 1.717, I do not reject H ₀ : H _a : s _p ² t, test statistic rejection region α df f	$\begin{array}{c c} 1.771 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 10.519558773 \\ \hline 10.519558773 \\ \hline 10.519558773 \\ \hline 10.51958773 \\ \hline 10.51958773 \\ \hline 10.5195873 \\ \hline 10.5195873 \\ \hline 10.5195873 \\ \hline 10.519713215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.51971215 \\ \hline 10.519715215 \\ \hline 10.519715215 \\ \hline 10.519715215 \\ $	s no c Null Alte	Hyr rnat diff	oothesis = Thei e Hypothesis = erence betwee pothesis = Thei	re is n = The en the	e Un	ifference betw a difference b ntreated and th ifference betw	een the	he l en t	Intreated popula he CFU input pop	ns	and t	he Treate	ed popul:	Population
t _a p-value Since 1.2875 < 1.771, I do not reject H ₀ : H ₃ : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0323 < 1.717, I do not reject H ₀ : H _a : s _p ² t, test statistic rejection region α α α α α α α α α α α α α	$\begin{tabular}{ c c c c c } \hline 1.771 & 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.519558773 \\ \hline 0.5195873 \\ \hline 0.5195873 \\ \hline 0.519713215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.51971215 \\ \hline 0.519715215 \\ \hline 0.519715$	s no c Null Alte	Hyr rnat diff	oothesis = Thei e Hypothesis = erence betwee pothesis = Thei	re is n = The en the	e Un	ifference betw a difference b ntreated and th ifference betw	een the	he l en t	Intreated popula he CFU input pop	ns	and t	he Treate	ed popul:	Population



Drotocol E Analysia															
Protocol 5 Analysis			-						-						
Data											_				
Strain					Muta	ant	#5								
CFU Input	34	10	41		Iviute		#J				-				
			30	17	21	43	17	20	36	22	21	20			
Untreated Samples	33												¢		
15 Hr Treated Samples	27		40	42		30			33		20		6		_
20 Hr Treated Samples	32	33	39	30	30	28	32	22	24	27	33	26			
All colony counts at 10 ^{-4 dilution}															
Statistics									-						
	-		1	-	42		-	42		-	42				-
	n _{5 -CFU input}	3		n _{5-Untreated}	12		n _{5 -Treated 15 Hr}	12		n _{5 -Treated 20 Hr}	12				
	x-bar _{5-CFU input}	41.0		x-bar _{5-Untreated}	29.6		x-bar _{5-Treated 15 H}	33.0		x-bar _{5-Treated 20 Hr}	29.7				
	S _{5-CFU input}	7.0		S _{5-Untreated}	9.2		S _{5-Treated 15 Hr}	7.0		S _{5-Treated 20 Hr}	4.6				
	S-CFU input				5.2		-S-Treated 15 Hr			~5-Treated 20 Hr					
Population Compariso	ons														
Comparison Set 1 - Strain 5															
H _o :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} = 0$	Null	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne C	FU input populat	ion a	nd th	ne Untreat	ed Popula	ation
H _a :	$\mu_{1-CFU input} = \mu_{1-Untreated} > 0$									he CFU input pop					
n _a .	µ1-CFU input = µ1-Untreated > 0	Aite		e nypotnesis -	- me		a uniterence be	lwee		ne cro mput pop	uratit	Jii ai		iealeu Fu	pulation
e ²	79.6090														
t, test statistic	1.9823		-			-			-						
	1.9023		-			-			-						
rejection region	t > t _a		-								_				
~	0.05		-												
u			-			-			-						
df	13		-			_			-						
t _α	1.771														
p-value	0.519558773														
Since 1.9823 > 1.771, I do reject the n	ull hypothesis, there is a d	iffere	ence	e between the	CFU	Inp	ut population a	nd the	e Ur	ntreated Populati	on				
							ifforanco hotuv			laterate da secola	lana		ho Troatod		
u .				othocic = Thou					0.1						
H ₀ :	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0$														
H ₀ : H _a :															
		Alte													
H _a : \$ _p ²	μ _{1-untreated} - μ _{1-treated 5 Hr} >0 67.3144	Alte													
H _a :	$\mu_{1-untreated}$ - $\mu_{1-treated 5 Hr}$ >0	Alte													
H _a : s _p ² t, test statistic	μ _{1-untreated} - μ _{1-treated} 5 Hr >0 67.3144 -1.0201	Alte													
H _a : S _ρ ²	μ _{1-untreated} - μ _{1-treated} 5 Hr >0 67.3144 -1.0201 t > t _α	Alte													
H _a : s _p ² t, test statistic rejection region α	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 5 \ Hr} > 0 \\ \hline 67.3144 \\ -1.0201 \\ t > t_{\alpha} \\ \hline 0.05 \end{array}$	Alte													
H _a : s _p ² t, test statistic	μ _{1-untreated} - μ _{1-treated} 5 Hr >0 67.3144 -1.0201 t > t _α	Alte													
H _a : s _p ² t, test statistic rejection region α	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 5 \ Hr} > 0 \\ \hline 67.3144 \\ -1.0201 \\ t > t_{\alpha} \\ \hline 0.05 \end{array}$	Alte													
H _a : sp ² t, test statistic rejection region α df t _a	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\ - 1.0201 \\ t > t_{\alpha} \\ \hline 0.05 \\ 22 \\ 1.717 \end{array}$	Alte													
H _a : s _p ² t, test statistic rejection region α	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\ \hline -1.0201 \\ t > t_{\alpha} \\ \hline 0.05 \\ 22 \\ \hline 1.717 \\ 0.519713215 \end{array}$	Alte	rnat	e Hypothesis -	= The	reis	s a difference be	etwee	en t	he CFU input pop	ulatio				
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject 1	μ _{1-untreated} - μ _{1-treated 5 Hr} >0 67.3144 -1.0201 t > t _α 0.05 22 1.717 0.519713215 the null hypothesis, there	Alte	diff	e Hypothesis : erence betwe	en th	e U	s a difference be	e 15 F	en t	he CFU input pop	ns	on ar	nd the Untr	reated Po	pulation Image: state sta
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject t H ₀ :	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\ - 1.0201 \\ t > t_{\alpha} \\ \hline 1.0201 \\ t > t_{\alpha} \\ 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline the null hypothesis, there \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} = 0 \end{array}$	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : s _p ² t, test statistic rejection region α df t _a p-value	μ _{1-untreated} - μ _{1-treated 5 Hr} >0 67.3144 -1.0201 t > t _α 0.05 22 1.717 0.519713215 the null hypothesis, there	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject t H ₀ :	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\1.0201 \\ t > t_{\alpha} \\ \hline 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline the null hypothesis, there \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} = 0 \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} > 0 \end{array}$	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject I H _a : H _a : s _p ²	μ1-untreated - μ1-treated 5 Hr >0 67.3144 -1.0201 t > t _a 0.05 22 1.717 0.519713215 the null hypothesis, there μ1-untreated - μ1-treated 10 Hr = 0 μ1-untreated - μ1-treated 10 Hr > 0 53.2538	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : sp ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject I H _a :	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\1.0201 \\ t > t_{\alpha} \\ \hline 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline the null hypothesis, there \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} = 0 \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} > 0 \end{array}$	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject I H _a : H _a : s _p ² t, test statistic	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline & 67.3144 \\ - 1.0201 \\ t > t_{\alpha} \\ \hline & 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline & 1.0519713215 \\ \hline & the null hypothesis, there \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} = 0 \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} > 0 \\ \hline & 53.2538 \\ - 0.0280 \\ \hline \end{array}$	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject I H _a : H _a : s _p ² t, test statistic	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\ - 1.0201 \\ t > t_{\alpha} \\ \hline 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline \text{the null hypothesis, there} \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} = 0 \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} > 0 \\ \hline 53.2538 \\ - 0.0280 \\ t > t_{\alpha} \end{array}$	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject I H _a : H _a : s _p ² t, test statistic rejection region α	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\1.0201 \\ t > t_{\alpha} \\ \hline 1.0201 \\ t > t_{\alpha} \\ \hline 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline \text{the null hypothesis, there} \\ \hline \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} > 0 \\ \hline \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} > 0 \\ \hline 53.2538 \\ - 0.0280 \\ \hline t > t_{\alpha} \\ \hline 0.05 \\ \hline \end{array}$	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject I H _a : H _a : s _p ² t, test statistic rejection region α	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\1.0201 \\ t > t_{\alpha} \\ \hline 1.0001 \\ t > t_{\alpha} \\ \hline 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline 1.717 \\ \hline 1.717 \\ 0.519713215 \\ \hline 1.717 \\ \hline 1.717 \\ 0.519713215 \\ \hline 1.717$	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject I H _a : H _a : s _p ²	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\1.0201 \\ t > t_{\alpha} \\ \hline 1.0201 \\ t > t_{\alpha} \\ \hline 1.0201 \\ 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline \text{the null hypothesis, there} \\ \hline \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} > 0 \\ \hline \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 10 \text{ Hr}} > 0 \\ \hline 53.2538 \\ - 0.0280 \\ \hline t > t_{\alpha} \\ \hline 0.05 \\ \hline \end{array}$	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco
H _a : s _p ² t, test statistic rejection region α df t _a p-value Since -1.0201 < 1.717, I do not reject I H _a : H _a : s _p ² t, test statistic rejection region α	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated} 5 \text{ Hr}} > 0 \\ \hline 67.3144 \\1.0201 \\ t > t_{\alpha} \\ \hline 1.0001 \\ t > t_{\alpha} \\ \hline 0.05 \\ 22 \\ 1.717 \\ 0.519713215 \\ \hline 1.717 \\ \hline 1.717 \\ 0.519713215 \\ \hline 1.717 \\ \hline 1.717 \\ 0.519713215 \\ \hline 1.717$	Alte	diff Hyp	e Hypothesis -	en th	e Un	s a difference be ntreated and th	e 15 H	en t	he CFU input pop	ulation a	on ar	hd the Untr	reated Po	pulation Image: Second seco



Protocol 5 Analys	le														
	015		-			-			-						_
Data															
Strain					Muta	ant	#8		-				1		
CFU Input	47	30	46		TVICAL					1					
			31	20	20	20	20	24	27	24	40	24			
Untreated Samples	22			20		29			27						
15 Hr Treated Samples	37		23	31		54			27						_
20 Hr Treated Samples	28	36	29	33	26	35	18	18	5	18	30	31			
All colony counts at 10 ^{-4 dilution}															
Statistics			-						-						
56663663			-			-		<u> </u>	-						_
	n _{8 -CFU input}	3		n _{8-Untreated}	12		n _{8 -Treated 15 Hr}	12		n _{8 -Treated 20 Hr}	12				
	x-bar _{8-CFU input}	44.0		x-bar _{8-Untreated}	27.1		x-bar _{8-Treated 15 H}	33.2		x-bar _{8-Treated 20 Hr}	25.6				
		4.4			6.5			9.6			9.1				
	S _{8-CFU} input	4.4		S _{8-Untreated}	0.5		S _{8-Treated 15 Hr}	9.0		S _{8-Treated} 20 Hr	9.1				
Population Compar	isons														
Comparison Set 3 - Strain 8			-			-			-						_
H _o :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} = 0$	Null	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne C	FU input populat	ion a	nd th	ne Untreat	ed Popul	ation
H _a :										he CFU input pop					
'a ·	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} > 0$	Aite	Indl	e riypotnesis	- me	101	a unreferice De		=11 C	пе сто присрор	uidtli	JII dl	ia the onti	eateu PC	pulation
s ²	39.1474														
t, test statistic	4.1886		-			-			-						_
	4.1860		-						-						-
rejection region	t>t _a		-			-									
~	0.05		-			-									
4			-			-			-						
df	13		-			-			-						_
tα	1.771														
p-value	0.519558773														
Since 4.1886 > 1.771, I do reject	the null hypothesis, there is a	liffer	enc	e between the	CFU	Inp	ut population a	nd th	e U	ntreated Populat	ion				
H ₀ :	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0$	NUULI	Lur	othoric - Tho	ic ic r		ifforanco hotuv	on th		Intropted popula	tion	nd t	ho Troator	l nonulat	ion
H _a :	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} > 0$	Alte	rnat	e Hypothesis	= The	re i	a difference be	etwee	en t	he CFU input pop	ulatio	on ar	nd the Unti	reated Po	pulation
			_			_			_						_
sp ²	67.2992														
t, test statistic	-1.8164														
rejection region	t > t _α														
-	0.05		-			-									
α	0.03		-			-									
α df	22							_							-
α df	22		-											1	
t _α	1.717														
α df t _{α} p-value															
t _α p-value	1.717 0.519713215		diff	erence betwe	en th	e U	ntreated and th	e 15 H	ir Ti	reated Populatio	ns				
t _α	1.717 0.519713215	is no										ind t	he Treatec	l populat	ion
t _α p-value Since -1.8164 < 1.717, I do not re	1.717 0.519713215 ject the null hypothesis, there μ _{1-untreated} - μ _{1-treated 10 Hr} = 0	is no Null	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				
t <u>a</u> p-value Since -1.8164 < 1.717, I do not re H ₀ :	1.717 0.519713215 ject the null hypothesis, there	is no Null	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				
t <u>a</u> p-value Since -1.8164 < 1.717, I do not re H ₀ :	1.717 0.519713215 ject the null hypothesis, there µ1-untreated - µ1-treated 10 Hr = 0 µ1-untreated - µ1-treated 10 Hr > 0	is no Null Alte	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				
t _a p·value Since -1.8164 < 1.717, I do not re H ₀ : H ₀ : s _p ²	1.717 0.519713215 ject the null hypothesis, there μ1-untreated - μ1-treated 10 Hr = 0 μ1-untreated - μ1-treated 10 Hr > 0 62.9924	is no Null Alte	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				
t _a p·value Since -1.8164 < 1.717, I do not re H ₀ : H ₉ :	1.717 0.519713215 ject the null hypothesis, there µ1-untreated - µ1-treated 10 Hr = 0 µ1-untreated - µ1-treated 10 Hr > 0	is no Null Alte	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				
t_a p-value Since -1.8164 < 1.717, I do not re $H_0:$ $H_0:$ s_p^2 t, test statistic	1.717 0.519713215 ject the null hypothesis, there µ1-untreated - µ1-treated 10 Hr = 0 µ1-untreated - µ1-treated 10 Hr > 0 62.9924 0.4629	is no Null Alte	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				
t _a p-value Since -1.8164 < 1.717, I do not re H ₀ : H ₀ : s ² s ² t, test statistic	1.717 0.519713215 ject the null hypothesis, there μ1_untreated ~ μ1-treated 10 Hr = 0 μ1_untreated ~ μ1-treated 10 Hr > 0 62.9924 0.4629 t > t_α	Null Alter	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				
t_{α} p-value Since -1.8164 < 1.717, I do not re $H_0:$ $H_0:$ s_p^2 t, test statistic rejection region α	1.717 0.519713215 ject the null hypothesis, there μ1-untreated - μ1-treated 10 Hr = 0 μ1-untreated - μ1-treated 10 Hr > 0 62.9924 0.4629 t > t_α 0.055	is no Null Alter	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				
t_{α} p-value Since -1.8164 < 1.717, I do not re H_0 : H_0 : s_p^2 t, test statistic rejection region α	$\begin{array}{c c c c c c c c c c c c c c c c c c c $	Null Alter	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				
t _a p·value Since -1.8164 < 1.717, I do not re H ₀ : H ₀ : s _p ²	1.717 0.519713215 ject the null hypothesis, there μ1-untreated - μ1-treated 10 Hr = 0 μ1-untreated - μ1-treated 10 Hr > 0 62.9924 0.4629 t > t_α 0.055	Null Alte	Hyp	othesis = The	re is r	no d	ifference betwe	en th	ne l	Intreated popula	tion a				



_			-			-			-						
Data															
Strain					Muta	nt	#11		_						
CFU Input	38	46	38												
Untreated Samples	50	37	44	33	38	42	56	42	34	52	47	20			
15 Hr Treated Samples	36	33	37	55	43	34	46	35	43	38	36	30			
20 Hr Treated Samples	41		39		37	37	29	50	39	46	30	25			
All colony counts at 10 ^{-4 dilution}		-			_				-			-			
Statistics			-			-			-		-				
Statistics			-		_	-									
	n _{11-CFU input}	3		n _{11-Untreated}	12		n _{11 - Treated 15 Hr}	12		n _{11 -Treated 20 Hr}	12				
	x-bar _{11-CFU input}	40.7		x-bar _{11-Untreated}	41.3		x-bar _{11-Treated 15 Hr}	38.8		x-bar _{11-Treated 20 Hr}	38.2				
		4.6			9.8			6.9			7.3				
	S _{11-CFU} input	4.0		S _{11-Untreated}	5.0		S _{11-Treated 15 Hr}	0.9		S _{11-Treated} 20 Hr	7.5				
Population Compari	sons														
Comparison Set 4 - Strain 11			-			-					_				
						Ļ									
H _o :	$\mu_{1-CFU \text{ input}} - \mu_{1-Untreated} = 0$	Null	Hyp	pothesis = There	e is no	o di	fference betwee	n the	CFL	J input populatio	n and	the	Untreated F	opulation	1
Ha :	$\mu_{1-CFU input} - \mu_{1-Untreated} > 0$	Alte	rnat	e Hypothesis =	There	e is	a difference betw	veen	the	CFU input popul	ation	and	the Untreat	ed Popula	tion
						_									
. 2	04.0044		-								-				
^p p	84.2244		-			-									
t, test statistic	-0.0985		-			-									
rejection region	t > t _a														
α	0.05														
df	13														
	1.771														
-α	0.519558773		-			-									
p-value				• .											
Since0985 < 1.771, I do not reje	ct the null hypothesis, there is	no d	iffe	rence between	the (CFU	Input population	n and	the	Untreated Popu	lation				
H ₀ :	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} = 0$	Null	Hyp	othesis = There	e is no	o di	fference betwee	n the	Un	treated population	on and	l the	Treated po	pulation	
H _a :	$\mu_{1-untreated} - \mu_{1-treated 5 Hr} > 0$														tion
na .	P1-untreated - P1-treated 5 Hr - 0	Aite	inat	e riypotriesis =	men	C 13	a uniterence betw	veen	une	ci o input popul	ation	anu	uie ontreat	europula	nuon
-			_			-			_						
Sp ²	71.3598														
t, test statistic	0.7008														
rejection region	t > t _a					Γ									
~	0.05	-	-								-	-			
u 		-	-			-					-	-			
df	22		-			-									
t _α	1.717														
p-value	0.519713215														
Since .07008 < 1.717, I do not reje	ct the null hypothesis, there is	s no d	liffe	erence betweer	the	Unt	treated and the 1	5 Hr 1	rea	ted Populations					
H ₀ :	$\mu_{1-untreated} - \mu_{1-treated \ 10 \ Hr} = 0$	Null	Hyp	othesis = There	e is no	b di	fference betwee	n the	Un	treated population	on and	l the	Treated po	pulation	
	μ _{1-untreated} - μ _{1-treated 10 Hr} >0														tion
Η ·	M1-untreated M1-treated 10 Hr V	Ane	al		men	- 13			- Te	. c. c mput popul		anu	e ontredt		
H _a :															
H _a :	74 5417										-	-			
	74.5417 0.8748														
δ _p ² t, test statistic	0.8748														
sp ² ; test statistic	0.8748 t > t _α														
sp ² ; test statistic	0.8748														
s _ρ ² t, test statistic rejection region α	0.8748 t > t _α														
s _ρ ² t, test statistic rejection region α	0.8748 t>t _a 0.05 22														
s _p	0.8748 t > t _α 0.05														



W All colony counts at 10 ^{-4 dilution} n1	/т												ARX 1 1 1		
and the second statement of th											WT		CFU input control	446666.7	32145.502
All colony counts at 10 ⁻⁴ discontinent	1 -CFU input	3	0 n1 -Untreated	12	0	n1 - Treated 15 Hr	12	0	n1 - Treated 20 Hr	12			non-irradiated control	379166.7	87225.760
	bar1-CFU input	44.66666667	0 x-bar1-Untreated			x-bar1-Treated 15 H	42.5		x-bar1-Treated 20 Hr	40.75			15 hr	425000	126670.65
	L-CFU input	3.214550254	0 s1-Untreated	8.722576072		s1-Treated 15 Hr	12.66706538		s1-Treated 20 Hr	7.275425636			20 hr	407500	72754.256
				·											
M	lutant #5										Muta	ant #5	CFU input control	410000	700
n!	5 - CFU input	3	0 n5 - Untreated	12	0	n5 -Treated 15 Hr	12	0	n5 - Treated 20 Hr	12			*non-irradiated control	295833.3	92289.892
x-	-bar5-CFU input	41	0 x-bar5-Untreated	29.58333333	0	x-bar5-Treated 15 H	33		x-bar5-Treated 20 Hr	29.66666667			15 hr	330000	70323.925
s5	5-CFU input	7	0 s5-Untreated	9.228989242	0	s5-Treated 15 Hr	7.032392584	0	s5-Treated 20 Hr	4.618802154			20 hr	296666.7	46188.021
M	lutant #8										Muta	ant #8	CFU input control	440000	43588.989
nf	8-CFU input	3	0 n8-Untreated	12	0	n8 - Treated 15 Hr	12	0	n8-Treated 20 Hr	12			*non-irradiated control	270833.3	65429.814
x-	-bar8-CFU input	44	0 x-bar8-Untreated	27.08333333	0	x-bar8-Treated 15 H	33.16666667	0	x-bar8-Treated 20 Hr	25.58333333			15 hr	331666.7	95805.990
sg	3-CFU input	4.358898944	0 s8-Untreated	6.542981435	0	s8-Treated 15 Hr	9.580599083	0	s8-Treated 20 Hr	9.119991361			20 hr	255833.3	91199.913
M	lutant #11										Muta	ant #11	CFU input control	406666.7	46188.021
	11 - CFU input	3	0 n11-Untreated	12	0	n11 -Treated 15 Hr	12	0	n11 -Treated 20 Hr	12			non-irradiated control	412500	97805.465
x-	-bar11-CFU inpu	40.66666667	0 x-bar11-Untreate	41.25	0	x-bar11-Treated 15 H	38.83333333	0	x-bar11-Treated 20 Hr	38.16666667			15 hr	388333.3	68600.733
s1	L1-CFU input	4.618802154	0 s11-Untreated	9.780546555	0	s11-Treated 15 Hr	6.860073328	0	s11-Treated 20 Hr	7.309188903			20 hr	381666.7	73091.889
	11 Local CFU	0000 0000 1000 100													
		1 GFU input control	non-tradiated control 15 hr 20 hr	CFU input control		on-irrad lated control [®] 15 hr 20 hr	CFU input control		on-irradiated control* 15 hr 20 hr	CFU input control	non-fradiated control 15 hr	20 hr			
						÷.			÷						



Protocol 6 Analysis	6									_			-
Data													
Strain					1 (WT)		-					
Untreated Samples	332	415		410									
5 Hr Treated Samples	423	167		473									_
10 Hr Treated Samples	391	415	_	439									_
15 Hr Treated Samples	348	356		366									-
20 Hr Treated Samples	473	447	407	437									_
All colony counts at 10 ^{-5 dilution}			_										
Statistics										_			-
	n _{1-Untreated}	4		n _{1 - Treated 5 Hr}	4	n _{1 -Treated 10 Hr}	4	n _{1 -Treated 15 Hr}	4		n _{1 - Treated 20}	4	Ì
	x-bar _{1-Untreated}	377.3		x-bar _{1-Treated 5 H}	362.5	x-bar _{1-Treated 10 H}	416.3	x-bar _{1-Treated 15 Hr}	348.0		x-bar _{1-Treat}	441.0	
		41.6			135.0		19.8		18.8			27.3	
	S _{1-Untreated}	41.0		S ₁ -Treated 5 Hr	155.0	S _{1-Treated} 10 Hr	15.0	S _{1-Treated} 15 Hr	10.0		S _{1-Treated} 201	27.5	
Population Comparis	ons												
Comparison Set 1 - Strain 1(WT)										_			
H ₀ :	$\mu_{1-Untreated}$ - $\mu_{1-Treated 5 Hr}$ = 0												
H _a :	$\mu_{1-Untreated}$ - $\mu_{1-Treated 5 Hr}$ > 0	Altern	ate I	Hypothesis = T	'here is a	difference betw	een the l	Untreated popula	tion and	d the	5 Hr Treate	ed Popula	tion
2 p	9978.9583												
, test statistic	0.2088												
ejection region	t > t _a												
X	0.05												
lf	6												
α	1.943												
p-value	0.519127341												
				nce between	the Untre	eated and the 5 H	Ir Treate	d Populations					
		\mathbf{X}	_	-					X	X	\sim	\sim	\geq
-t _a -			X	\sim	\times	\sim	\succ	\sim	and the	×	Hr Treated		
	$\mu_{1-untreated}$ - $\mu_{1-treated \ 10 \ Hr}$ = 0	Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
		Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
	$\mu_{1-\text{untreated}} - \mu_{1-\text{treated } 10 \text{ Hr}} = 0$ $\mu_{1-\text{untreated}} - \mu_{1-\text{treated } 10 \text{ Hr}} > 0$	Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
H _a :	μ _{1-untreated} - μ _{1-treated 10 Hr} = 0 μ _{1-untreated} - μ _{1-treated 10 Hr} > 0 1058.9167	Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
H _a :	$\mu_{1-\text{untreated}} - \mu_{1-\text{treated } 10 \text{ Hr}} = 0$ $\mu_{1-\text{untreated}} - \mu_{1-\text{treated } 10 \text{ Hr}} > 0$	Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
H _a : 5. ² t, test statistic	μ _{1-untreated} - μ _{1-treated 10 Hr = 0 μ_{1-untreated} - μ_{1-treated 10 Hr > 0 1058.9167 -1.6949}}	Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
H _a : , p ² , test statistic	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0 \\ \\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0 \\ \\ \hline 1058.9167 \\ - 1.6949 \\ \\ t > t_{\alpha} \end{array}$	Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
H _a : ⁵ p ² t, test statistic rejection region α	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0 \\ \\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0 \\ \\ \hline \\ 1058.9167 \\ - 1.6949 \\ \\ t > t_{\alpha} \\ \\ 0.05 \end{array}$	Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
H _a : ⁵ p ² t, test statistic rejection region α	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0 \\ \\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0 \\ \\ \hline 1058.9167 \\ - 1.6949 \\ \\ t > t_{\alpha} \\ 0.05 \\ 6 \end{array}$	Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
H _a : p ² t, test statistic rejection region α df t _a	$\begin{array}{c} \mu_{1\text{-untreated}} - \mu_{1\text{-treated 10Hr}} = 0 \\ \\ \mu_{1\text{-untreated}} - \mu_{1\text{-treated 10Hr}} > 0 \\ \\ \hline \\ 1058.9167 \\ \hline \\ -1.6949 \\ \\ t > t_{\alpha} \\ \\ t > t_{\alpha} \\ \hline \\ 0.05 \\ \hline \\ 6 \\ \hline \\ 1.943 \end{array}$	Null H	X ypot	hesis = There	is no diff	erence between	the Untr	eated population					
H _a : s _p ² t, test statistic rejection region α df t _a -value	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0\\ \\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \\ \hline \\ 1058.9167\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.05\\ \hline \\ 6\\ 1.943\\ 0.519127341 \end{array}$	Null H Altern	ypot ate I	hesis = There Hypothesis = T	is no diff here is a	difference between	the Untreen the I	eated population					
H _a : s _p ² t, test statistic rejection region α df t _a -value	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0\\ \\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \\ \hline \\ 1058.9167\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.05\\ \hline \\ 6\\ 1.943\\ 0.519127341 \end{array}$	Null H Altern	ypot ate I	hesis = There Hypothesis = T	is no diff here is a	difference between	the Untreen the I	eated population					
H _a : ⁵ p ² (, test statistic rejection region α ff t _a - o-value Since - 1.6949 < 1.943, I do not reject	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0\\ \\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \\ \hline \\ 1058.9167\\ - 1.6949\\ \\ t > t_{\alpha} \\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ 1.943\\ 0.59\\ - 1.6949\\ \\ 1.943\\ 0.59\\ - 1.9127341\\ \\ t the null hypothesis, there i$	s no di	ypot ate I	hesis = There Hypothesis = T	the Untr	erence between difference betw	the Untr een the I	eated population		d the	10 Hr Trea	ted Popul	
H _a : sp ² rejection region a ff t _a p-value Since -1.6949 < 1.943, I do not reject	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0\\ \\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \\ 1058.9167\\ - 1.6949\\ \\ t > t_{\alpha} \\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ t > t_$	s no di	ypot ate I	hesis = There Hypothesis = T ence between hesis = There	the Untr	erence between	OHr Treat	eated population Jntreated popula	and the	e 15 H	10 Hr Trea	ted Popul	n
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H _a : ; test statistic rejection region x if 	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0\\ \\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \\ 1058.9167\\ - 1.6949\\ \\ t > t_{\alpha} \\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ t > t_{\alpha} \\ 0.59\\ - 1.6949\\ \\ t > t_{\alpha} \\ t > t_$	s no di	ypot ate I	hesis = There Hypothesis = T ence between hesis = There	the Untr	erence between	OHr Treat	eated population Jntreated popula	and the	e 15 H	10 Hr Trea	ted Popul	n
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H _a : ^p ² ; test statistic rejection region x if 	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0 \\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0 \\ \hline \\ 1058.9167 \\1.6949 \\ t > t_{\alpha} \\ 0.05 \\ 6 \\ 1.943 \\ 0.519127341 \\ t the null hypothesis, there i \\ \mu_{1-untreated} - \mu_{1-treated 15 Hr} = 0 \\ \mu_{1-untreated} - \mu_{1-treated 15 Hr} > 0 \\ \end{array}$	s no di	ypot ate I	hesis = There Hypothesis = T ence between hesis = There	the Untr	erence between	OHr Treat	eated population Jntreated popula	and the	e 15 H	10 Hr Trea	ted Popul	n
H _a : ^p ² ; test statistic rejection region x if 	$\label{eq:h1-untreated} \begin{split} & \mu_{1-untreated} - \mu_{1-treated 10\text{Hr}} = 0 \\ & \mu_{1-untreated} - \mu_{1-treated 10\text{Hr}} > 0 \\ & 1058.9167 \\ & 1.058.9167 \\ & 1.6949 \\ & t > t_{\alpha} \\ & 0.05 \\ & 0.519127341 \\ & t > t_{\alpha} \\ & 0.519127341 \\ & t the null hypothesis, there is \\ & \mu_{1-untreated 15\text{Hr}} = 0 \\ & \mu_{1-untreated 15\text{Hr}} > 0 \\ & 1041.1250 \\ & 1041.1250 \\ & 1041.1250 \\ \end{split}$	s no di	ypot ate I	hesis = There Hypothesis = T ence between hesis = There	the Untr	erence between	OHr Treat	eated population Jntreated popula	and the	e 15 H	10 Hr Trea	ted Popul	n
H _a : p ² rejection region x ff ra -value since - 1.6949 < 1.943, I do not reject 4 c : + d : + d : + d : + c : +	$\label{eq:h1-untreated} \begin{split} & \mu_{1-untreated} - \mu_{1-treated 10\text{Hr}} = 0 \\ & \mu_{1-untreated} - \mu_{1-treated 10\text{Hr}} > 0 \\ & 1058.9167 \\ & 1.058.9167 \\ & 1.6949 \\ & t > t_{\alpha} \\ & 0.05 \\ & 0.519127341 \\ & t > t_{\alpha} \\ & 0.519127341 \\ & t the null hypothesis, there is \\ & \mu_{1-untreated 15\text{Hr}} = 0 \\ & \mu_{1-untreated 15\text{Hr}} > 0 \\ & 1041.1250 \\ & 1041.1250 \\ & 1041.1250 \\ \end{split}$	s no di	ypot ate I	hesis = There Hypothesis = T ence between hesis = There	the Untr	erence between	OHr Treat	eated population Jntreated popula	and the	e 15 H	10 Hr Trea	ted Popul	n
H _a : p ² rejection region x ff ra -value since - 1.6949 < 1.943, I do not reject 4 c : + d : + d : + d : + c : +	$\label{eq:product} \begin{array}{l} \mu_{1-untreated} - \mu_{1-treated10Hr} = 0 \\ \mu_{1-untreated} - \mu_{1-treated10Hr} > 0 \\ \hline \\ 1058.9167 \\ - 1.6949 \\ \hline \\ t > t_{\alpha} \\ \hline \\ t > t_{\alpha} \\ 0.519127341 \\ t the null hypothesis, there i \\ \mu_{1-untreated} - \mu_{1-treated15Hr} = 0 \\ \mu_{1-untreated} - \mu_{1-treated15Hr} > 0 \\ \hline \\ 1041.1250 \\ \hline \\ 1.2820 \\ \hline \end{array}$	s no di	ypot ate I	hesis = There Hypothesis = T ence between hesis = There	the Untr	erence between	OHr Treat	eated population Jntreated popula	and the	e 15 H	10 Hr Trea	ted Popul	n
H _a : p ² rejection region x ff 	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0\\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \hline \\ 1058.9167\\ - 1.6949\\ \hline \\ t > t_{\alpha} \\ 0.59127341\\ \hline \\ t the null hypothesis, there i\\ \mu_{1-untreated} - \mu_{1-treated 15Hr} = 0\\ \hline \\ \mu_{1-untreated} - \mu_{1-treated 15Hr} > 0\\ \hline \\ 1041.1250\\ 1.2820\\ \hline \\ t > t_{\alpha} \end{array}$	s no di	ypot ate I	hesis = There Hypothesis = T ence between hesis = There	the Untr	erence between	OHr Treat	eated population Jntreated popula	and the	e 15 H	10 Hr Trea	ted Popul	n
H _a : s_p^2 z_i , test statistic rejection region α df r_a $p_p-value Since -1.6949 < 1.943, I do not rejection Ha : s_p^2z_i, test statisticrejection region\alpha$	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0 \\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0 \\ \hline \\ 1058.9167 \\ - 1.6949 \\ \hline \\ t > t_{\alpha} \\ 0.519127341 \\ \hline \\ 0.519127341 $	s no di	ypot ate I	hesis = There Hypothesis = T ence between hesis = There	the Untr	erence between	OHr Treat	eated population Jntreated popula	and the	e 15 H	10 Hr Trea	ted Popul	n
H _a : s_p^2 rejection region α df t _a p-value Since - 1.6949 < 1.943, I do not rejection H _a : s_p^2 t, test statistic rejection region α df t _a s_p^2 t, test statistic	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0 \\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0 \\ \hline \\ 1058.9167 \\ -1.6949 \\ t > t_{\alpha} \\ 0.519127341 \\ t > t_{\alpha} \\ 0.519127341 \\ t the null hypothesis, there i \\ \hline \\ \mu_{1-untreated} - \mu_{1-treated 15 Hr} = 0 \\ \mu_{1-untreated} - \mu_{1-treated 15 Hr} > 0 \\ 1041.1250 \\ 1.2820 \\ t > t_{\alpha} \\ 0.05 \\ 6 \\ 6 \\ \end{array}$	s no di	ypot ate I	hesis = There Hypothesis = T ence between hesis = There	the Untr	erence between	OHr Treat	eated population Jntreated popula	and the	e 15 H	10 Hr Trea	ted Popul	n
H _a : r_{p}^{2} rejection region r_{a} r_{a} r_{a} r_{a} r_{b} : r_{b} :	$\label{eq:h1-untreated - } \begin{array}{c} \mu_{1-untreated 10Hr} = 0 \\ \\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0 \\ \\ \hline \\ 1058.9167 \\ \\ -1.6949 \\ \\ \hline \\ t > t_{\alpha} \\ \\ \hline \\ t > t_{\alpha} \\ \\ 0.519127341 \\ \\ \hline \\ tthe null hypothesis, there i \\ \\ \mu_{1-untreated} - \mu_{1-treated 15Hr} = 0 \\ \\ \mu_{1-untreated} - \mu_{1-treated 15Hr} > 0 \\ \\ \hline \\ 10441.1250 \\ \\ 1.2820 \\ \\ t > t_{\alpha} \\ \\ 0.519127341 \\ \end{array}$	Null H Altern s no di Null H Altern	ffer ypot	hesis = There Hypothesis = T ence between hesis = There Hypothesis = T	the Untr	eated and the 10	DHr Treat	eated population Jntreated popula ed Populations eated populations Untreated populat	and the	e 15 H	10 Hr Trea	ted Popul	n
H _a : r_{p}^{2} rejection region r_{a} r_{a} r_{a} r_{a} r_{b} : r_{b} :	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0\\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \hline \\ 1058.9167\\ - 1.6949\\ \hline \\ t > t_{\alpha} \\ 0.519127341\\ 0.519127341\\ \hline \\ t the null hypothesis, there is a divide the set of the $	Null H Altern s no di Null H Altern	ffer ypot ate I ypot ate I	hesis = There Hypothesis = T ence between hesis = There Hypothesis = T etween the U	the Untr	erence between difference betw reated and the 10 erence between difference betw	DHr Treat	eated population Jntreated popula ed Populations eated populations Untreated populat	and the	e 15 H	10 Hr Trea	ted Popul	n
4. : ²	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10Hr} = 0\\ \mu_{1-untreated} - \mu_{1-treated 10Hr} > 0\\ \hline \\ 1058.9167\\ - 1.6949\\ \hline \\ t > t_{\alpha} \\ 0.519127341\\ \hline \\ 0.519127341\\ \hline \\ 0.519127341\\ \hline \\ 0.519127341\\ \hline \\ 0.519127341\\ \hline \\ 1.4tte null hypothesis, there i \\ \hline \\ \mu_{1-untreated} - \mu_{1-treated 15Hr} = 0\\ \hline \\ \mu_{1-untreated} - \mu_{1-treated 15Hr} = 0\\ \hline \\ 1.2820\\ \hline \\ 1.2820\\ \hline \\ t > t_{\alpha} \\ \hline \\ 0.519127341\\ \hline \\ 0.519127341\\ \hline \\ 0.519127341\\ \hline \\ 0.519127341\\ \hline \end{array}$	S no di	ffera ypot	hesis = There Hypothesis = T hesis = There Hypothesis = T etween the U	the Untraction of the Untracti	eated and the 10	HIT Treat	eated population Untreated popula ede Populations eated population Untre	and the	d the	10 Hr Trea	ted Popul	n
H _a : p ² y, test statistic ejection region x ff a >-value since - 1.6949 < 1.943, I do not reject	$\begin{array}{c} \mu_{1-untreated} - \mu_{1-treated 10 Hr} = 0 \\ \mu_{1-untreated} - \mu_{1-treated 10 Hr} > 0 \\ \hline \\ 1058.9167 \\ - 1.6949 \\ \hline \\ t > t_{\alpha} \\ 0.519127341 \\ \hline \\ t > t_{\alpha} \\ 0.519127341 \\ \hline \\ t the null hypothesis, there i \\ \mu_{1-untreated} - \mu_{1-treated 15 Hr} = 0 \\ \mu_{1-untreated} - \mu_{1-treated 15 Hr} > 0 \\ \hline \\ 1.2820 \\ \hline \\ t > t_{\alpha} \\ 0.519127341 \\ \hline \\ null hypothesis, there is a di \\ 0.519127341 \\ - 0.519127341 \\ \hline \\ 1.2820 \\ \hline \\ t > t_{\alpha} \\ 0.519127341 \\ \hline \\ null hypothesis, there is a di \\ \mu_{1-untreated} - \mu_{1-treated 15 Hr} = 0 \\ \hline \end{array}$	Null H Altern S no di Null H Altern fferen	ffere ypot	hesis = There Hypothesis = T hesis = There Hypothesis = T Hypothesis = T hesis = There Hypothesis = There	the Untr	erence between difference between erence between difference between difference between erence between	Hte Untr een the Untr DHr Treat	eated population Untreated populat eated populations eated population Untreated population Untreated population eated population eated population	and the	d the	Hr Treated	populatio ted Popul	natio
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Ha A summentated - μ-summentated 15 Hr A least set to track and 15 Hr A least set t	Since 4.8106 > 1.943, I do reject the H ₀ : H ₀ : p ² z test statistic rejection region x df f b-value	e null hypothesis, there is a c μ _{5-untreated} - μ _{5-treated 15 μr = 0 μ_{5-untreated} - μ_{5-treated 15 μr > 0 427.4583 -2.7874 t > t_a 0.05 6 1.943 0.519127341}}	Null H Alterr	Aypot aate l	thesis = There Hypothesis = T	is no dif here is a	ference between a difference between	the Unt	reated population					
μ_suntreated ~ μ_surate distr Alter rate Hypothesis = There is a difference between the Untreated population and the 20 Hr Treated Population μ_suntreated ~ μ_surate distr Mater rate (Mater rate) Mater rate (Mater rate) Mater rate (Mater rate) μ_suntreated ~ μ_surate distr Mater rate Hypothesis = There is a difference between the Untreated population and the 20 Hr Treated Population Mater rate <th< td=""><td>Since 4.8106 > 1.943, I do reject the 4.5 : 4.5 : 5.7 2 5.7 5</td><td>e null hypothesis, there is a c μ_{5-untreated} - μ_{5-treated 15 μr = 0 μ_{5-untreated} - μ_{5-treated 15 μr > 0 427.4583 -2.7874 t > t_a 0.05 6 1.943 0.519127341}}</td><td>Null H Alterr</td><td>Aypot aate l</td><td>thesis = There Hypothesis = T</td><td>is no dif here is a</td><td>ference between a difference between</td><td>the Unt</td><td>reated population</td><td></td><td></td><td></td><td></td></th<>	Since 4.8106 > 1.943, I do reject the 4.5 : 4.5 : 5.7 2 5.7 5	e null hypothesis, there is a c μ _{5-untreated} - μ _{5-treated 15 μr = 0 μ_{5-untreated} - μ_{5-treated 15 μr > 0 427.4583 -2.7874 t > t_a 0.05 6 1.943 0.519127341}}	Null H Alterr	Aypot aate l	thesis = There Hypothesis = T	is no dif here is a	ference between a difference between	the Unt	reated population					
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Lest statistic 0.9614 Image: Constraint of the statistic of the	Since 4.8106 > 1.943, I do reject the H_0 : H_0 : h_1 : h_2 : h_2 : h_2 : h_3 : h_2 : h_2 : h_2 : h_3 :	e null hypothesis, there is a c $\mu_{S-untreated} - \mu_{S-treated 15 Hr} = 0$ $\mu_{S-untreated} - \mu_{S-treated 15 Hr} = 0$ 427.4583 -2.7874 $t > t_{\alpha}$ 0.05 6 1.943 0.519127341 t the null hypothesis, there is $\mu_{S-untreated} - \mu_{S-treated 15 Hr} = 0$	Null H Alterr	liffer	rence between thesis = There	is no dif here is a n the Un is no dif	ference between	5 Hr Tre	eated Population	and the	e 20	15 Hr Treated Po	pulation	
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x 0.05 off 6 ia_ 1.943	Since 4.8106 > 1.943, I do reject the H_0 : H_0 : H_0 : h_1 : h_2 : h_2 : h_3 : h_4 : h_2 : h_4 : h_5 : h_6 : H_0 :	e null hypothesis, there is a c $\mu_{5-untreated} - \mu_{5-treated 15 Hr} = 0$ $\mu_{5-untreated} - \mu_{5-treated 15 Hr} > 0$ 427.4583 -2.7874 $t > t_{\alpha}$ 0.055 6 1.943 0.519127341 t the null hypothesis, there is $\mu_{5-untreated} - \mu_{5-treated 15 Hr} = 0$ $\mu_{5-untreated} - \mu_{5-treated 15 Hr} > 0$ 454.9167	Null H Alterr	liffer	rence between thesis = There	is no dif here is a n the Un is no dif	ference between	5 Hr Tre	eated Population	and the	e 20	15 Hr Treated Po	pulation	
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	Since 4.8106 > 1.943, I do reject the 1 ₀ : 1 ₂ : 1 ₂ : 1 ₃ : 1 ₄ : 1 ₅ : 1 ₅ : 1 ₅ : 1 ₆ : 1 ₆ : 1 ₆ : 1 ₆ : 1 ₇ : 1 ₈ : 1 ₉ :	e null hypothesis, there is a c $\mu_{5-untreated} - \mu_{5-treated 15 Hr} = 0$ $\mu_{5-untreated} - \mu_{5-treated 15 Hr} > 0$ 427.4583 -2.7874 $t > t_{\alpha}$ 0.05 6 1.943 0.519127341 t the null hypothesis, there is $\mu_{5-untreated} - \mu_{5-treated 15 Hr} = 0$ $\mu_{5-untreated} - \mu_{5-treated 15 Hr} > 0$ 454.9167 0.9614 $t > t_{\alpha}$ 0.05	Null H Alterr	liffer	rence between thesis = There	is no dif here is a n the Un is no dif	ference between	5 Hr Tre	eated Population	and the	e 20	15 Hr Treated Po	pulation	
0.510127241	a - a - b - a - c - c - c - c - c - c - c - c - c - c - c - c - c - d -	e null hypothesis, there is a c $\mu_{5-untreated} - \mu_{5-treated 15 Hr} = 0$ $\mu_{5-untreated} - \mu_{5-treated 15 Hr} > 0$ 427.4583 -2.7874 $t > t_{\alpha}$ 0.05 6 1.943 0.519127341 t the null hypothesis, there is $\mu_{5-untreated} - \mu_{5-treated 15 Hr} = 0$ $\mu_{5-untreated} - \mu_{5-treated 15 Hr} > 0$ 454.9167 0.9614 $t > t_{\alpha}$ 0.05	Null H Alterr	liffer	rence between thesis = There	is no dif here is a n the Un is no dif	ference between	5 Hr Tre	eated Population	and the	e 20	15 Hr Treated Po	pulation	
p-value 0.519127341	Since 4.8106 > 1.943, I do reject the H_0 : H_0 : H_2 : h_2 : h_3 : h_4 : h_5 : h_5 : h_6 : h_6 : H_0 : H_0 : H_0 : H_0 : H_0 : h_5 :	e null hypothesis, there is a c $\mu_{5-untreated} - \mu_{5-treated 15 Hr} = 0$ $\mu_{5-untreated} - \mu_{5-treated 15 Hr} > 0$ 427.4583 -2.7874 $t > t_{\alpha}$ 0.05 6 1.943 0.519127341 tt he null hypothesis, there is $\mu_{5-untreated} - \mu_{5-treated 15 Hr} = 0$ $\mu_{5-untreated} - \mu_{5-treated 15 Hr} > 0$ 454.9167 0.9614 $t > t_{\alpha}$ 0.05 6	Null H Alterr	liffer	rence between thesis = There	is no dif here is a n the Un is no dif	ference between	5 Hr Tre	eated Population	and the	e 20	15 Hr Treated Po	pulation	



Protocol 6 Analysis			_									
Data												
itrain					Mutant	#8		- *		_		
Untreated Samples	333	311	382	276								
5 Hr Treated Samples	317	364	345	307								
10 Hr Treated Samples	333	331		317								
15 Hr Treated Samples	316	329		285								
20 Hr Treated Samples	233	332	320	269								
All colony counts at 10 ^{-5 dilution}												
Statistics			_									
5141151165	n _{8-Untreated}	4		n _{8 -Treated 5 Hr}	4	n _{8 -Treated 10 Hr}	4	n _{8-Treated 15 Hr}	4		n _{8 -Treated 20 Hr}	4
		325.5		x-bar _{8-Treated 5 F}	333.3	x-bar _{8-Treated 10 H}	321 3	x-bar _{8-Treated 15 Hr}	307.5		x-bar _{8-Treated 20 Hr}	288.5
		44.4										46.0
	S _{8-Untreated}	44.4		S8-Treated 5 Hr	26.1	S _{8-Treated} 10 Hr	13.5	S _{8-Treated 15 Hr}	19.1		S _{8-Treated} 20 Hr	40.0
Population Comparise	ons		_									
•												
Comparison Set 1 - Strain 1(WT)												
H ₀ :	$\mu_{8-Untreated}$ - $\mu_{8-Treated 5 Hr}$ = 0											
1 _a :	μ _{8-Untreated} - μ _{8-Treated 5 Hr} > 0	Altern	ate ⊦	lypothesis = T	here is a	difference betw	een the	Untreated popula	tion an	d the	e 5 Hr Treated Pop	oulation
2	1324.2917											
p			_				\vdash					
, test statistic	-0.3012											
ejection region	t > t _α					-						
1	0.05											
df	6											
~	1.943											
α o-value	0.519127341					-						
ince3012 < 1.943, I do not reject	the null hypothesis, there is	no dif	Foror									
			erer	ice between i	ne Untr	eated and the 5 H	r Treateo	d Populations				
	>	\approx	X			eated and the 5 H	r Treated	d Populations	\times	X	$>\!$	$>\!\!\!>\!\!\!>$
H ₀ :	$\mu_{8-untreated} - \mu_{8-treated 10 Hr} = 0$	\times	X	\sim	\gg	\sim	>>	\sim	and the	X e 10	Hr Treated popula	ation
		Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
	$\mu_{8-untreated} - \mu_{8-treated 10 Hr} = 0$ $\mu_{8-untreated} - \mu_{8-treated 10 Hr} > 0$	Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
		Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
H _a : 	μ _{8-untreated} - μ _{8-treated 10 Hr} > 0 1076.2917	Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
H _a :	μ _{8-untreated} - μ _{8-treated 10 Hr} >0	Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
H _a : 5. ² t, test statistic	U8-untreated - U8-treated 10 Hr >0 1076.2917 0.1832	Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
H _a : 5. ² t, test statistic	μ _{8-untreated} - μ _{8-treated 10 Hr >0 1076.2917 0.1832 t > t_α}	Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
H _a : ^{p²} , test statistic rejection region α	U8-untreated - U8-treated 10 Hr >0 1076.2917 0.1832	Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
H _a : ^{p²} , test statistic rejection region α	$\begin{array}{c} \mu_{\text{B-untreated}} \sim \mu_{\text{B-treated 10 Hr}} > 0 \\ \hline \\ 1076.2917 \\ \hline \\ 0.1832 \\ \hline \\ t > t_{\alpha} \\ \hline \\ 0.05 \end{array}$	Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
ν _P rejection region α df	$\begin{array}{c} \mu_{\text{B-untreated}} & - \mu_{\text{B-treated 10 Hr}} > 0 \\ \hline \\ & 1076.2917 \\ \hline \\ 0.1832 \\ \hline \\ t > t_{\alpha} \\ \hline \\ t > t_{\alpha} \\ 0.05 \\ \hline \\ 6 \\ \hline \\ 1.943 \end{array}$	Null H	X ypoti	hesis = There	XX is no dif	ference between	the Unti	reated population				
H _a : ^{p²} , test statistic rejection region α	μ _{8-untreated} - μ _{8-treated 1D Hr} >0 1076.2917 0.1832 t > t _α 0.05 6 1.943 0.519127341	Null H Altern	ypotl ate F	hesis = There łypothesis = T	kere is a	ference between difference betw	the Untri een the	reated population				
H _a : p p rejection region x df -value	μ _{8-untreated} - μ _{8-treated 1D Hr} >0 1076.2917 0.1832 t > t _α 0.05 6 1.943 0.519127341	Null H Altern	ypotl ate F	hesis = There łypothesis = T	is no difi here is a	ference between difference betw	the Untri een the	reated population				
H _a : p ² p ² rejection region a ff i _a o-value Since .1832 < 1.943, I do reject the p	$\begin{array}{c} \mu_{8-untreated} \sim \mu_{8-treated \ 1D \ Hr} > 0 \\ \\ \hline 1076.2917 \\ 0.1832 \\ t > t_{\alpha} \\ \hline t > t_{\alpha} \\ 0.05 \\ \hline 6 \\ 1.943 \\ 0.519127341 \\ null hypothesis, there is a ditert$	Null H Altern	ypotl ate F	hesis = There Hypothesis = T Hypothesis = T	treated	ference between difference betw and the 10 Hr Tree	the Untri een the	reated population		the state of the s	e 10 Hr Treated Po	pulation
H _a : p ² rejection region a ff ca p-value Since .1832 < 1.943, I do reject the P	$\label{eq:heat} \begin{array}{c} \mu_{\text{B-untreated}} - \mu_{\text{B-treated 1D Hr}} > 0 \\ \hline \\ 1076.2917 \\ 0.1832 \\ \hline \\ 1076.2917 \\ 0.1832 \\ \hline \\ 1076.2917 \\ 0.59127341 \\ 0.519127341 \\ 0.519127341 \\ 0.519127341 \\ 0.519127341 \\ \hline \\ null hypothesis, there is a different of the second se$	Null H Altern	ypotl ate F	tween the Ur thesis = There	is no diff	ference between addifference betw and the 10 Hr Tree ference between	ated Pop	reated population Untreated popula	and the	e 15	e 10 Hr Treated Po	pulation
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H _a : p ² test statistic rejection region x ff fa -value since .1832 < 1.943, I do reject the P	μ _{8-untreated} - μ _{8-treated 1D Hr} >0 1076.2917 0.1832 t > t _α 0.05 6 1.943 0.519127341 null hypothesis, there is a difference is a difference in the second is the	Null H Altern	ypotl ate F	tween the Ur thesis = There	is no diff	ference between addifference betw and the 10 Hr Tree ference between	ated Pop	reated population Untreated popula	and the	e 15	e 10 Hr Treated Po	pulation
4. : ¹ / _p : ¹ / _p : ¹ / _p : ¹ / ₂ : ¹ / ₂ : ¹ / ₂ : ¹ / ₂ : ¹ / _p : ¹ /	$\begin{array}{c} \mu_{8-untreated} - \mu_{8-treated \ 1D \ Hr} > 0 \\ \hline \\ 1076.2917 \\ 0.1832 \\ t > t_{\alpha} \\ \hline \\ t > t_{\alpha} \\ 0.05 \\ 0.519127341 \\ null hypothesis, there is a different of the second sec$	Null H Altern	ypotl ate F	tween the Ur thesis = There	is no diff	ference between addifference betw and the 10 Hr Tree ference between	ated Pop	reated population Untreated popula	and the	e 15	e 10 Hr Treated Po	pulation
$\begin{array}{l} H_a: \\ & \\ p_a^2 \\ \text{rejection region} \\ \alpha \\ \text{df} \\ & \\ p_a^2 \\ \text{df} \\ & \\ p_a^2 \\ \text{df} \\ $	μ _{8-untreated} - μ _{8-treated 1D Hr} >0 1076.2917 0.1832 t > t _α 0.05 6 1.943 0.519127341 null hypothesis, there is a difference is a difference in the second is the	Null H Altern	ypotl ate F	tween the Ur thesis = There	is no diff	ference between addifference betw and the 10 Hr Tree ference between	ated Pop	reated population Untreated popula	and the	e 15	e 10 Hr Treated Po	pulation
4 _a : ² test statistic ejection region α ^α ·value ince .1832 < 1.943, I do reject the r 4 _b : 4 _b : ² ² ² ³ ⁴ · ···································	µs-untreated ~ µs-treated 10 Hr >0 1076.2917 0.1832 t > t _a 0.05 6 1.943 0.519127341 null hypothesis, there is a dif µs-untreated ~ µs-treated 15 Hr = 0 µs-untreated ~ µs-treated 15 Hr >0 1167.6667 0.7450	Null H Altern	ypotl ate F	tween the Ur thesis = There	is no diff	ference between addifference betw and the 10 Hr Tree ference between	ated Pop	reated population Untreated popula	and the	e 15	e 10 Hr Treated Po	pulation
4. : . test statistic rejection region x ff 	$\label{eq:subrate} \begin{array}{c} \mu_{\$-untreated} - \mu_{\$-treated \ 1D \ Hr} > 0 \\ \hline \\ 1076.2917 \\ 0.1832 \\ \hline \\ 1076.2917 \\ 0.1832 \\ \hline \\ 1076.2917 \\ 0.519127341 \\ 0.519127341 \\ 0.519127341 \\ 0.519127341 \\ 0.519127341 \\ 0.519127341 \\ \hline \\ null hypothesis, there is a difter the set of t$	Null H Altern	ypotl ate F	tween the Ur thesis = There	is no diff	ference between addifference betw and the 10 Hr Tree ference between	ated Pop	reated population Untreated popula	and the	e 15	e 10 Hr Treated Po	pulation
H _a : ^{p2} / _{p2} rejection region x ff -value since .1832 < 1.943, I do reject the a H ₀ : H _a : (p ² / _p) (t est statistic rejection region x	$\label{eq:heat} \begin{array}{c} \mu_{\text{B-untreated}} - \mu_{\text{B-treated 1D Hr}} > 0 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 10.19127341 \\ 0.519127341 \\ \hline 10.19127341 \\ \hline $	Null H Altern	ypotl ate F	tween the Ur thesis = There	is no diff	ference between addifference betw and the 10 Hr Tree ference between	ated Pop	reated population Untreated popula	and the	e 15	e 10 Hr Treated Po	pulation
$H_{a}:$ p_{p}^{2} (rejection region (x) (rejection region (x) (x) (x) (x) (x) (x) (x) (x) (x) (x)	$\label{eq:rested_org} \begin{array}{c} \mu_{\$.untreated} - \mu_{\$.treated \ 1D \ Hr} > 0 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 0.1832 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 1076.2917 \\ \hline 10.1832 \\ 0.519127341 \\ \hline 10.1943 \\ 0.519127341 \\ \hline 10.1943 \\ \hline 0.519127341 \\ \hline 10.1943 \\ \hline 0.519127341 \\ \hline 10.1943 \\ \hline 0.519127341 \\ \hline 10.1943 $	Null H Altern	ypotl ate F	tween the Ur thesis = There	is no diff	ference between addifference betw and the 10 Hr Tree ference between	ated Pop	reated population Untreated popula	and the	e 15	e 10 Hr Treated Po	pulation
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H _a : r_{a}^{b} r_{a}^{c} r_{a}^{c} r_{a}^{c} r_{a}^{c} r_{a}^{c} r_{a}^{c} r_{a}^{c} r_{a}^{c} r_{a}^{c} r_{b}^{c}	$\label{eq:heat} \begin{array}{c} \mu_{\text{B-untreated}} - \mu_{\text{B-treated 1D Hr}} > 0 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 0.1832 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 1096 \\ 0.1943 \\ 0.519127341 \\ \hline 1096 \\ \mu_{\text{B-untreated}} - \mu_{\text{B-treated 15 Hr}} = 0 \\ \mu_{\text{B-untreated}} - \mu_{\text{B-treated 15 Hr}} > 0 \\ \hline 1167.6667 \\ 0.7450 \\ \hline 1187 \\ 0.7450 \\ \hline 1.943 \\ 0.519127341 \\ \hline 0.519127341 $	iference	ypotl ate F	tween the Ur typothesis = T typothesis = T typothesis = T typothesis = T	here is a	and the 10 Hr Tre	ated Pop	eated population Untreated popula ulations eated population Untreated population Untreated population	and the	e 15	e 10 Hr Treated Po	pulation
$a_1 = \frac{1}{2}$ $a_2 = \frac{1}{2}$ $a_2 = \frac{1}{2}$ $a_3 = \frac{1}{2}$ $a_4 = \frac{1}{2}$ $a_4 = \frac{1}{2}$ $a_5 = \frac{1}{2}$ $a_1 = \frac{1}{2}$ $a_2 = \frac{1}{2}$ $a_3 = \frac{1}{2}$ $a_4 = \frac{1}{2}$ $a_5 $	$\label{eq:heat} \begin{array}{c} \mu_{\text{B-untreated}} - \mu_{\text{B-treated 1D Hr}} > 0 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 0.1832 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 1096 \\ 0.1943 \\ 0.519127341 \\ \hline 1096 \\ \mu_{\text{B-untreated}} - \mu_{\text{B-treated 15 Hr}} = 0 \\ \mu_{\text{B-untreated}} - \mu_{\text{B-treated 15 Hr}} > 0 \\ \hline 1167.6667 \\ 0.7450 \\ \hline 1187 \\ 0.7450 \\ \hline 1.943 \\ 0.519127341 \\ \hline 0.519127341 $	iference	ypotl ate F	tween the Ur typothesis = T typothesis = T typothesis = T typothesis = T	here is a	and the 10 Hr Tre	ated Pop	eated population Untreated popula ulations eated population Untreated population Untreated population	and the	e 15	e 10 Hr Treated Po	pulation
4 _a : p p, test statistic ejection region x -value ince .1832 < 1.943, I do reject the r	$\label{eq:rested_1} \begin{array}{c} \mu_{\text{B-untreated}} & - \ \mu_{\text{B-treated}} & 10 \ \text{He} > 0 \\ \hline & & 1076.2917 \\ \hline & & 0.1832 \\ \hline & & & \\ t > t_{\alpha} & & \\ \hline & & & \\ t > t_{\alpha} & & \\ \hline & & & \\ 0.519127341 \\ null hypothesis, there is a different of the second sec$	iference	ypotl ate F ypotl ate F	tween the Ur hesis = There hypothesis = T hesis = There hypothesis = T	treated	and the 15 Hr Tree	ated Pop	valations	and thi	e 15 d the	e 10 Hr Treated Po	pulation
4.a : p y, test statistic ejection region x -value ince .1832 < 1.943, I do reject the r	$\begin{array}{c} \mu_{8-untreated} - \mu_{8-treated 10 Hr} > 0\\ \hline \\ 1076.2917\\ \hline \\ 0.1832\\ \hline \\ t > t_{\alpha} \\ \hline \\ t > t_{\alpha} \\ \hline \\ 0.519127341\\ \hline \\ null hypothesis, there is a different of the second $	iferenn Null H Altern Null H Altern	ypotl ate F ypotl ate F	tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur	treated treated	and the 15 Hr Tree ference between	ated Pop	valations valati	and the	e 15 d the	e 10 Hr Treated Po	pulation
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$H_a:$ p_a^2 $rejection region x ff g_a g_a g_a g_a g_a g_a g_a g_a g_a g_a H_a: g_a$	$\begin{array}{c} \mu_{\text{B-untreated}} & - \mu_{\text{B-treated 1D Hr}} > 0 \\ \hline & & & & \\ & & & & \\ & & & & \\ & & & &$	iferenn Null H Altern Null H Altern	ypotl ate F ypotl ate F	tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur	treated treated	and the 15 Hr Tree ference between	ated Pop	valations valati	and the	e 15 d the	e 10 Hr Treated Po	pulation
$H_a : \\ H_a : \\ P_a^{2}$ $F_a = \\ P_$	$\label{eq:heat} \begin{array}{c} \mu_{\text{B-untreated}} - \mu_{\text{B-treated} 10 \ \text{Hr}} > 0 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 10.19127341 \\ \hline 10.191273$	iferenn Null H Altern Null H Altern	ypotl ate F ypotl ate F	tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur	treated treated	and the 15 Hr Tree ference between	ated Pop	valations valati	and the	e 15 d the	e 10 Hr Treated Po	pulation
4. : y _p ² y _p y _p rejection region x ff -a -a-value ince .1832 < 1.943, I do reject the r	$\begin{array}{c} \mu_{\text{B-untreated}} & - \mu_{\text{B-treated 1D Hr}} > 0 \\ \hline & & & & \\ & & & & \\ & & & & \\ & & & &$	iferenn Null H Altern Null H Altern	ypotl ate F ypotl ate F	tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur	treated treated	and the 15 Hr Tree ference between	ated Pop	valations valati	and the	e 15 d the	e 10 Hr Treated Po	pulation
4_a : p_p^2 p_p^2 rejection region x ff a p_p^2 p_p^2 q_0 : 4_a : p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 q_0 : <t< td=""><td>$eq:rested_streated_st$</td><td>iferenn Null H Altern Null H Altern</td><td>ypotl ate F ypotl ate F</td><td>tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur</td><td>treated treated</td><td>and the 15 Hr Tree ference between</td><td>ated Pop</td><td>valations valations ><td>and the</td><td>e 15 d the</td><td>e 10 Hr Treated Po</td><td>pulation</td></t<>	$eq:rested_streated_st$	iferenn Null H Altern Null H Altern	ypotl ate F ypotl ate F	tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur	treated treated	and the 15 Hr Tree ference between	ated Pop	valations valati	and the	e 15 d the	e 10 Hr Treated Po	pulation
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4_a : p^2	$\label{eq:rested_optimization} \begin{array}{c} \mu_{\text{B-untreated}} & - \ \mu_{\text{B-treated}} & 10 \ \text{He} > 0 \\ \hline & 1076.2917 \\ \hline & 0.1832 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.7450 \\ \hline & 0.7450 \\ \hline & 0.7450 \\ \hline & 0.7450 \\ \hline & 0.7450 \\ \hline & 0.519127341 \\$	iferenn Null H Altern Null H Altern	ypotl ate F ypotl ate F	tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur	treated treated	and the 15 Hr Tree ference between	ated Pop	valations valati	and the	e 15 d the	e 10 Hr Treated Po	pulation
4_a : p_p^2 p_p^2 rejection region x ff a p_p^2 p_p^2 q_0 : 4_a : p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 p_p^2 q_0 : <t< td=""><td>$\label{eq:rested_optimization} \begin{array}{c} \mu_{\text{B-untreated}} - \mu_{\text{B-treated} 10 \ \text{Hz}} > 0 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 0.1076.2917 \\ 0.1832 \\ \hline 1076.2917 \\ \hline 0.1832 \\ \hline 1.943 \\ 0.519127341 \\ \hline 0.519127341 \\ \hline 0.519127341 \\ \hline 0.519127341 \\ \hline 0.519127341 \\ \hline 0.7450 \\ \hline 1167.6667 \\ \hline 1167.667 \\ \hline 1167.667 \\ \hline 1167.667 \\ \hline 1177.117 \\ \hline 1177.$</td><td>iferenn Null H Altern Null H Altern</td><td>ypotl ate F ypotl ate F</td><td>tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur</td><td>treated treated</td><td>and the 15 Hr Tree ference between</td><td>ated Pop</td><td>valations valations ><td>and the</td><td>e 15 d the</td><td>e 10 Hr Treated Po</td><td>pulation</td></t<>	$\label{eq:rested_optimization} \begin{array}{c} \mu_{\text{B-untreated}} - \mu_{\text{B-treated} 10 \ \text{Hz}} > 0 \\ \hline 1076.2917 \\ 0.1832 \\ \hline 0.1076.2917 \\ 0.1832 \\ \hline 1076.2917 \\ \hline 0.1832 \\ \hline 1.943 \\ 0.519127341 \\ \hline 0.519127341 \\ \hline 0.519127341 \\ \hline 0.519127341 \\ \hline 0.519127341 \\ \hline 0.7450 \\ \hline 1167.6667 \\ \hline 1167.667 \\ \hline 1167.667 \\ \hline 1167.667 \\ \hline 1177.117 \\ \hline 1177.$	iferenn Null H Altern Null H Altern	ypotl ate F ypotl ate F	tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur	treated treated	and the 15 Hr Tree ference between	ated Pop	valations valati	and the	e 15 d the	e 10 Hr Treated Po	pulation
4_a : p^2	$\label{eq:rested_optimization} \begin{array}{c} \mu_{\text{B-untreated}} & - \ \mu_{\text{B-treated}} & 10 \ \text{He} > 0 \\ \hline & 1076.2917 \\ \hline & 0.1832 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.519127341 \\ \hline & 0.7450 \\ \hline & 0.7450 \\ \hline & 0.7450 \\ \hline & 0.7450 \\ \hline & 0.7450 \\ \hline & 0.519127341 \\$	iferenn Null H Altern Null H Altern	ypotl ate F ypotl ate F	tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur tween the Ur	treated treated	and the 15 Hr Tree ference between	ated Pop	valations valati	and the	e 15 d the	e 10 Hr Treated Po	pulation



Jintreated Samples	ntreated - H11-Treated 5 Hr = ntreated - H11-Treated 5 Hr > 1756.2500 -1.7379	420 411 435 301 4 4 338.8 47.0	łypot	358 421 269 486 326 	36.1 s no dif	n11-Treated 10 Hr x-bar 11-Treated 10 Hr x-bar 11-Treated 10 Hr 511-Treated 10 Hr	58.2 the Unt	n11-Treated 15 Hr k-DaF 11-Treated 15 Hr 511-Treated 15 Hr	35.3		n _{11-Treated 20 Hr} X-Daf _{11-Treated 20 Hr} S _{11-Treated 20 Hr}	4 293.0 45.9
Statistics Statistics n11.00 x-bar \$11.00 Population Comparisons \$100 Comparison Set 1 - Strain 1(WT) \$100 40 : \$11.00 40 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$11.00 10 : \$100 10 : \$100 10 : \$100 10 : \$100 10 : \$100 10 : \$100 10 : \$100 10 : \$100 10 :	349 339 416 226 /////////////////////////////////	420 411 435 301 4 4 338.8 47.0	371 330 407 319	358 421 269 486 326 	4 390.3 36.1	n11-Treated 10 Hr x-bar 11-Treated 10 Hr x-bar 11-Treated 10 Hr 511-Treated 10 Hr	337.3 58.2	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	436.0		x-bar _{11-Treated 20 Hr}	293.0
iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples iii Hr Treated Samples Statistics Population Comparisons comparison Set 1 - Strain 1(WT) 40 : µ µ µ µ i, test statistic ejection region x if a b-value iince -1.7379 < 1.943, I do not reject the nu	349 339 416 226 /////////////////////////////////	420 411 435 301 4 4 338.8 47.0	371 330 407 319	421 269 486 326 n _{11-Treated 5 Hr} x-bar _{11-Treated 5} Hr S _{11-Treated 5} Hr	390.3 36.1	x-bar _{11-Treated 10} + S _{11-Treated 10} Hr	337.3 58.2	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	436.0		x-bar _{11-Treated 20 Hr}	293.0
10 Hr Treated Samples 15 Hr Treated Samples 20 Hr Treated Samples 20 Hr Treated Samples 21 Hr Treated Samples 20 Hr Treated Samples 21 How Statistics 21 How Statistics 21 How Statistics 21 How Statistics 22 How Statistic 23 How Statistic 24 How Statistic 24 How Statistic 25 How Statistic 26 How Statistic 27 How Statistic 27 How Statistic 27 How Statistic 27 How Statistic 27 How Statistic 28 How Statistic 29 How Statistic 29 How Statistic 20 How Statistic 20 How Statistic 29 How Statistic 20 How Statist	339 416 226 intreated r11-Untreated r11-Untreated r11-Treated 5 Hr = 1756.2500 -1.7379 4 0.05 6	411 435 301 4 338.8 47.0 Null H Alterr	330 407 319	269 486 326 n11-Treated 5 Hr x-bar11-Treated 5 Hr 511-Treated 5 Hr thesis = There i	390.3 36.1	x-bar _{11-Treated 10} + S _{11-Treated 10} Hr	337.3 58.2	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	436.0		x-bar _{11-Treated 20 Hr}	293.0
L5 Hr Treated Samples 20 Hr Treated Samples 20 Hr Treated Samples All colony counts at 10 ^{-5 dilution} Statistics Statistics Population Comparisons Comparison Set 1 - Strain 1(WT) 40 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un 50 : H1:-Un </td <td>416 226 intreated f1:-Untreated ntreated - µ1- Treated 5 Hr = ntreated - µ1- Treated 5 Hr > 1756.2500 -1.7379 4 0.05 6</td> <td>435 301 4 338.8 47.0 Null H Alterr</td> <td>407 319</td> <td>486 326 n₁₁-Treated 5 Hr x-baf₁₁-Treated 5 S₁₁-Treated 5 Hr thesis = There i</td> <td>390.3 36.1</td> <td>x-bar_{11-Treated 10} + S_{11-Treated 10} Hr</td> <td>337.3 58.2</td> <td>x-bar_{11-Treated 15 Hr} S_{11-Treated 15 Hr}</td> <td>436.0</td> <td></td> <td>x-bar_{11-Treated 20 Hr}</td> <td>293.0</td>	416 226 intreated f1:-Untreated ntreated - µ1- Treated 5 Hr = ntreated - µ1- Treated 5 Hr > 1756.2500 -1.7379 4 0.05 6	435 301 4 338.8 47.0 Null H Alterr	407 319	486 326 n ₁₁ -Treated 5 Hr x-baf ₁₁ -Treated 5 S ₁₁ -Treated 5 Hr thesis = There i	390.3 36.1	x-bar _{11-Treated 10} + S _{11-Treated 10} Hr	337.3 58.2	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	436.0		x-bar _{11-Treated 20 Hr}	293.0
20 Hr Treated Samples All colony counts at 10 ^{-5 dilution} Statistics Statistics Population Comparisons Comparison Set 1 - Strain 1(WT) 40 : 41 - Unit 41 : 41 - Unit 42 : 41 - Unit 43 : 41 - Unit 44 : 41 - Unit 45 : 41 - Unit 46 : 41 - Unit 47 : 41 - Unit 48 : 41 - Unit 49 : 41 - Unit 40 :	226 //treated f1:-Untreated /treated /treated //tr	301 4 338.8 47.0 Null H Alterr	319	326 n _{11-Treated 5 Hr} x-bar _{11-Treated 5} S _{11-Treated 5 Hr} thesis = There i	390.3 36.1	x-bar _{11-Treated 10} + S _{11-Treated 10} Hr	337.3 58.2	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	436.0		x-bar _{11-Treated 20 Hr}	293.0
All colony counts at 10 ^{-5 dilution} Statistics Population Comparisons Comparison Set 1 - Strain 1(WT) 40 :	Intreated 「1:-Untreated Intreated → µ1:-Treated 5 Hr = ITreated → µ1:-Treated 5 Hr > 1756.2500 -1.7379 -0.05 6	4 338.8 47.0 Null H Alterr	łypot	n _{11-Treated 5 Hr} x-bar _{11-Treated 5} S _{11-Treated 5 Hr} thesis = There i	390.3 36.1	x-bar _{11-Treated 10} + S _{11-Treated 10} Hr	337.3 58.2	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	436.0		x-bar _{11-Treated 20 Hr}	293.0
Statistics Statistics n11.00 x-bar \$11.00 Population Comparisons \$11.00 Comparison Set 1 - Strain 1(WT) \$100 40 : \$11.00 40 : \$11.00 10	r_11-Untreated threated intreated - µ11- Treated 5 Hr = intreated - µ11- Treated 5 Hr > 1756.2500 -1.7379 -0.05 6	338.8 47.0 Null H Alterr	łypot	x-bar _{11-Treated 5} S _{11-Treated 5} Hr	390.3 36.1	x-bar _{11-Treated 10} + S _{11-Treated 10} Hr	337.3 58.2	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	436.0		x-bar _{11-Treated 20 Hr}	293.0
$\begin{array}{c} n_{11-Ur} \\ x-bar \\ s_{11-Urr} \\ \hline \end{array}$	r_11-Untreated threated intreated - µ11- Treated 5 Hr = intreated - µ11- Treated 5 Hr > 1756.2500 -1.7379 -0.05 6	338.8 47.0 Null H Alterr	łypot	x-bar _{11-Treated 5} S _{11-Treated 5} Hr	390.3 36.1	x-bar _{11-Treated 10} + S _{11-Treated 10} Hr	337.3 58.2	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	436.0		x-bar _{11-Treated 20 Hr}	293.0
x-bar S11-UM Population Comparisons Comparison Set 1 - Strain 1(WT) H_0 : μ_{11-UM} H_0 : μ_{11-UM} μ_{2} μ_{2} μ_{2} μ_{2} μ_{3} : μ_{3} μ_{2} μ_{3}	r_11-Untreated threated intreated - µ11- Treated 5 Hr = intreated - µ11- Treated 5 Hr > 1756.2500 -1.7379 -0.05 6	338.8 47.0 Null H Alterr	łypot	x-bar _{11-Treated 5} S _{11-Treated 5} Hr	390.3 36.1	x-bar _{11-Treated 10} + S _{11-Treated 10} Hr	337.3 58.2	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	436.0		x-bar _{11-Treated 20 Hr}	293.0
$x - bar \\ S_{11-UM} \\ \hline Population Comparisons \\ Comparison Set 1 - Strain 1(WT) \\ H_0 : \qquad \mu_{11-UM} \\ H_a : \qquad \mu_{11-UM} \\ H_a : \qquad \mu_{11-UM} \\ \vdots \\ \vdots \\ z_2 \\ z_1 \\ z_2 \\ z_2 \\ z_3 \\ z_4 \\ z_4 \\ z_5 \\ z_6 \\ z_6 \\ z_6 \\ z_6 \\ z_6 \\ z_6 \\ z_6 \\ z_7 \\ z_6 \\ z_7 \\ z_6 \\ z_7$	r_11-Untreated threated intreated - µ11- Treated 5 Hr = intreated - µ11- Treated 5 Hr > 1756.2500 -1.7379 -0.05 6	47.0 Null H Alterr	łypot	x-bar _{11-Treated 5} S _{11-Treated 5} Hr	36.1 s no dif	x-bar _{11-Treated 10} + S _{11-Treated 10} Hr	58.2 the Unt	x-bar _{11-Treated 15 Hr} S _{11-Treated 15 Hr}	35.3		x-bar _{11-Treated 20 Hr}	
S11-Um Population Comparisons Comparison Set 1 - Strain 1(WT) 4_0 : 4_0 : μ_{11-Un} μ_a : μ_{11-Un} μ_a^2 $\mu_a^$	ntreated - H11-Treated 5 Hr = ntreated - H11-Treated 5 Hr > 1756.2500 -1.7379 -0.05 6	47.0 Null H Alterr	łypot	S _{11-Treated 5 Hr}	36.1 s no dif	S _{11-Treated 10 Hr}	58.2 the Unt	S _{11-Treated 15 Hr}	35.3			
Population Comparisons Comparison Set 1 - Strain 1(WT) 40: 40: 41. 41. 42. 42. 43. 44. 44. 44. 45. 45. 45. 45. 45	ntreated ⁻ µ11-Treated 5 Hr ⁼ ntreated ⁻ µ11-Treated 5 Hr ^{>} 1756.2500 -1.7379 c 0.05 6	Null H Alterr	łypot	thesis = There i	s no dif	ference between	the Unti				S11-Treated 20 Hr	45.9
Comparison Set 1 - Strain 1(WT) 4 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 40: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00 50: 41:00	ntreated - µ11-Treated 5 Hr > 1756.2500 -1.7379 4 0.05 6	Alterr						reated population				
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	ntreated - µ11-Treated 5 Hr > 1756.2500 -1.7379 4 0.05 6	Alterr						reated nonulation				
4a: μ11-Un p y test statistic ejection region t > t _a a -value	ntreated - µ11-Treated 5 Hr > 1756.2500 -1.7379 4 0.05 6	Alterr						noitelugon hoteo				
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p p, test statistic ejection region t > t _α x ff α -value since -1.7379 < 1.943, I do not reject the nu	-1.7379 0.05 6]					een the	Untreated populat	ion an	d the	e 5 Hr Treated Pop	ulation
p p, test statistic ejection region t > t _α x ff α -value since -1.7379 < 1.943, I do not reject the nu	-1.7379 0.05 6]										
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Since -1.7379 < 1.943, I do not reject the nu	1.943											
Since -1.7379 < 1.943, I do not reject the nu												
	0.519127341											
a: µ11-un 2	ntreated - µ _{11-treated 10 Hr} > 2797.9167											
, test statistic	0.0401											
ejection region $t > t_{\alpha}$												
	0.05											
lf	6											
α	1.943											
o-value	0.519127341			·								ļ
Since .0401 < 1.943, I do reject the null hyp	pothesis, there is a di	fferen		stween the Un	treated	and the 10 Hr Tre		bulations	\sim	$\overline{}$	\sim	
		\sim	\sim	\sim	\sim	\sim	\sim	\sim	\sim	\sim	\sim	\sim
	ntreated - $\mu_{11-\text{treated }15 \text{ Hr}}$ =											
H _a : μ _{11-un}	ntreated - $\mu_{11-\text{treated }15 \text{ Hr}}$ >	Alterr	nate I	Hypothesis = T	here is a	a difference betwo	een the	Untreated populat	ion an	d the	e 15 Hr Treated Po	pulation
2 p	1729.4583											
, test statistic	-3.3071											
ejection region t > t _α	4											
1	0.05											
If	6											
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			ろ		\times		$\underline{\sim}$	\sim	N	ム		
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iince -3.3071 < 1.943, I do reject the null hy 4 ₀ : μ _{11-un} 4 _a : μ _{11-un}	ypothesis, there is a number of the set of	Alterr		Hypothesis = T	here is a							
μ _a : μ _{11-un}	ypothesis, there is a ntreated - μ _{11-treated} 15 Hr = ntreated - μ _{11-treated} 15 Hr > 2158.7917	Alterr		Hypothesis = T	here is a							
ince -3.3071 < 1.943, I do reject the null hy t ₀ : μ _{11-un} t ₀ : μ _{11-un}	ypothesis, there is a number of the set of	Alterr		Hypothesis = T	here is a							
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ince -3.3071 < 1.943, I do reject the null hy 0 : μ _{11-un} 2 test statistic	ypothesis, there is a ntreated - μ ₁₁ treated 15 Hr = ntreated - μ ₁₁ treated 15 Hr > 2158.7917 1.3925	Alterr		Hypothesis = T	here is a							
ince -3.3071 < 1.943, I do reject the null hy 0: μ _{11-un} 2 2 2 2 2 2 2 2 2 2 2 2 2	ypothesis, there is a in ntreated - µ11-treated 15 Hr = ntreated - µ11-treated 15 Hr > 2158.7917 1.3925	Alterr		Hypothesis = T	here is a							



Data									_	
Strain				EC					2.49.44	
Jntreated Samples	15			16 24 1					colony counts at 10 ^{-2 dilution}	
5 Hr Treated Samples	2		3	3 5					colony counts at 10 ^{-2 dilution}	
10 Hr Treated Samples	2		3	4 8					colony counts at 10 ^{-2 dilutio}	
15 Hr Treated Samples	1	1	7	3 2	1 3	2			colony counts at 10 ^{-2 dilutio}	
20 Hr Treated Samples	8	5	10	12 7	3 17	9			colony counts at 10 ^{-2 dilutio}	n
Statistics										
	n _{EC -Untreated}	8	n _{EC -Treated 5 H}	8	n _{EC -Treated 10 Hr}	8	n _{EC-Treated 15 Hr}	8	n _{EC-Treated 20 Hr}	8
	x-bar _{EC-Untreated}	15.8	x-bar _{EC-Treate}	d 5 4.0	x-bar _{EC-Treated 10 F}	4.0	x-bar _{EC-Treated 15 Hr}	2.5	x-bar _{EC-Treated 20 Hr}	8.9
	S _{EC-Untreated}	5.1	S _{EC-Treated 5 Hr}	1.5	S _{EC-Treated 10 Hr}	1.9	S _{EC-Treated 15 Hr}	2.0	S _{EC-Treated 20 Hr}	4.3
Population Comparis	ons									
Comparison Set 1 - Strain 1(WT)										
H ₀ :	μ _{EC-Untreated} - μ _{EC-Treated 5 Hr} =	Null H	pothesis = The	e is no dif	ference between	the Untr	eated population	and the	5 Hr Treated Population	
4a:									the 5 Hr Treated Population	
. 2	44.072									
sp ⁻ t, test statistic	14.1071 6.2567									
ministrian ragion	+>+									
ejection region	t > t _α 0.05									
df	14									
~	1.761				1					
a-value	0.519585629									
		ifferen	ce between the	Untreated	l and the 5 Hr Trea	ited Popu	ulations	\sim		\sim
ince 6.2567 > 1.761, I do reject the I ₀ :	HeC-untreated ⁻ μ _{EC-treated} 10 Hr =	Null H	ypothesis = The	e is no dif	ference between	the Untr	eated population			
since 6.2567 > 1.761, I do reject the H ₀ : H _a :	HeC-untreated ⁻ μ _{EC-treated} 10 Hr =	Null H	ypothesis = The	e is no dif	ference between	the Untr	eated population		10 Hr Treated population the 10 Hr Treated Population	
6 ince 6.2567 > 1.761, I do reject the H₀:	HeC-untreated ⁻ μ _{EC-treated} 10 Hr =	Null H Altern	ypothesis = The	e is no dif	ference between	the Untr	eated population			
since 6.2567 > 1.761, I do reject the H ₀ : H _a :	Hull hypothesis, there is a d μ _{EC-untreated} - μ _{EC-treated} 10 Hr = μ _{EC-untreated} - μ _{EC-treated} 10 Hr >	Null H Altern	ypothesis = The	e is no dif	ference between	the Untr	eated population			
Since 6.2567 > 1.761, I do reject the H ₀ : H ₄ : p ² p ² p, test statistic	Pull hypothesis, there is a d HEC-untreated - HEC-treated 10H = HEC-untreated - HEC-treated 10H > 14.8214 6.1041	Null H Altern	ypothesis = The	e is no dif	ference between	the Untr	eated population			
Since 6.2567 > 1.761, I do reject the H ₀ : H ₄ : p ² p ² p, test statistic	null hypothesis, there is a d HEC-untreated = HEC-treated 10 H = HEC-untreated = HEC-treated 10 H > 14.8214 6.1041 t > t_a	Null H Altern	ypothesis = The	e is no dif	ference between	the Untr	eated population			
Since 6.2567 > 1.761, I do reject the $H_0:$ $H_a:$ F_a^2 F_a^2 F_a	Pull hypothesis, there is a d HEC-untreated - HEC-treated 10 H = HEC-untreated - HEC-treated 10 H = 14.8214 6.1041 t > t _a 0.05	Null H Altern	ypothesis = The	e is no dif	ference between	the Untr	eated population			
Since 6.2567 > 1.761, I do reject the H_0 : H_0 : S_p^2 L_1 test statistic rejection region α	Hull hypothesis, there is a d μccuntreated μccurated to H μccurated μccurated to H μccurated μccurated to H 14.8214 6.1041 t t u 0.05 14 14.8214	Null H Altern	ypothesis = The	e is no dif	ference between	the Untr	eated population			
Since 6.2567 > 1.761, I do reject the 40: 41, : 22, 2 24, test statistic rejection region 21 21 21 22 22 23 24 24 25 25 25 25 25 25 25 25 25 25	Hull hypothesis, there is a d HEC-untreased - HEC-breased 10H = HEC-untreased - HEC-breased 10H = HEC-untreased - HEC-breased 10H = 14.8214 6.1041 t > t_a 0.055 14 14.761	Null H Altern	ypothesis = The	e is no dif	ference between	the Untr	eated population			
Since 6.2567 > 1.761, I do reject the H ₀ : H ₄ : p ² t, test statistic rejection region x ff 	null hypothesis, there is a d µEC-untreated - VEC-treated 10 Hr µEC-untreated - VEC-treated 10 Hr 14.8214 6.1041 t > t _a 0.05 14 1761 0.519585629	Null H Altern	ypothesis = There	e is no dif	ference between difference between	the Untro	eated population Intreated populat			
Since 6.2567 > 1.761, I do reject the H_0 : H_a : h_a^2 : h_b^2 : h_a^2 :	null hypothesis, there is a d µEC-untreated - VEC-treated 10 Hr µEC-untreated - VEC-treated 10 Hr 14.8214 6.1041 t > t _a 0.05 14 1761 0.519585629	Null H Altern	ypothesis = There	e is no dif	ference between difference between	the Untro	eated population Intreated populat			
Since 6.2567 > 1.761, I do reject the H_0 : H_0 : h_a :	Hull hypothesis, there is a d Htcomtreated - Htc treated 10 Hr Htcomtreated - Htc treated 10 Hr 14.8214 6.1041 t > t_a 0.05 14 14.8214 6.1041 t.761 0.519585629 enull hypothesis, there is a c	Null H	ypothesis = Then ate Hypothesis =	e is no dif	erence between difference betwee	eated Po	eated population Intreated populat	ion and	the 10 Hr Treated Population	
Since 6.2567 > 1.761, I do reject the H_0 : s_p^2 , t_i test statistic rejection region α df f_s p_p -value Since 6.1041 > 1.761, I do reject the H_0 :	Hull hypothesis, there is a d HtCurtreated - HtC breated 10 Hr HtCurtreated - HtC breated 10 Hr HtCurtreated - HtC breated 10 Hr 14.8214 6.1041 t > t_a 0.005 14.8214 0.1041 0.05 14.8214 0.05 14.8214 0.05 14.8214 0.05 14.8214 0.05 14.8214 0.05 14.8214 14.8214 0.05 14.8214 14.8214 0.05 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 14.8214 <	Null H	ypothesis = Then ate Hypothesis =	• is no dif	erence between difference between	the Untro een the U	pulations	and the	the 10 Hr Treated Population	
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Since 6.2567 > 1.761, I do reject the 4_0 : 4_a : p^2 , test statistic rejection region x ff a_a	null hypothesis, there is a d Hccuntreated - HcCreated 10 H Hccuntreated - HcCreated 10 H Hccuntreated - HcCreated 10 H 14.8214 6.1041 t > t_a 0.05 14.8214 6.1041 t > t_a 0.05 14.8214 0.052 14.8214 0.052 14.8214 0.052 14.8214 0.19585629 11.761 0.519585629 Paccutreated - HcCreated 15 H Hccutreated - HcCreated 15 H Hccutreated - HcCreated 15 H 14.9643	Null H	ypothesis = Then ate Hypothesis =	• is no dif	erence between difference between	the Untro een the U	pulations	and the	the 10 Hr Treated Population	
Since 6.2567 > 1.761, I do reject the $A_0:$ $A_a:$ $A_a:$ $A_a:$ $A_a:$ $A_a:$ $A_a:$ to reject on region x fi $A_a:$ $A_$	null hypothesis, there is a d Hccurtrated = HcCreated 10 H = Hccurtrated = HcCreated 10 H = Hccurtrated = HcCreated 10 H > 14.8214 6.1041 t > ta 0.05 14.8214 0.05 14 1.761 0.519585629 e null hypothesis, there is a c HcCurtrated = HcCreated 15 H = HcCurtrated = HcCreated 15 H = HcCurtrated = HcCreated 15 H = HcCurtrated = HcCreated 15 H > HcCurtrated = HcCrea	Null H	ypothesis = Then ate Hypothesis =	• is no dif	erence between difference between	the Untro een the U	pulations	and the	the 10 Hr Treated Population	
Since 6.2567 > 1.761, I do reject the H_0 : H_a : p^2 p	null hypothesis, there is a d Hccuntreated - HcCureated 10 H = HcCuntreated - HcCureated 10 H - HcCuntreated - HcCureated 10 H - HcCurtreated - HcCureated 10 H - 14.8214 6.1041 t > ta 0.05 14.8214 0.005 14 1.7661 0.519585629 enull hypothesis, there is a a HcCurtreated - HcCureated 15 H - HcCurtreateed - HcCureated 15	Null H	ypothesis = Then ate Hypothesis =	• is no dif	erence between difference between	the Untro een the U	pulations	and the	the 10 Hr Treated Population	
Since 6.2567 > 1.761, I do reject the H_0 : μ_a : μ_a^2 : μ_b^2 : rejection region χ rejection region χ χ μ_a^2 : μ_a^2 :	null hypothesis, there is a d Hccuntreated - HcCureated OH = Hccuntreated - HcCureated OH = Hccuntreated - HcCureated OH = 14.8214 6.1041 t > ta 0.05 14.8214 0.05 14.921 t > ta 0.519585629 e null hypothesis, there is a co HcCurtreated - HcCureated IS M = HcCurtreated - HcCureated IS M = HcCurtreated - HcCureated IS M = 14.9643 6.8504 t > ta t > ta	Null H	ypothesis = Then ate Hypothesis =	• is no dif	erence between difference between	the Untro een the U	pulations	and the	the 10 Hr Treated Population	
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Since 6.2567 > 1.761, I do reject the 4_0 : 4_a : p^2 p	null hypothesis, there is a d Hc_untreated ⁻ HcC-treated 10 H [−] HcC-untreated ⁻ HcC-treated 10 H [−] HcC-untreated ⁻ HcC-treated 10 H [−] 14.8214 6.1041 t > t _a 0.05 14 1.761 0.519585629 enull hypothesis, there is a d HcC-untreated ⁻ HcC-treated 15 H [−] HcC-untreated ⁻ HcC-treated 15 H [−] HcC-untreated ⁻ HcC-treated 15 H [−] 14.9643 6.8504 t > t _a 0.05 14	Null H Altern Null H Altern	ypothesis = Then ate Hypothesis =	• is no dif	erence between difference between	the Untro een the U	pulations	and the	the 10 Hr Treated Population	
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Since 6.2567 > 1.761, I do reject the H_0 : H_1 : s_p^2 t_i test statistic rejection region α f_1 f_2 f_2 f_3 f_4 h_0 : H_0 : H_0 : H_0 : H_0 : H_0 : H_1 : s_p^2 t_i test statistic rejection region α f_1 f_2 f_2 f_2 f_2 f_2 f_3 f_4 f_2 f_2 f_4 f_2 f_2 f_4 f_2 f_2 f_4 f_2 f_4 f_2 f_4 f_2 f_4 f_2 f_4 f_5 f_4 f_5 f_4 f_5 f_4 f_5 f_4 f_5 f_4 f_5 f_5 f_4 f_5	null hypothesis, there is a d HtContreated - HtC-treated 10 H = HtContreated - HtC-treated 10 H = HtContreated - HtC-treated 10 H = 14.8214 6.1041 t > t_a 0.05 14.8214 0.05 14.8214 0.05 14 0.1761 0.519585629 NULl hypothesis, there is a c HtContreated - HtC-treated 15 H = HtContreated - HtC-treated 15 H = 14.9643 6.8504 t > t_a 0.05 14 1.761 0.052 14.9643 0.519585629	Null H Altern Iifferer Null H Altern	ypothesis = There ate Hypothesis = cee between the ypothesis = There ate Hypothesis =	Untreate	d and the 10 Hr Trn	eated Po	pulations	and the	the 10 Hr Treated Population	
Since 6.2567 > 1.761, I do reject the H_0 : H_1 : h_2 : h_2 : h_3 : h_4 : h_5^2 : h_5^2 : h_5^2 : h_5^2 : h_6 : h_7 :	null hypothesis, there is a d HtContreated - HtC-treated 10 H = HtContreated - HtC-treated 10 H = HtContreated - HtC-treated 10 H = 14.8214 6.1041 t > t_a 0.05 14.8214 0.05 14.8214 0.05 14 0.1761 0.519585629 NULl hypothesis, there is a c HtContreated - HtC-treated 15 H = HtContreated - HtC-treated 15 H = 14.9643 6.8504 t > t_a 0.05 14 1.761 0.052 14.9643 0.519585629	Null H Altern Iifferer Null H Altern	ypothesis = There ate Hypothesis = cee between the ypothesis = There ate Hypothesis =	Untreate	d and the 10 Hr Tre	eated Po	pulations	and the	the 10 Hr Treated Population	
since 6.2567 > 1.761, I do reject the H_0 : μ_1 : μ_2 : μ_2 : μ_2 : μ_2 : μ_2 : μ_2 : μ_2 : μ_2 : μ_2 : μ_2 : μ_2 : μ_3 : μ_4 : μ_4 : μ_4 : μ_4 : μ_5 : μ_4 : μ_5 : μ_5 : μ_6 :	null hypothesis, there is a d HtContreated - HtC-treated 10 H = HtContreated - HtC-treated 10 H = HtContreated - HtC-treated 10 H = 14.8214 6.1041 t > t_a 0.05 14.8214 0.05 14.8214 0.05 14 0.1761 0.519585629 NULl hypothesis, there is a c HtContreated - HtC-treated 15 H = HtContreated - HtC-treated 15 H = 14.9643 6.8504 t > t_a 0.05 14 1.761 0.052 14.9643 0.519585629	Null H Altern Null H Altern Null H Altern	ypothesis = Then ate Hypothesis = ace between the ypothesis = Then ate Hypothesis = the Hypothesis = ate Hypothesis =	Untreatee	erence between difference between a and the 10 Hr Trr erence between difference between difference between and the 15 Hr Tre	eated Poo	pulations	and the ion and	the 10 Hr Treated Population 15 Hr Treated population 15 Hr Treated population the 15 Hr Treated Population	
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since 6.2567 > 1.761, I do reject the 4_0 : 4_a : p^2 p	null hypothesis, there is a d HtC-untreated - HtC-treated 10 H = HtC-untreated - HtC-treated 10 H = HtC-untreated - HtC-treated 10 H = 14.8214 6.1041 t > t_a 0.05 14.8214 6.1041 t > t_a 0.05 14 0.05 14 0.1761 0.51958629 NULl hypothesis, there is a c HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H = 14.9643 0.519585629 null hypothesis, there is a d 0.519585629 null hypothesis, there is a d HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H =	Null H Altern Null H Altern Mull H Altern	ypothesis = Then ate Hypothesis = we between the ypothesis = Then ate Hypothesis = Then ate Hypothesis = Then ate Hypothesis = Then ate Hypothesis = Then	Untreated Untreated Untreated Untreated	and the 10 Hr Tro	eated Po	pulations	and the	the 10 Hr Treated Population 15 Hr Treated population 15 Hr Treated population 15 Hr Treated population 20 Hr Treated population 20 Hr Treated population	
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since 6.2567 > 1.761, I do reject the I_0 : I_a : I_a : I_a : I_b : I_a : I_b : I_a : I_b : I_a : I_b : I_a : I_b : I_a : I_b :	null hypothesis, there is a d HtC-untreated - HtC-treated 10 H = 14.8214 6.1041 t > t _a 0.05 14.8214 0.1041 t > t _a 0.05 14 0.519585629 HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H = 14.9643 0.519585629 t > t _a 0.519585629 mull hypothesis, there is a C 0.519585629 mull hypothesis, theread 15 H = HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H = HtC-untreated - HtC-treated 15 H =	Null H Altern Null H Altern Ifferen Null H Altern	ypothesis = Then ate Hypothesis = we between the ypothesis = Then ate Hypothesis = Then ate Hypothesis = Then ate Hypothesis = Then ate Hypothesis = Then	Untreated Untreated Untreated Untreated	and the 10 Hr Tro	eated Po	pulations	and the	the 10 Hr Treated Population 15 Hr Treated population 15 Hr Treated population 15 Hr Treated population 20 Hr Treated population 20 Hr Treated population	



													CFU	Std. Dev.
WT											WT	non-irradiated control		4156420.73
n1-Untreated	4	n1 - Treated 5 Hr	4	n1-Trea	ited 10 Hr	4	n1 - Treated 15 Hr	4	n1 -Treated 20 Hr	4		5 hr	36250000	13501975.1
x-bar1-Untreated	377.25	x-bar1-Treated 5 Hr	362.5		reated 10 Hr	416.25	x-bar1-Treated 15 Hr	348	x-bar1-Treated 20 Hr	441		10 hr		1975474.62
s1-Untreated	41.56420736	s1-Treated 5 Hr	135.0197516	s1-Treat	ed 10 Hr	19.75474627	s1-Treated 15 Hr	18.83259586	s1-Treated 20 Hr	27.27636339		15 hr		1883259.58
												20 hr	44100000	2727636.33
Mutant #5														
n5 - Untreated	4	n5 -Treated 5 Hr	4		ited 10 Hr	4	n5 - Treated 15 Hr	4	n5 -Treated 20 Hr	4		non-irradiated control		1187083.2
x-bar5-Untreated	343.25	x-bar5-Treated 5 Hr	346.75		reated 10 Hr	307.75	x-bar5-Treated 15 Hr	384	x-bar5-Treated 20 Hr	328.75		5 hr		2656281.86
s5-Untreated	11.8708326	s5-Treated 5 Hr	26.56281863	s5-Treat	ed 10 Hr	8.770214745	s5-Treated 15 Hr	26.72077843	s5-Treated 20 Hr	27.72934667		*10 hr*		877021.474
												15 hr		2672077.84
Mutant #8 n8 - Untreated	4	n8 - Treated 5 Hr		-0. Teres	ited 10 Hr	4	n8 - Treated 15 Hr		n8 - Treated 20 Hr			20 hr	328/5000	2772934.66
x-bar8-Untreated	325.5	x-bar8-Treated 5 Hr	333.25		reated 10 Hr	321.25	x-bar8-Treated 15 Hr	307.5	x-bar8-Treated 20 Hr	288.5	Mutant #8	non-irradiated control	22550000	4438092.68
s8-Untreated	44.38092683	s8-Treated 5 Hr	26.05602937		ed 10 Hr	13.52466882	s8-Treated 15 Hr	19.12241268	s8-Treated 20 Hr	45.98912915		5 hr		2605602.93
so-oncreated	44.38032083	so-meated 5 m	20.03002337	30-freat	20 1011	13.32400882	30-Treated 15Th	13.12241200	so-meated 20m	43.36312313		10 hr		1352466.88
Mutant #11												15 hr		1912241.26
n11 - Untreated	4	0 n11 - Treated 5 Hr	4	0n11-Tre	ated 10 Hr	4	0 n11-Treated 15 Hr	4	0 n11-Treated 20 Hr	4		20 hr		4598912.91
x-bar11-Untreated	338.75	0 x-bar11-Treated 5 Hr	390.25		Treated 10 H	337.25	0 x-bar11-Treated 15 H	436	0 x-bar11-Treated 20 H	293				
s11-Untreated	47.02747424	0 s11-Treated 5 Hr	36.06822239		ated 10 Hr	58.17430704	0 s11-Treated 15 Hr		0 s11-Treated 20 Hr	45.89117562	Mutant #11	non-irradiated control	33875000	4702747.42
												5 hr	39025000	3606822.23
EC												10 hr	33725000	5817430.70
nEC -Untreated	8	0 nEC - Treated 5 Hr	8	0 nEC -Tre	ated 10 Hr	8	0 nEC-Treated 15 Hr	8	0 nEC-Treated 20 Hr	8		15 hr	43600000	3531760.65
x-barEC-Untreated	15.75	0 x-barEC-Treated 5 Hi	4	0 x-barEC-	Treated 10 H	4	0 x-barEC-Treated 15 H	2.5	0 x-barEC-Treated 20 H	8.875		20 hr	29300000	4589117.56
sEC-Untreated	5.092010549	0 sEC-Treated 5 Hr	1.511857892	0 sEC-Trea	ated 10 Hr	1.927248223	0 sEC-Treated 15 Hr	2	0 sEC-Treated 20 Hr	4.323936698				
											EC	non-irradiated control	1575	509.201054
												5 hr	400	151.185789
			FILCompa	risons for	3rd Neutro	on Exnerime	ent							
		C	FU Compa	risons for	3rd Neutr	on Experime	ent					*10 hr*	400	192.724822
100000000		C	FU Compa	risons for	3rd Neutr	on Experime	ent					*10 hr* *15 hr*	400 250	192.724822 20
	111		FU Compa	risons for	3rd Neutr	on Experime	ent					*10 hr*	400 250	192.724822
10000000	111		FU Compa	risons for	3rd Neutr	on Experime	ent					*10 hr* *15 hr*	400 250	192.724822 20
10000000			FU Compa	risons for	3rd Neutr	on Experime						*10 hr* *15 hr*	400 250	192.724822 20
			FU Compa	risons for	3rd Neutr	on Experime						*10 hr* *15 hr*	400 250	192.724822 20
10000000			FU Compa	risons for	3rd Neutr	on Experime						*10 hr* *15 hr*	400 250	192.724822 20
10000000			FU Compa	risons for	3rd Neutro	on Experime						*10 hr* *15 hr*	400 250	192.724822 20
10000000			FU Compa	risons for	3rd Neutro	on Experime						*10 hr* *15 hr*	400 250	192.724822 20
10000000			FU Compa	risons for	3rd Neutro	on Experime						*10 hr* *15 hr*	400 250	192.724822 20
10000000 1000000 100000 E 100000 E			FU Compa	risons for	3rd Neutro	on Experime		Ŧ				*10 hr* *15 hr*	400 250	192.724822 20
10000000			FU Compa	risons for	3rd Neutro	on Experime		i.				*10 hr* *15 hr*	400 250	192.724822 20
10000000 1000000 100000 20 100000 20 10000 20			FU Compa	risons for	3rd Neutro	on Experime		İ.				*10 hr* *15 hr*	400 250	192.724822 20
10000000 1000000 1000000 100000 100000 100000			FU Compa	risons for	3rd Neutro	on Experime		lı				*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 0000 000 1000 1000 1000			FU Compa	risons for	3rd Neutri	on Experime		İi				*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 100000 20 10000 20 10000 1000			FU Compa	risons for	3rd Neutri	on Experime		İi				*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 0000 000 1000 1000 1000			FU Compa	risons for	3rd Neutri	on Experime		İi				*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 0000 000 1000 1000 1000												*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 0000 000 1000 1000 1000						e e e e e e e e e e e e e e e e e e e		and the second se				*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 0000 000 1000 1000 1000	d control 0 5 M 10 M							a ontrad				*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 100000 20 10000 1000 1000	lated corrors 5 h 10 h							Liked control *5 h*	Y T T T T T T T T T T T T T T T T T T T			*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 0000 000 1000 1000 1000	fradiend contro 5 h 10 h							• • • • • • • • • • • • • • • • • • •				*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 20 10000 20 1000 1000 100	on + railent contro 5 h 10 h							entro basilori + entro				*10 hr* *15 hr*	400 250	192.724822 20
1000000 100000 0000 000 1000 1000 1000	mon-traditated control of the second se	13h 20m Pon-trafaed onto 5h				15 M						*10 hr* *15 hr*	400 250	192.724822 20



Data											
											+
Strain Control 1 - CFU Input	11	16 11	1 (WT)								
Control 2 - Untreated, No Vacuum	10	13 12	12 9 21								
Control 3 - Untreated. Vacuum 10 Gy Treated Samples	1	8 12	5 8 6 6 10 6	9							_
100 Gy Treated Samples			12 13 13	9 12							
500 Gy Treated Samples			4 5 9	9 7							
1000 Gy Treated Samples 2500 Gy Treated Samples	1	11 14 8 15	12 8 8 7 8 8	11 8 1 15							-
10000 Treated Samples		8 14	16 9 12	12 1							
All colony counts at 10 ^{-5 diation}											_
											-
Statistics											
	n _{1-control 1}	3 n _{1-or}	191912 6 n _{1-co}	ntrol 3 7 n ₁₋₁₀	_{cy} 7 n _{1-100 c}	, 8	n _{1-500 Gy} 8	n1-2000 Gy 8	n1 - 2500 Gy	8 n _{1-10000 Gy}	~
	x-bar _{1-control 1}		r _{1-control 2} 12.8 x-ba	Ir _{1-control 3} 8.0 x-bar	r _{1-33 Gy} 7.4 x-bar ₁	100 Gy 10.6	x-bar _{1-500 Gy} 7.1	x-bar _{1-1000 Gy} 10.0	x-bar ₁₋₂₅₀₀	_{0 Gy} 8.8 x-bar ₁₋₁₀₀	000 Gy
	S _{1-control 1}	2.9 Si-cont	trai2 4.3 \$1-cor	mola 2.2 s ₁₋₁₀₀	_{2y} 2.8 S _{1-100 Gy}	2.3	s _{1-500 Gy} 2.0	\$ _{1-1000 Gy} 2.3	\$1-2500 Gy	4.7 \$1-10000 Gy	
Population Comparisons											
н _о :	μ _{1-Control 1} - μ _{1-Control 2} = 0	Null Hypothesis =	There is no difference	between the Control	1 (CFU Input) populatio	n and the Contro	al 2 (Untreated / Uno	pened Lid) Populatio	n		
Н, :	µ1-Control 1 * µ1-Control 2 > 0	Null Hypothesis = 1	There is a difference b	between the Control 1	(CFU Input) population	and the Control	2 (Untreated / Unop	ened Lid) Population			-
s ₀ ²	15.357										
t, test statistic	0.541										
											-
rejection region α	t > t _a										-
df											
t <u>a</u>	1.89		-+++			-					_
p-value Since 0.5413 < 1.895, I do not reject the nu	0.51924041 ull hypothesis, there is n	o difference betwe	en the Control 1 and C	Control 2						+	-
	> <				$\sim \sim \sim$	∞	$\sim \!$	$\sim \propto$	\times	∞	\bigcirc
H ₀ :	µ1-Control 2 - µ1-Control 2 = 0	Null Hypothesis = 1	There is no difference	between the Control	2 (Untreated / Unopen	ed Lid) populatio	n and the Control 3 (On Treatment Lid) Pe	opulation		
ң,:	μ _{1-Control 2} - μ _{1-Control 3} > 0	Null Hypothesis =	There is a difference b	between the Control 2	(Untreated / Unopened	Lid) population	and the Control 3 (O	n Treatment Lid) Pop	oulation		_
s. ²	10.984									+	-
s _p t, test statistic	2.621										
											-
rejection region	t > t _x										-
- df	0.0										
t _a	1.79										
p-value Since 2.6212 > 1.943. I do reject the null hy	0.51949062		- Control 2 and Control	12 December 1							-
3arte 2.6212 > 1.943, 1 do reject the ridh ny	pouresis, urere is s uni				$\sim \sim \sim$	$\propto x$	>>>>	\sim	\sim	\propto	\sim
H ₀ :	μ _{1-Control 1} - μ _{1-10 Gy} = 0				3 (Untreated / On Treat						-
н, :	$\mu_{1-Control 3} - \mu_{1-10 Gy} > 0$	Null Hypothesis =	There is a difference b	etween the Control 3	(Untreated / On Treatm	ent Lid Lid) popu	ulation and the 10 Gy	treatment Population	on		
2											-
sp t, test statistic	6.476										-
i, test statistic	0.420.	1									
rejection region	$t > t_{\alpha}$										_
a di	0.0										-
t,	1.78										
p-value	0.51952750										_
Since 0.4201 < 1.782, I do not reject the n	ull hypothesis, there is					∞	$\sim \sim$	\sim	$\sim \sim$	\sim	\sim
H ₀ :	H1-Control 3 * H1-100 Gy = 0	Null Hypothesis = 1	There is no difference	between the Control	3 (Untreated / On Treat	ment Lid) popula	ation and the 100 Gy	treatment Populatio	n		~
Н,:	μ _{1-Control 3} - μ _{1-100 Gy} > 0	Null Hypothesis =	There is a difference b	etween the Control 3	(Untreated / On Treatm	ent Lid Lid) popu	ulation and the 100 G	iy treatment Populat	ion		
3											_
sp [*] t, test statistic	5.221										-
rejection region	$t > t_{\alpha}$										_
α df	0.0										-
t _a	1.77										
p-value	0.51955877										
Since -2.2197 < 1.771, I do not reject the n	ull hypothesis, there is	o difference betwe	en the Control 3 and	the 100 Gy Treated Pop		\sim	$\sim \sim$	\sim	$\sim \sim$	\propto	\rightarrow
He:	μ _{1-Control 3} - μ _{1-S00 Gy} = 0									\sim	\sim
н,:	μ _{1-Cantral 3} · μ _{1-S00 Gy} >0	Null Hypothesis = '	There is a difference b	etween the Control 3	(Untreated / On Treatn	ent Lid Lid) popu	ulation and the 500 G	y treatment Populat	ion		
5 _p	4.375										_
sp ² t, test statistic	4.375										
sp ² t, test statistic rejection region	0.808										
	0.808 t > t _a 0.0										
	0.808										
rejection region a df t_ p-value	0.808 t>ts 0.00 12 1.777 0.519558773										
rejection region a df t_ p-value	0.808 t>ts 0.00 12 1.777 0.519558773			he 500 Gy Treated Pop	ulations						
rejection region a df t_ p-value	0.808 t > ts 0.01 1: 77: 0.51958977 ull hypothesis, there is n	o difference betwee	$\sim \infty$	$\sim \infty >$	$\sim \sim \sim$			treatment Provider	20		
rejection region α df 5-yalue	0.808 t > t _a 0.00 1: 1.777 0.51955877 0.51955875 rs n µ ₁ https://www.sec.org	o difference betwee	There is no difference	between the Control	3 (Untreated / On Treat	ment Lid) popula	ation and the 1000 G	v treatment Populati	Da tion		<
rejection region a df t_ p-value	0.808 t > t_a 0.01 1.777 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.5195597 0.5195797 0.5195777 0.5195777 0.5195777 0.5195777 0.5195777 0.51957777 0.51957777 0.51957777 0.51957777 0.51957777 0.51957777 0.51957777 0.51957777	o difference betwee Null Hypothesis = 1 Null Hypothesis = 1	There is no difference	between the Control	$\sim \sim \sim$	ment Lid) popula	ation and the 1000 G	rtreatment Populati	DA tion		<
rejection region a d 	0.808 1> t _a 0.01 1.77 0.51955877 all hypothesis, there is n piccaring 1 - µi- s000 c ₀ = 0 Pic caring 1 - µi- s000 c ₀ > 0 5.2300	o difference betwee Null Hypothesis = 1 Null Hypothesis = 1	There is no difference	between the Control	3 (Untreated / On Treat	ment Lid) popula	ation and the 1000 G	treatment Populati Gy treatment Popula	on tion		~
rejection region a df t _a p-value K _b : H _b : h _b	0.808 t > t_a 0.01 1.777 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.51955977 0.5195597 0.5195797 0.5195777 0.5195777 0.5195777 0.5195777 0.5195777 0.51957777 0.51957777 0.51957777 0.51957777 0.51957777 0.51957777 0.51957777 0.51957777	o difference betwee Null Hypothesis = 1 Null Hypothesis = 1	There is no difference	between the Control	3 (Untreated / On Treat	ment Lid) popula	ation and the 1000 G	treatment Populati	on tition		
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$\label{eq:approximation} rejection region $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$	0.000 t > 5 a 0.00	o difference betwee Null Hypothesis = 1 Null Hypothesis = 1 Null Hypothesis = 1 Null Hypothesis = 1	een the Control 3 and	the 1000 Gy Treated P	a (Untreated / On Treat (Untreated / On Treat opulations 3 (Untreated / On Treat	ment Lid) popula rent Lid Lid) popu ment Lid Lid) popula ment Lid) popula	ation and the 1000 G ulation and the 1000 station and the 2000 G	Gy treatment Populat			
$\label{eq:approximation} rejection region $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$	0.000 t > 5_0 0.01 11 12 13 14 15 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	difference betwee Null Hypothesis = 1 Null Hypothesis = 1 Null Hypothesis = 1 Null Hypothesis = 1 Null Hypothesis = 1	een the Control 3 and	the 1000 Gy Treated P	a (Untreated / On Treat (Untreated / On Treat opulations 3 (Untreated / On Treat	ment Lid) popula rent Lid Lid) popu ment Lid Lid) popula ment Lid) popula	ation and the 1000 G ulation and the 1000 station and the 2000 G	Gy treatment Populat			
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Protocol 7 Analysis																		
Data		\vdash				+											+-	
train			Mut	ant #5														
Control 1 - CFU Input Control 2 - Untreated, No Vacuum	18			10 10	0 8 10	_		_									_	
Control 3 - Untreated, No Vacuum	7				0 10													
100 Gy Treated Samples	3		8 9			_		_		_							_	
500 Gy Treated Samples 1000 Gy Treated Samples	8					-		-									-	
2500 Gy Treated Samples	4	10	7 12		21 6												_	
All colony counts at 10 ^{-5 dilution}																		
Statistics																		
	n _{5-control 1}	3	n _{5-control 2}	8	n _{5-control 3} 3		100 Gy 8	_	n _{5-500 Gy}	7	n _{5-1000 Gy}	7	n _{5 - 2500 Gy}	8			_	
	x-bar _{5-control 1} s _{5-control 1}	13.7 3.8	x-bar _{5-control 2}	8.9 2.4	x-bar _{5-control 3} 6.7 s _{5-control 3} 1.5	x-b s _{5.1}	oar _{5-100 Gy} 6.1	-	x-bar _{5-500 Gy} s _{5-500 Gy}	4.2	x-bar _{5-1000 Gy}	2.4	x-bar _{5-2500 Gy} \$ _{5-2500 Gy}	9.8 5.2				
Population Comparisons						-				-							-	
ropulation compansons						-												
H ₀ :	$\mu_{\text{S-Control 1}} - \mu_{\text{S-Control 2}} = 0$	Null Hypot	thesis = There i	s no diffe	erence between th	e Cont	rol 1 (CFU Inp	ut) p	opulation ar	nd the Co	ontrol 2 (Untre	ated / Un	pened Lid) P	opulatio	'n			
4 <u>.</u> :	$\mu_{5-Control 1} - \mu_{5-Control 2} > 0$	Null Hypot	thesis = There i	s a diffen	ence between the	Contro	ol 1 (CFU Inpu	t) po	pulation and	the Cor	itrol 2 (Untrea	ed / Uno	ened Lid) Pop	oulation				
2	7.7269					-											-	
, test statistic	2.5462																	
ejection region	t>t _a	\vdash								_				++			-	
I	0.05																	
if	9			++						_		\square		HT			-	
t _α p-value	1.833 0.519392768					+											-	
Since 2.5462 > 1.833, I do reject the null h			ween the Contr			~						~~						
4.	μ _{S-Control 2} - μ _{S-Control 3} = 0							<u>×</u>			Lation and the					\sim	\propto	\sim
4₀: 4₀:	$\mu_{\text{S-Control 2}} - \mu_{\text{S-Control 3}} = 0$ $\mu_{\text{S-Control 2}} - \mu_{\text{S-Control 3}} > 0$	Null Hypot	thesis = There i	s a diffen	ence between the	Contro	ol 2 (Untreate	.cu/ d/U	nopened Lic	i) popula	tion and the C	ontrol 3 (On Treatment	Lid) Por	opulation			
-																		
2 p	5.0602										-						_	
, test statistic	1.4501	\vdash				-								++			-	
rejection region	t > t _a																	
ı If	0.05						— H				-							
α	1.833																	
o-value	0.519392768																	
Since 1.4501 < 1.833, I do not reject the nu	all hypothesis, there is n	difference	e between the	Control 2	and Control 3 Pop			X	\sim	XX	\sim	XX	\sim	X	\sim	\sim	\sim	\sim
H ₀ :	$\mu_{5-Control 3} - \mu_{5-100 Gy} = 0$	Null Hypot	thesis = There i	s no diffe	erence between th	e Cont			On Treatme	nt Lid) po	opulation and	he 100 G	treatment Po	pulatio	n			
Н":	$\mu_{\text{S-Control 3}} - \mu_{\text{S-100 Gy}} > 0$	Null Hypot	thesis = There i	s a diffen	ence between the	Contro	ol 3 (Untreate	d / C	n Treatment	Lid Lid)	population an	d the 100	Sy treatment	Populat	ion			
2	4.3935																	
, test statistic	0.3817																	
						_											_	
rejection region α	t > t _a 0.05		_			-											-	
f	9																	
t _α p-value	1.833 0.519392768					-				_							_	
Since 0.3817 < 1.833, I do not reject the n			e between the	Control	3 and the 100 Gy T	reated	Populations											
	>	>>	\sim	$\mathbf{x}\mathbf{x}$	$\sim x$	X)	$\sim x$	X	\sim	XX	\sim	XX	\sim	\mathbf{X}	\sim	\sim	\propto	\sim
Ho:	$\mu_{5-Control 3} - \mu_{5-500 \text{ Gy}} = 0$ $\mu_{5-Control 3} - \mu_{5-500 \text{ Gy}} > 0$	Null Hypot	thesis = There i	s no diffe	erence between the	e Contr	rol 3 (Untreat	ted /	On Treatme	nt Lid) po	opulation and	the 500 G	treatment Po	pulatio Ropulat	n			
NT	PS-Control 3 PS-500 Gy 20							570	en		ponotion di		e, acounent	. opuidt				
2 0	13.5476																	
, test statistic	-1.5373	\vdash				_				_	-			\vdash			-	
			-															
ejection region	t > t _a																	
ejection region	0.05																-	
ejection region x if	0.05					-												
x if -value	0.05 8 1.860 0.519325892																	
x df :a p-value	0.05 8 1.860 0.519325892		ce between the		3 and the 500 Gy T	reated	Populations	Y	~	~	~	~	~	~	~		~	~
x df :a p-value	0.05 8 1.860 0.519325892 ull hypothesis, there is n	no differenc	\sim	\times	>>	Q	$\sim \propto$	X ted /	>>> On Treatme	nt Lid) po	opulation and	.he 1000 (y treatment F	Populati	on	\sim	~	\sim
1 ff ∋-value šince -1.5373 < 1.860, I do not reject the n do:	0.05 8 1.860 0.519325892	Null Hypot	thesis = There i	s no diffe	erence between th	e Cont	crol 3 (Untreat	ted /	On Treatmen	nt Lid) po	opulation and population and	the 1000 0	y treatment F	Population t Popula	on etion	~	~	><
r 16 - value iince - 1.5373 < 1.860, I do not reject the n 4.	0.05 8 0.519325892 ull hypothesis, there is n µ _{5 Control 3} - µ _{5-1000 Gy} = 0 µ _{5 Control 3} - µ _{5-1000 Gy} > 0	Null Hypot	thesis = There i	s no diffe	erence between th	e Cont	crol 3 (Untreat	ted / d / C	On Treatment	nt Lid) po t Lid Lid)	opulation and	the 1000 C	y treatment F	Populati t Popula	on ation	~	~	~
x # value % % 4 	0.05 8 1.860 0.519325892 will hypothesis, there is n H _{5 Control 3} - H _{5 1000 Gy} = 0 H _{5 Control 3} - H _{5 1000 Gy} > 0 4.7619	o differenc Null Hypot Null Hypot	thesis = There i	s no diffe	erence between th	e Cont	crol 3 (Untreat	ted / d / C	On Treatment	nt Lid) po	opulation and	the 1000 d	y treatment F	Populati t Popula	on ation	~	~	
a ff i i i i i i i i i i i i i	0.05 8 1.860 0.519325892 will hypothesis, there is n Hs_connet 3 - Hs_1000 Gy = 0 Hs_connet 3 - Hs_1000 Gy > 0 4.7619 -2.4033	o differenc Null Hypot Null Hypot	thesis = There i	s no diffe	erence between th	e Cont	crol 3 (Untreat	Xted / d / C	On Treatmen	nt Lid) po	opulation and	the 1000 d	y treatment F	Populati t Popula	on ation	~		><
t ff 	0.05 8 1.860 0.519325892 ull hypothesis, there is n H ₅ Control 1 - H ₅ 1000 Gy = 0 H ₅ Control 1 - H ₅ 1000 Gy > 0 4.7619 -2.4033 t > t _a	Null Hypot	thesis = There i	s no diffe	erence between th	e Cont	crol 3 (Untreat	X ted / C	On Treatment	nt Lid) po	opulation and	the 1000 d	y treatment P	Populati t Popula	on tition		~	
t ff 	0.05 8 1.860 0.519325892 will hypothesis, there is n Hs_connet 3 - Hs_1000 Gy = 0 Hs_connet 3 - Hs_1000 Gy > 0 4.7619 -2.4033	Null Hypot	thesis = There i	s no diffe	erence between th	e Cont	crol 3 (Untreat	ted / d / C	On Treatmen	nt Lid) po	oppulation and population an	the 1000	y treatment P	Populati t Popula	on tion			
z # -value ince -1.5373 < 1.860, I do not reject the n 40: 40: 40: 40: 40: 40: 40: 40:	0.05 8 1.860 0.51932589 Wpothesis, there is a W_Control 1 M 51000 pc 0 4.7619 -2.403 t > t_a 0.05 8 1.50	Null Hypot	thesis = There i	s no diffe	erence between th	e Cont	crol 3 (Untreat	ted/	On Treatmen	nt Lid) po	oppulation and	the 1000 d	iy treatment F Gy treatmen	Populati t Popula	on			
x ff subset fine = 1.5373 < 1.860, I do not reject the n for for for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1	0.05 8 1.860 0.51922589 H ² _{control} - P _{3.0000} - PO H ₂ _{control} - P _{5.0000} - PO 4.7619 -2.4033 t > t _a 0.05 8 1.860 0.519255892	Null Hypot	thesis = There i	s no diffe	erence between the	e Contro	ol 3 (Untreate	d / C	On Treatment	nt Lid) po	population and	the 1000 d	y treatment F	Populati	on tition			
x # 5 -value 5 5 5 5 5 5 5 5 5 5 5 5 5	0.05 8 1.860 0.51922589 H ² _{control} - P _{3.0000} - PO H ₂ _{control} - P _{5.0000} - PO 4.7619 -2.4033 t > t _a 0.05 8 1.860 0.519255892	Null Hypot	thesis = There i thesis = There i	s no diffen	erence between the	e Contro	ol 3 (Untreate	d / C	On Treatmen	nt Lid) po	pulation and population an	the 1000 G	y treatment F	Populati Populati	on ttion			
x # 5 -value 5 5 5 5 5 5 5 5 5 5 5 5 5	0.05 8 1.860 0.5192269 H ₂ General - H _{3.1000} = 0 H ₄ General - H _{3.1000} = 2 H ₄ General - H _{3.1000} = 2 t > t ₄ 1.860 0.5192589 0.055 8 1.912589 1	o difference Null Hypot Null Hypot	thesis = There i thesis = There i thesis = There i	Control	and the 1000 Gy	e Contro Contro	d Populationary rol 3 (Untreate	d / C	n Treatment	t Lid Lid)	population an	d the 100	y treatment F	t Popula	on			><
x ff subset fine = 1.5373 < 1.860, I do not reject the n for for for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for e 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1.860, I do not reject the n for 1.5573 < 1	0.05 8 1.500 0.51325802 ull hypothesis, there is ri H _{2.60003} - H _{2.50006} = 0 4.7619 -2.4033 t > t _a 0.05 8 8 1.500 0.51322582 ull hypothesis, there is ri	o difference Null Hypot Null Hypot	thesis = There i thesis = There i thesis = There i	Control	and the 1000 Gy	e Contro Contro	d Populationary rol 3 (Untreate	d / C	n Treatment	t Lid Lid)	population an	d the 100	y treatment F	t Popula	on			>>>
x # 5 -value 5 5 5 5 5 5 5 5 5 5 5 5 5	0.05 8 1.500 0.51922569 UII hypothesis, there is in 14, course 1 - 14, 1000 m = 0 14, course 1 - 14, 1000 m = 0 14, 7619 -2.4033 t > t_ 1, 8 0.05925692 UII hypothesis, there is in 1, 5000 m = 1, 14, 2000 m = 0 14, course 1 - 14, course 1 - 14, course 1 - 14, course 1 - 14, course 1 - 14, course 1 - 14, course 1 - 14, course 1	o difference Null Hypot Null Hypot	thesis = There i thesis = There i thesis = There i	Control	and the 1000 Gy	e Contro Contro	d Populationary rol 3 (Untreate	d / C	n Treatment	t Lid Lid)	population an	d the 100	y treatment F	t Popula	on	~		
2 3 4 5 5 5 5 5 5 5 5 5 5 5 5 5	0.05 8 1.860 0.5192269 H ₂ General - H _{3.1000} = 0 H ₄ General - H _{3.1000} = 2 H ₄ General - H _{3.1000} = 2 t > t ₄ 1.860 0.5192589 0.055 8 1.912589 1	o difference Null Hypot Null Hypot Null Hypot Null Hypot	thesis = There i thesis = There i thesis = There i	Control	and the 1000 Gy	e Contro Contro	d Populationary rol 3 (Untreate	d / C	n Treatment	t Lid Lid)	population an	d the 100	y treatment F	t Popula	on	~		
2 3 4 5 5 5 5 5 5 5 5 5 5 5 5 5	0 005 8 1,860 0.5192269 H ₅ General ⁻¹ H ₅ 1000 g ⁻¹⁰ H ₅ General ⁻¹ H ₅ 1000 g ⁻¹⁰ H ₅ General ⁻¹ H ₅ 1000 g ⁻¹⁰ -2.4033 t > t _a 1,860 0.5192269 H ₅ General ⁻¹ H ₅ 2000 g ⁻¹⁰ H	o difference Null Hypot Null Hypot Null Hypot Null Hypot	thesis = There i thesis = There i thesis = There i	Control	and the 1000 Gy	e Contro Contro	d Populationary rol 3 (Untreate	d / C	n Treatment	t Lid Lid)	population an	d the 100	y treatment F	t Popula	on			
1 4 5 5 5 5 5 5 5 5 5 5 5 5 5	0.05 8 1.860 0.51922692 Will hypothesis, there is 1 H ₂ -const - H ₃ -store - 20 H ₄ -const - H ₃ -store - 20 1.25 1.2	o difference Null Hypot Null Hypot Null Hypot Null Hypot	thesis = There i thesis = There i thesis = There i	Control	and the 1000 Gy	e Contro Contro	d Populationary rol 3 (Untreate	d / C	n Treatment	t Lid Lid)	population an	d the 100	y treatment F	t Popula	on			
1 4 5 5 5 5 5 5 5 5 5 5 5 5 5	0.05 8. 1.860 0.51932889 We could be a set of the s	o difference Null Hypot Null Hypot Null Hypot Null Hypot	thesis = There i thesis = There i thesis = There i	Control	and the 1000 Gy	e Contro Contro	d Populationary rol 3 (Untreate	d / C	n Treatment	t Lid Lid)	population an	d the 100	y treatment F	t Popula	on			
rejection region a a d	0.05 8 1.860 0.51922892 III hypothesis, there is in 9, consult - 14, 2000; = 0 14, consult - 14, 2000; = 0 14, consult - 14, 2000; = 0 1, 24, 003 1, 24,	o difference Null Hypot	thesis = There i thesis = There i thesis = There i	Control	and the 1000 Gy	e Contro Contro	d Populationary rol 3 (Untreate	d / C	n Treatment	t Lid Lid)	population an	d the 100	y treatment F	t Popula	on			



Data						+		-									+		+
Strain			м	utant #8				_											
Control 1 - CFU Input	10			20 22 1		2 22													-
Control 2 - Untreated, No Vacuum Control 3 - Untreated. Vacuum	18			20 23 1 6	1 1	3 22				_							+ +-		+
100 Gy Treated Samples	4	6	6	11 7		95													
500 Gy Treated Samples 1000 Gy Treated Samples	7		14 5	7 9 8 4 1		3 7 8 12		_		_									_
2500 Gy Treated Samples	11			8 12		7 6													
All colony counts at 10 ^{5 diution}										_									-
Statistics																			
Statistics	n _{8-control 1}	3	n _{8-control 2}	8	n _{8-control 3}	4	n _{8-100 Gy}	8	n _{8-500 Gy}	8	n _{8-1000 Gy}	8	n _{8 - 2500 Gy}	8					+
	x-bar _{8-control 1}	11.3	x-bar _{8-control}	17.6	x-bar _{8-control}	3 4.8	x-bar _{8-100 Gy}	5.5		9.4	x-bar _{8-1000 Gv}	7.6	x-bar _{8-2500 Gy}	8.0					
	S _{8-control 1}	1.2	S8-control 2	4.7	S8-control 3	2.1		2.4		2.9	S _{8-1000 Gy}	2.8	S _{8-2500 Gy}	2.8					
B								-											+
Population Comparisons								_		_									+
H- :	μ _{5-Control 1} - μ _{5-Control 2} = 0	Null Hypot	hesis = There	is no diff	erence hetwo	on the l	ontrol 1 (CELL	Innut)	nonulation and	the Con	trol 2 (Lintre:	ted / Hr	onened Lid) Pr	nulatio	on.				+
Ha:	$\mu_{\text{5-Control 1}} = \mu_{\text{5-Control 2}} > 0$	Null Hypot	thesis = There	is a diffe	rence betwee	n the Co	ontrol 1 (CFU Ir	nput) p	opulation and t	he Contr	ol 2 (Untreat	ed / Unc	opened Lid) Pop	ulation	1				
Sp ²	17.1713																		
t, test statistic	-2.2427					+ +		-						\vdash				-	+
rejection region	t>t _a			+ +		+ +-		-									+		+
α	0.05																		
df	9																		
t _a	1.833							_		_									+
p-value Since -2.2427 < 1.833, I do not reject the ու	0.519392768 ull hypothesis, there is n		nce betwee	1 the Cont	rol 1 and Con	trol 2													+
						XX	\geq	X	\sim	\propto	\geq	∞	\sim	X	\geq	\geq	XX	\geq	\supset
н _о :	$\mu_{\text{S-Control 2}} - \mu_{\text{S-Control 3}} = 0$															n			
H _a :	$\mu_{5-Control 2} - \mu_{5-Control 3} > 0$	Null Hypot	thesis = There	e is a diffe	ence betwee	n the Co	ontrol 2 (Untre	ated /	Jnopened Lid)	populati	on and the Co	ontrol 3	(On Treatment	Lid) Po	pulation				
2				_				_		_									+
sp ² t, test statistic	16.4625 5.1818		_	+		+		-						\square					+
	5.1010					+													+
rejection region	t > t _α																		
α. df	0.05					++	T			+									-
df to	10					+										-		-	+
^{να} p-value	0.519446506																		+
Since 5.1818 > 1.812, I do reject the null hy	ypothesis, there is a diffe	erence bet	ween the Con		Control 3 Pop	oulation	5			~ ~		_					_	_	
	>	\sim	\sim	$\overline{\mathbf{x}}$			\sim			<u> X</u>	\sim	\mathbf{x}	\sim	X	\simeq	\sim	XX	\sim	
H ₀ :													By treatment Po D Gy treatment I						
· · · ·	PS-Control 3 PS-100 Gy 7 0	Hunnypo	incuis – mere	. is a diffe	chec betwee					la Lla, pe	paractorrant	100	o oy a councile						
s _ρ ²	5.4750																		
t, test statistic	-1.2213			_				_		_									_
rejection region								-											+
α																			-
	t > t _a 0.05																		
df	0.05																		
df t _a	0.05																		
df t _a p-value Since -1.2213 < 1.812. Ldo, not reject the r	0.05 10 1.812 0.519446506		ice between 1	the Contro	and the 10	0 Gy Tre	ated Populati	ons											
	0.05 10 1.812 0.519446506		ice between	the Contro	I 3 and the 10	10 Gy Tre	ated Populati	ons	\sim	~~	\mathbf{x}	x >	~~	x	~	\sim	<u> </u>	\sim	5
df t _a p-value Since -1.2213 < 1.812, I do not reject the n H ₀ :	0.05 10 1.812 0.519446506 null hypothesis, there is	no differer	\sim	∞	\sim	∞	\sim	X	On Treatment	Lid) pop	ulation and t	XX he 500 G	y treatment Po		<u>></u>	\sim	<u>××</u>	\sim	2
	0.05 10 1.812 0.519446506	no differer	thesis = There	is no diff	erence betwe	en the	Control 3 (Untr	eated ,	On Treatment	Lid) pop id Lid) po	ulation and t	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	Correctment Po D Gy treatment I	pulatic Populat	>>> on tion	~	<u> </u>	~	2
	$\begin{array}{c} 0.05\\ 10\\ 1.812\\ 0.519446506\\ \text{null hypothesis, there is}\\ \mu_{5\ \text{Control 3}}\cdot\mu_{5\ 500\ 6\gamma}=0\\ \mu_{5\ \text{Control 3}}\cdot\mu_{5\ 500\ 6\gamma}>0 \end{array}$	Null Hypot	thesis = There	is no diff	erence betwe	en the	Control 3 (Untr	eated ,	On Treatment	Lid) pop id Lid) po	ulation and t	200 G he 500 G I the 500	Sy treatment Po O Gy treatment I	pulatic Populat	>>> tion	>	<u>××</u>	~	2
Since -1.2213 < 1.812, I do not reject the r H ₀ : H ₄ : S _p ²	0.05 10 1.812 0.519446506 null hypothesis, there is µ _{5 Control 3} · µ _{5 500 Gy} = 0 µ _{5 Control 3} · µ _{5 500 Gy} > 0 7.2625	Null Hypot	thesis = There	is no diff	erence betwe	en the	Control 3 (Untr	eated ,	On Treatment L	Lid) pop	ulation and t	he 500 G	by treatment Po	X pulatic Populat	on tion	><		~	>
Since -1.2213 < 1.812, I do not reject the r H ₀ : H ₄ : S _p ²	$\begin{array}{c} 0.05\\ 10\\ 1.812\\ 0.519446506\\ \mbox{null hypothesis, there is}\\ \mu_{5\ Control 3} - \mu_{5\ 500\ 6\gamma} = 0\\ \mu_{5\ Control 3} - \mu_{5\ 500\ 6\gamma} > 0 \end{array}$	Null Hypot	thesis = There	is no diff	erence betwe	en the	Control 3 (Untr	eated ,	On Treatment	Lid) pop	ulation and t	he 500 G	Gy treatment Po	X ppulatic Populat	>>> tion	><	××	~	>
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Since -1.2213 < 1.812, 1 do not reject the r H ₀ : H ₁ : S ₀ ² t, test statistic rejection region a df H ₂ -value	0.05 1.1312 0.515446556 Inter thypothesis, there is 1.6 ₅₀₀₀₀ = 70 1.6 ₅₀₀₀ = 70 1.6 ₅₀₀₀₀ = 70 1.6 ₅₀₀₀ =	no differen	thesis = There thesis = There between the	e is no diffe e is a diffe	and the 50	een the Co	Control 3 (Untre	ated / 1	Dn Treatment L	id Lid) po	opulation and	the 500	0 Gy treatment I	Populat	tion	~		~	
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	Mutant #5															
	n5-control 1	3	n5-control 2	8	n5 -control 3	3	n5 - 100 Gy	8	n5- 500 Gy	7	n5 - 1000 Gy	7		n5 - 2500 Gy	8	
	x-bar5-control 1	13.66666667	x-bar5-control 2	8.875	x-bar5-control 3	6.66666667	x-bar5-100 Gy	6.125	x-bar5-500 Gy	10.57142857	x-bar5-1000 Gy	10.28571429		x-bar5-2500 Gy	9.75	
	s5-control 1	3.785938897	s5-control 2	2.416461403	s5-control 3	1.527525232	s5-100 Gy	2.232071427	s5-500 Gy	4.157609203	s5-1000 Gy	2.360387377		s5-2500 Gy	5.2030211	
	Mutant #8															
	n8-control 1	3	n8-control 2	8	n8 -control 3	4	n8 - 100 Gy	8	n8- 500 Gy	8	n8-1000 Gy	8		n8 - 2500 Gy	8	
	x-bar8-control 1	11.333333333	x-bar8-control 2	17.625	x-bar8-control 3	4.75	x-bar8-100 Gy	6.5	x-bar8-500 Gy	9.375	x-bar8-1000 Gy	7.625		x-bar8-2500 Gy	8	
	s8-control 1	1.154700538	s8-control 2	4.657942526	s8-control 3	2.061552813	s8-100 Gy	2.449489743	s8-500 Gy	2.924648941	s8-1000 Gy	2.774243784		\$8-2500 Gy	2.7774603	
1	10000000												CFU	Std. Dev.		
			CF	U Compariso	ins for Proton Expe	eriment					WT	Control 1	1433333.33			
	1000000		- T	T 🖬	- I	- T						Control 2	1283333.33			
				1			II					*Control 3*	80000			
												10 Gy	742857.142			
	100000								-			100 Gy	106250			
												500 Gy	71250			
	10000											1000 Gy	100000			
a	5											2500 Gy	87500	470372.1931		
Total CD	8											10000 Gy	98750	470372.1931		
P	² 1000								-							
											Mutant #5	Control 1	1366666.66			
	100											*Control 2*	88750			
												Control 3	666666.666			
												100 Gy	61250			
	20								-			500 Gy	1057142.85			
												1000 Gy	1028571.42			
												2500 Gy	97500	520302.11		
	1 N	* 8 3	500 G y 1000 G y 2500 G y	Control 1	Dantral 2* Contral 3 100 Gy 500 Gy	1000.6 y	Control 1 Control 2 Sontrol 3* 1006v	500Gy 1000Gy	2000							
	8 8	10 10	8 8 8	8 1	200 H	8 8	10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 8	8			Control 1	1133333.33			
	8 8	ğ		8 8	j 8	- 10	8 8 ğ		~			Control 2	176250			
			WT		Mutant #5		Mutar	+#5				*Control 3*	47500			
												100 Gy	65000	244948.9743		
												500 Gy	93750			
												1000 Gy	76250	277424.3784		
												2500 Gy	80000	277746.0299		



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14. ABSTRACT <i>Deinococcus radiodurans</i> is a robust bacterium that is known for its extraor In general, many of the investigations of this bacterium's resistance have re radiation, such as gamma and electron radiation. This study explored <i>Deim</i> high linear energy transfer radiation, specifically proton and neutron radiati dehydrated to reduce the effects of low linear energy transfer radiation. Th and proton radiation of varying amounts and rehydrated. The resulting colo colonies of non-irradiated control samples using a two population, t-statistic exceptions, the results of these comparisons showed, with 95% certainty, the between the non-irradiated controls and the irradiated samples.	volved around low linear energy transfer pcocccus radiodurans's ability to survive on. Deinococcus radiodurans was bacteria were exposed to both neutron onies were counted and compared to be test. With few, non-trend forming
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