

THE INTERACTION OF RADIO FREQUENCY AND LAMBDA DNA

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ABSTRACT

By exposing an aqueous DNA solution to a spectrum of radio frequency (RF) energy this research identifies frequencies, if any, where DNA interacts with RF energy. Interaction is determined by the amount of RF energy either absorbed or reflected by the DNA solution. Previous studies have shown that RF energy at high power levels causes destruction of DNA. The method outlined in this thesis will radiate a DNA solution at a low power level of non-ionizing RF energy. This will determine if DNA behavioral changes can be induced without heating the DNA solution. Any frequencies interacting with DNA within the frequency band areas will be identified as potential frequencies to induce change in genetic function. This thesis sets a foundational experimental protocol to test RF energy interaction with a variety of biological molecules.

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LIST OF ABBREVIATIONS

DNA.....	Deoxyribonucleic acid
<i>E. coli</i>	<i>Escherichia coli</i>
GHz	Gigahertz
kHz	kilohertz
MATLAB	Matrix Laboratory simulation software
MHz	Megahertz
RF.....	Radio Frequency
S ₂₁	Scattering parameter that measures forward gain voltage
THz.....	terahertz
μL	Microliters

1. INTRODUCTION

Because DNA is the fundamental building block of molecular function, it is important to ensure DNA does not become damaged by external environmental factors such as radio frequency (RF) energy. Therefore a need exists to better understand the effects of DNA being exposed to RF energy and the interaction between them.

Previous studies have shown that RF energy at high power levels can cause heating within cells [1] [2] [3]. The heating effects due to RF energy will cause cell and DNA damage which can then lead to serious health problems such as cancer [1] [4] [5]. Other experiments have focused on studying only one frequency in the RF range [3]. One research group exposed multiple types of DNA to frequency sweeps in the Terahertz range, which is where the DNA types have their resonance frequencies [6]. An extensively characterized DNA used in many research studies is Lambda DNA [7] [8].

Performing a RF sweep could identify any specific frequencies that have an increased rate of interaction with DNA throughout a range of frequencies. These isolated frequencies can be further studied to test if the increased interaction between RF energy and lambda DNA is constructive or destructive. If RF energy positively affects lambda DNA, then new techniques can be developed to repair DNA by altering switching mechanisms in genes. But, if RF negatively affect Lambda DNA then more studies can be performed, and expanded to human DNA, to derive correlations about how certain diseases originate.

No previous research has used a low power level of non-ionizing RF energy in order to avoid heating the DNA but looking for changes in DNA. Therefore a link between interaction of the DNA and RF energy may be discovered not due to heating effects.

This research is studying the interaction between RF energy and Lambda DNA. Interaction will be determined by the amount of RF energy that is absorbed or reflected by an aqueous DNA solution over a specified RF range and power level.

2. BACKGROUND THEORY

2.1. Introduction

This chapter will discuss general background information about some of the biological and electromagnetic aspects of this research. Lambda DNA was a primary part of this research, so it is worthwhile to overview how Lambda phage becomes Lambda DNA and how Lambda DNA regulates its gene expression. A brief overview of radio frequency energy and areas of electromagnetics relating to this research can also be found later in the chapter.

2.2. Lambda DNA

Lambda DNA has been thoroughly studied by biologists and other researchers over the past several decades. Lambda DNA was the first DNA molecule to have its genome fully sequenced. Later, a gene from Lambda DNA was the first bacterial gene ever to be cloned. With 48k base pairs, this DNA is considered long for a viral DNA. Lambda DNA is considered an important tool in virology and other applied sciences based on the numerous studies performed on the DNA. Lambda DNA was chosen to be used in this research because of its detailed history and well-known characteristics [7] [8].

Lambda DNA is extracted from the bacteriophage Lambda. A bacteriophage is a bacterial parasite that grows by inserting its genetic material into a host, in this case *E. coli*. It then overcomes the host cell and starts replicating and reproducing new strands of Lambda DNA. Lambda DNA, can be isolated from the *E. coli* cell by inducing cell lysis by exposing the cells to an environmental disturbance such as ultraviolet light [8].

Researchers exploit the parasitic characteristic of bacteriophage Lambda as a drug delivery system to transport vaccines and other medicines throughout the body. This model is successful because the bacteriophage Lambda naturally targets bacterial cells that are causing sickness within the body and upon infestation of these cells the medicines are also delivered [9].

2.3. Gene Expression of Lambda DNA

Previous research has shown gene expression is activated when the Lambda's DNA is exposed to ultraviolet radiation [8]. Some of these genes are in charge of up or down regulating functions of the DNA. This activation causes the cells containing Lambda DNA to express different genes on the DNA strand, which in turn causes different protein and amino acid combinations to synthesize, and overall for

the cell to change its function [8]. If the Lambda DNA preferentially absorbs or reflects significant amounts of radio frequency radiation, it could provide evidence that gene expression also takes place in the RF domain.

2.4. Radio Frequency Radiation

On the electromagnetic spectrum, radio frequency waves have the longest wavelength and are considered a source of low power, non-ionizing electromagnetic radiation [2]. Studies have proven ionizing radiation to be damaging to cells and DNA in the human body [1] [4] [5]. Although many studies have been conducted on the specific radio frequencies that electronics operate at, it is inconclusive if RF energy causes destructive effects of DNA [3] [4] [5]. This research can add to evidence showing that RF radiation has negative health effects, but this research may also find specific frequencies that have positive effects on DNA.

Another investigation is researching the phenomenon that bacterial molecules can communicate with other bacterial molecules by acting as a fractal antenna. This was observed within *E. coli* bacteria when the molecules were shifting into different energy states. The researchers concluded that electron energy was given off when the molecules shifted from one energy state to another. This electron energy could then be detected by surrounding cells [10].

2.5. Radio Frequency Absorption and Reflection

Absorption and reflection of RF energy can be experimentally measured by taking the ratio of the amount of voltage received divided by how much voltage was sent. This ratio, known as S_{21} , is part of a group of measurements called scattering parameters. In the following experiments a network analyzer computes this ratio by measuring the voltages sent and received by horn antennas. The formal equation to calculate S_{21} is defined as:

$$S_{21} = \frac{V_2}{V_1} = \frac{\text{voltage received}}{\text{voltage sent}} \quad (1)$$

Previous studies have concluded that the heating effects as a result of RF energy lead to damage in cells and DNA [1]. We want to use levels of RF that do not lead to heating effects that damage DNA according to the IEEE standards for RF heating, but may still activate genetic change [2].

2.6. Resonance Frequencies

Previous research has used radio spectroscopy to measure absorption rates in a variety of molecules, including Lambda DNA. A theoretical model was made for a DNA-water solution that was experiencing a decoupling phenomenon at a range of frequencies. The DNA-water solution was modeled as a mass and spring system [11]. A preliminary experiment wanted to determine if the length of DNA being exposed to specific microwave frequencies had an effect on DNA absorption characteristics. An aqueous solution of saline buffer and *E. coli* DNA, which is a DNA that is short in length, were tested in three separate experimental setups to test absorption rates. In each iteration of the set of experiments the length of DNA was changed. The first experiment was to induce microwave heating in the DNA sample by using laser. The next experiment was measuring reflection coefficients using a short coaxial cable model. And finally, repeating the second experiment but instead measuring reflection coefficients using an open cable model. The results of all three experiments showed that the shortest DNA strand lengths had a direct correlation with the increased amount of absorption of microwave energy measured [12].

In a recent study, however, researchers found high absorption rates by performing frequency sweeps at the resonance frequencies of DNA molecules of differing lengths. [6]. Resonance frequency is the frequency where the length of the material, in this case Lambda DNA, matches the wavelength of the electromagnetic energy.

2.7. Estimation of Electric Field

The electric field that was experienced by the DNA solution was estimated. First the power density was calculated using Friss equation:

$$P_r(\text{dBm}) = P_t(\text{dBm}) + G_t(\text{dB}) + G_r(\text{dB}) - 20\log R(\text{km}) - 20\log f(\text{MHz}) - 32.44 \quad (2)$$

Where P_r is the power received, P_t is the power transmitted, G_t is the gain of the transmitting antenna, G_r is the gain of the receiving antenna, R is the distance from the horns to the item of interest, and λ is the wavelength of the frequency in question [13]. P_r was calculated for the low and high frequency of the sweep, being 1.0 GHz and 17.0 GHz. The power transmitted is 0 dBm. The gain of the horns was 6.1 dB each at the low frequency and 11.6 dB at the high frequency [14]. The power density is calculated at the distance from the horn to the sample which is 31 cm.

Next, the power density, S , was estimated at both low and high frequency using the equation [13]:

$$S = \frac{P_r}{A} \quad (3)$$

Where A is the effective area of the horn antenna, which in this case was 0.0339 m². The calculated power density from low frequency to high frequency ranged between 2.9 mW/m² to 0.126 mW/m², respectively. After the power density was calculated, the electric field was calculated using the equation [15]:

$$E = \sqrt{S \times Z_0} \quad (4)$$

Where Z_0 was said to be the impedance of air and equal to 377Ω. Therefore between the frequency sweep range of 1.0 – 17.0 GHz the electric field experienced at the sample was estimated to be between 1.046 V/m – 0.218 V/m, respectively.

3. MATERIALS AND METHODS

3.1. Experimental Overview

This experiment protocol was: 1) exposing a 96 well cell-culturing tray filled with 200 μ L of aqueous DNA solution in each well, 2) using a 96 well tray with 200 μ L of 1:10 concentration of Lambda DNA and 1X TE buffer, respectively, 3) ran a frequency sweep from 1.0-8.5 GHz lasting 3 minutes, 4) collected 1601 frequency steps, 5) set the power level to 0 dBm.

Table 1. Material List.

Pyramidal Microwave Horn Antennas (2)
Network Analyzer (older model)
Network Analyzer (newer model)
Coaxial cables
Pyramidal Anechoic Material
Anechoic Chamber
Aluminum Aperture
Permanent Test Fixture (wood)
96 well cell-culture trays
Lambda DNA (linear)
1X TE Buffer

3.2. Preliminary Experimental Design

To gather initial data a plan was devised to expose a 96 well cell-culturing tray filled with a 1:10 concentration of Lambda DNA to 1X TE buffer, respectively, to RF energy between two pyramidal microwave horn antennas. An aluminum aperture with a cutout in the middle held the tray halfway between both horn antennas (Figure 1 below). The aluminum aperture was held in the middle of the two horn antennas by anechoic material. The frequency sweep was set up on the network analyzer and S₂₁ parameters recorded for 49 sweeps. The means of both the set of sweeps with buffer only and the sweeps with DNA plus buffer were calculated where \bar{X} is the point-by-point mean, X_i is the individual S₂₁ measurement, and n is the number of samples [16].

$$\bar{X} = \frac{\sum_{i=1}^{49} X_i}{n} \quad (5)$$

The signal due to DNA was determined by finding the difference of the means [16].

$$\bar{X}_{DNA+buffer} - \bar{X}_{buffer} = \frac{\sum_{i=1}^{49} X_{DNA+buffer}}{n} - \frac{\sum_{i=1}^{49} X_{buffer}}{n} \quad (6)$$

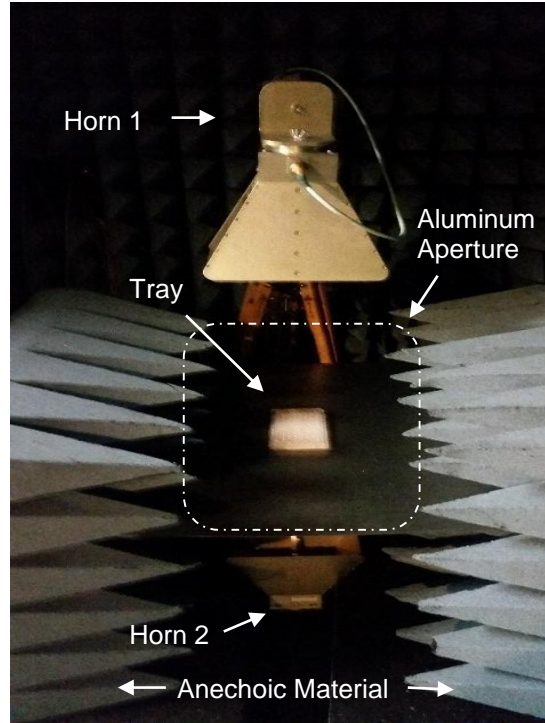


Figure 1. Above is the full view of experimental setup. Two horn antennas faced one another with an aluminum aperture holding the cell-culturing tray in between. Blue pyramidal material on the sides was anechoic material.

The preliminary experimental setup and some initial conclusions were presented at the 2015 Rocky Mountain Bioengineering Symposium [17].

3.3. Revised Experimental Setup

After the initial experimental runs, key problems of the original setup were addressed which led to a revised protocol. First, it was not known if the aluminum aperture was having any effects on the results, such as scattering the RF signal. Also, it was determined that since the effect of the Lambda DNA was going to be very small, the systematic error needed to be reduced as much as possible. A new experimental setup was proposed in an effort to eliminate systematic error in the system. Therefore a permanent test fixture was designed. The permanent test fixture was made from pretreated lumber and had two equidistant boards where the horn antennas were attached. Since the antennas were securely attached to the test fixture, this reduced the possibility of the horns accidentally being moved or bumped

out of place. Also, an equidistant spot was measured to attach the horns, ensuring that the experimental setup was replicable. Exactly halfway between the attached horn antennas was a jig to insert a 96 well cell-culturing tray. The insert was the dimensions of a cell-culturing tray, which reduced the possibility of placing the tray in a different location than a previous placed tray.

Another change in the experimental setup was the use of a new network analyzer. The network analyzer was new and had a range from 300 kHz to 20 GHz. This extended range is over double the amount of frequencies that the experiment was able to sweep with the older network analyzer. However, because of the limitations of the horn antennas, a range from 1.0-17.0 GHz was used to ensure reliable data readings.

The revised experimental setup was put into place after the design on the permanent test fixture. First, the RF equipment was setup in the anechoic chamber by attaching horn 1 to the top of the permanent test fixture, and horn 2 to the bottom. The horn antennas were clamped into position, and anechoic material was placed around the sides and bottom of the permanent test fixture to reduce RF interference from reflections in the anechoic chamber.

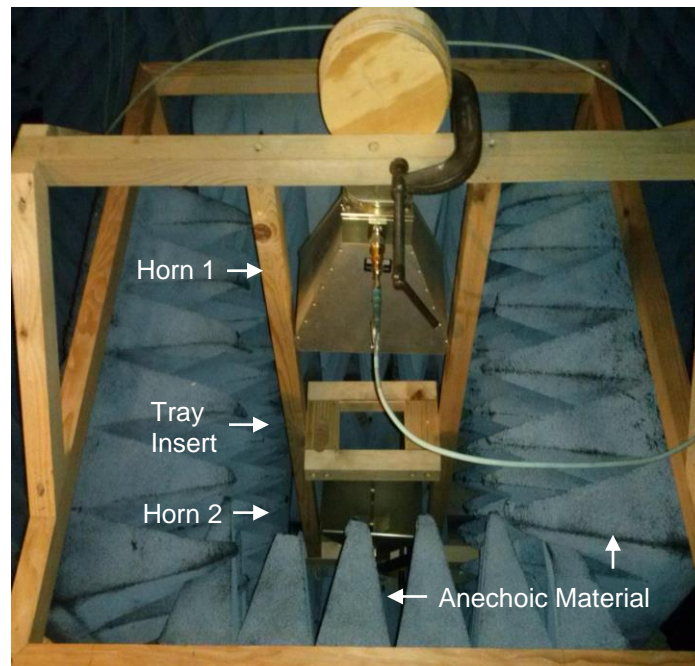


Figure 2. Above is the top view of the permanent test fixture. The top horn points down, directly above the insert for the cell-culturing tray and the second horn.

3.4. Calibration

The next step in the experimental design was to calibrate the system. First, to calibrate the coaxial cables on the network analyzer choose: 2 port calibration and then reflection. Then, vector-error calibration was used to calibrate port 1 using: open, short, load. Using the same method calibrate port 2 using: open, short, load. The final cable calibration step was to Thru calibrate by selecting: transmission, then Port 1-2 Thru. Then the coaxial cables were connected to the two horn antennas. By pressing the Sweep Setup button, select S21 as the measurement type and set the power level to 0 dBm. Also, the sweep parameters were set to: a start frequency of 1.0 GHz and stop frequency of 17.0 GHz with 1601 points and a sweep time of 3.0 minutes. Next, horn antenna 1 was connected to port 1 of the network analyzer using coaxial cables. Similarly, horn antenna 2 was connected to port 2 of the network analyzer. Then a cable-to-cable calibration test sweep was ran on the network analyzer by choosing a single continuous sweep. Once the test sweep is finished, the data was saved on flash drive as a .csv file. A second test sweep could be performed, to act as a reference, using the above specifications but measuring the S21 parameters from horn 1 to horn 2. These first two sweeps recorded the calibration of the system, shown in Figure 4.

3.5. Replacement Verification

The follow steps were taken to measure the amount of experimental error introduced into the experimental results. First, the permanent test fixture was placed in the anechoic chamber, and all the steps from the previous experiments were taken to calibrate the system. Once all calibration sweeps were complete, a cell-culturing tray filled with 200 μ L of 1X TE buffer was placed within the test fixture. Then, a single continuous sweep was taken from 1.0-17.0 GHz with 1601 points and a sweep time of 30 seconds. The results of each sweep were saved as .csv file. After each sweep was completed, the tray was removed and replaced in its exact, previous location. The replacement sweeps were repeated 20 times.

After the 20 sweeps were completed the cell-culturing tray was removed from the permanent test fixture. Then, all the buffer was removed from the cell-culturing tray. Before proceeding it was important to make sure each well of the tray was completely dried out. Next, the cell-culturing tray was refilled by pipetting 200 μ L of 1X TE buffer in each well. After pipetting was finished, the filled tray was replaced within the test fixture. Then, a single continuous sweep was ran from 1.0-17.0 GHz with 1601 points and

a sweep time of 30 seconds, and saved as .csv file. After each sweep is completed, the tray was removed and replaced in the exact location as before. The sweep was repeated 20 times. Both groups of 20 runs are shown in Figure 5. Finally, after the experimentation is completed, the experimental error was analyzed.

3.6. Experimental Protocol

After all calibration and error measurements were taken, the next part of the experiment took place. First, 200 μL of 1X TE buffer was pipetted into each of the 96 wells of a cell-culturing tray. The tray was replaced in the permanent test fixture and a single, continuous sweep was ran from 1.0-17.0 GHz with 1601 points and a sweep time of 3.0 minutes at the 0 dBm power level. The results were saved as a .csv file. The sweep was repeated for 20 sweeps. The buffer-filled cell-culturing tray was removed from the permanent test fixture.

Next, taking a vial containing Lambda DNA out of the -20°C freezer and began to thaw it. Once the entire vial was thawed, the vial was gently vortexed to ensure the Lambda DNA is thoroughly mixed. Then, 20 μL of buffer was removed from each of the 96 wells. Next, 20 μL of Lambda DNA was pipetted into each well, to obtain a 1:10 concentration of Lambda DNA to 1X TE buffer. The micropipette was used to gently titrate each well to mix the DNA solution completely. After titration is completed, the cell-culturing tray was replaced, which held the aqueous Lambda DNA and buffer solution, into the permanent test fixture. Again, a continuous sweep from 1.0-17.0 GHz was ran with 1601 points and a sweep time of 3.0 minutes at the 0 dBm power level. The data was saved with a .csv file extension, and the single sweep was repeated 20 times. Both groups of 20 sweeps are shown in Figure 8. Finally, the data was analyzed using MATLAB.

3.7. Derivations

All the calculations of the above experimental protocols were processed in MATLAB. Each frequency sweep created a matrix of values where a specific frequency was paired with its correlating S_{21} value. After importing each sweep into MATLAB, the point-by-point mean was calculated for the sweeps of Group 1 and Group 2 of the tray and buffer replacement measurements, from section 3.5.

The following equation was used, where \bar{X} is the point-by-point mean, X_i is the individual S_{21} measurement, and n is the number of samples [16].

$$\bar{X} = \frac{\sum_{i=1}^{i=20} X_i}{n} \quad (7)$$

After the means of these two groups were calculated, the difference of the means were calculated to observe where the greatest difference in sweeps between the two groups occurred, shown in Figure 6 [16].

$$\bar{X}_{Replacement\ Group\ 1} - \bar{X}_{Replacement\ Group\ 2} = \frac{\sum_{i=1}^{i=20} X_{Replacement\ Group\ 1}}{n} - \frac{\sum_{i=1}^{i=20} X_{Replacement\ Group\ 2}}{n} \quad (8)$$

Then the standard error of the sample mean, $\sigma_{\bar{X}}$, of both Group 1 and Group 2 were calculated and plotted in Figure 7 [16],

$$\sigma_{\bar{X}} = \frac{s}{\sqrt{n}} \quad (9)$$

where s is the sample standard deviation and is equal to the following [16].

$$s = \sqrt{\frac{\sum(X_i - \bar{X})^2}{n-1}} \quad (10)$$

After the error measurements were calculated, the point-by-point mean for the buffer only, and Lambda DNA plus buffer solution sweeps from section 3.6 were calculated using equation 7. The difference of the means were also calculated and shown in Figure 9 [16].

$$\bar{X}_{DNA+buffer} - \bar{X}_{buffer} = \frac{\sum_{i=1}^{i=20} X_{DNA+buffer}}{n} - \frac{\sum_{i=1}^{i=20} X_{buffer}}{n} \quad (11)$$

Next, the t - test statistic, t , was calculated on a two sample t - test [16].

$$t = \frac{\bar{X}_{DNA+buffer} - \bar{X}_{buffer}}{\sigma_{\bar{X}_{DNA+buffer}} - \sigma_{\bar{X}_{buffer}}} \quad (12)$$

Finally, the p -values, denoted as P , of the two sample t - test were calculated, where $\Phi(|t|)$ was the standard normal cumulative distribution function [16].

$$P = 2[1 - \Phi(|t|)] \quad (13)$$

Any p -value less than 0.05 were plotted, in Figure 10, and these areas were determined to be frequencies of interest.

4. RESULTS

4.1. Preliminary Experiment Results

Two separate 96 well cell-culturing trays were used in this experiment. First, all the wells in both trays were filled 200 μ l of 1X TE buffer. Then one tray was placed in the experimental setup and 49 sweeps were taken over the range of 1.0-8.5 GHz. This process was repeated for the second tray. After completing both sets of runs with only buffer in the trays, the contents were each replaced with a 1:10 concentration of Lambda DNA to 1X TE buffer. Again, the 49 sweeps were repeated on each tray. This resulted in four sets of data 49x1601 in size. Each set of data included 49 sweeps, which contained 1601 frequency steps of: tray 1 with buffer only, tray 1 with DNA and buffer, tray 2 with buffer only, and tray 2 with DNA and buffer. The means were calculated by finding the point-by-point mean of each column, as shown in equation 5. This resulted in a matrix of means (1x1601). Taking the mean of the DNA and buffer runs and subtracting the mean of the buffer only runs the difference of the means was calculated in equation 6. Figure 3 shows the difference of the means for each tray, the first tray to be run, noted as tray 1, is shown in black diamonds and the second tray, tray 2, is shown in gray circles.

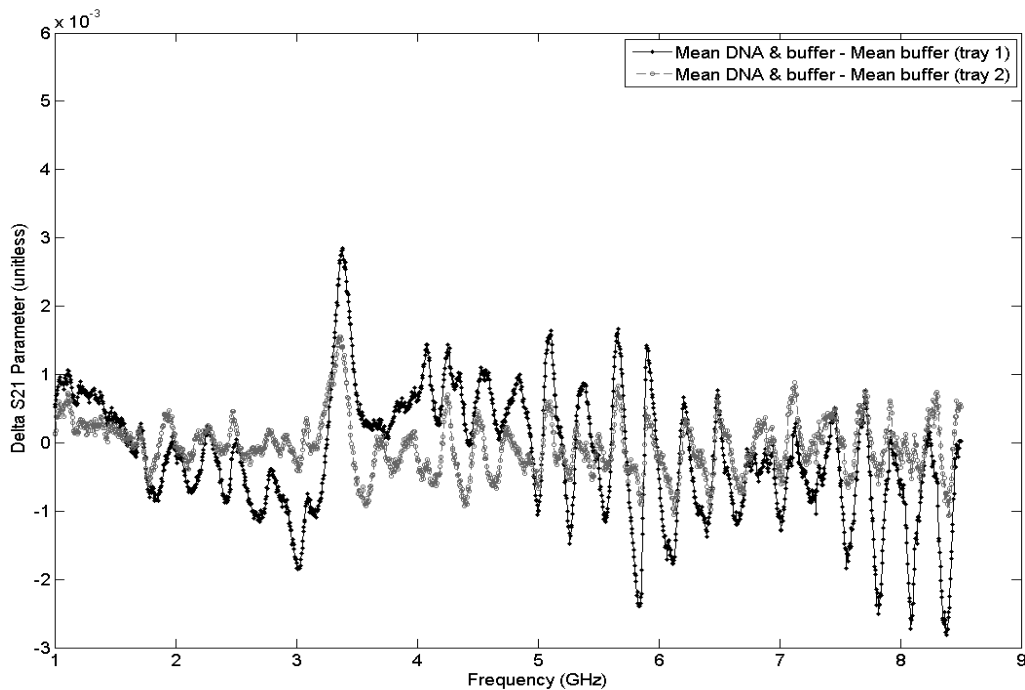


Figure 3. Above is the difference of the means, which were calculated by taking the mean of the DNA plus buffer runs (49 runs) and subtracting the mean of the runs with buffer only (49 runs) for each tray.

4.2. Experimental Error Measurements

Since there was variability in the preliminary experimental runs, a new test fixture was built to ensure the reproducibility of all future results (see section 3.3).

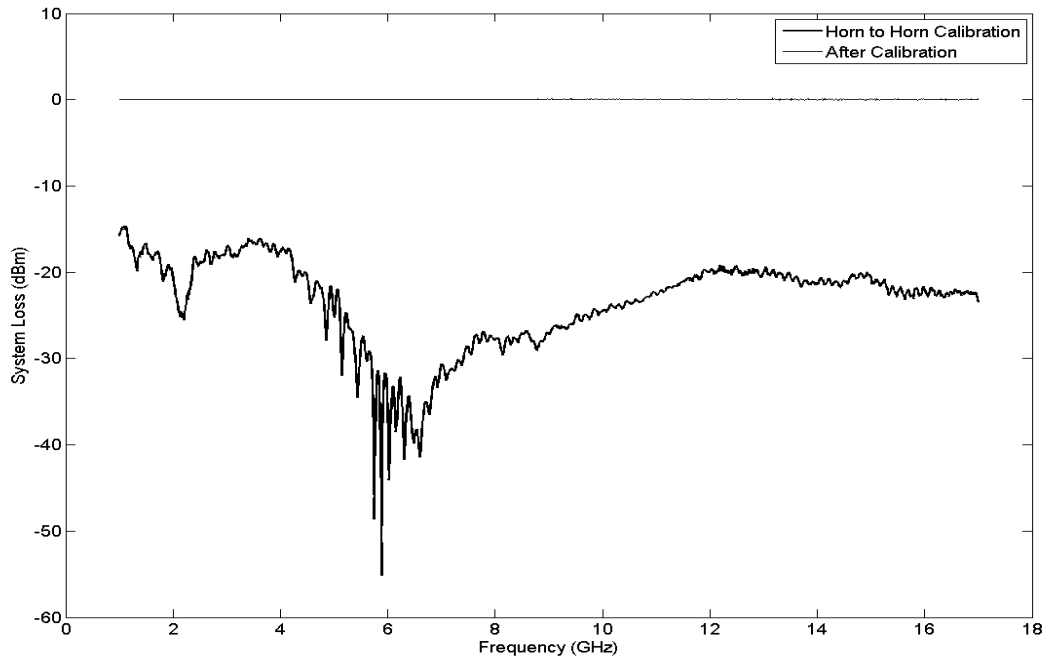


Figure 4. The thick black line shows the noise of the system, measured from the top horn to the bottom horn before calibration. After the calibration was complete, the thin black line shows that the majority of the noise has been calibrated out.

Next, the error due to tray replacement into the permanent test fixture was measured. 200 μ L of 1X TE buffer was placed inside of a cell-culturing tray and then placed within the permanent test fixture.

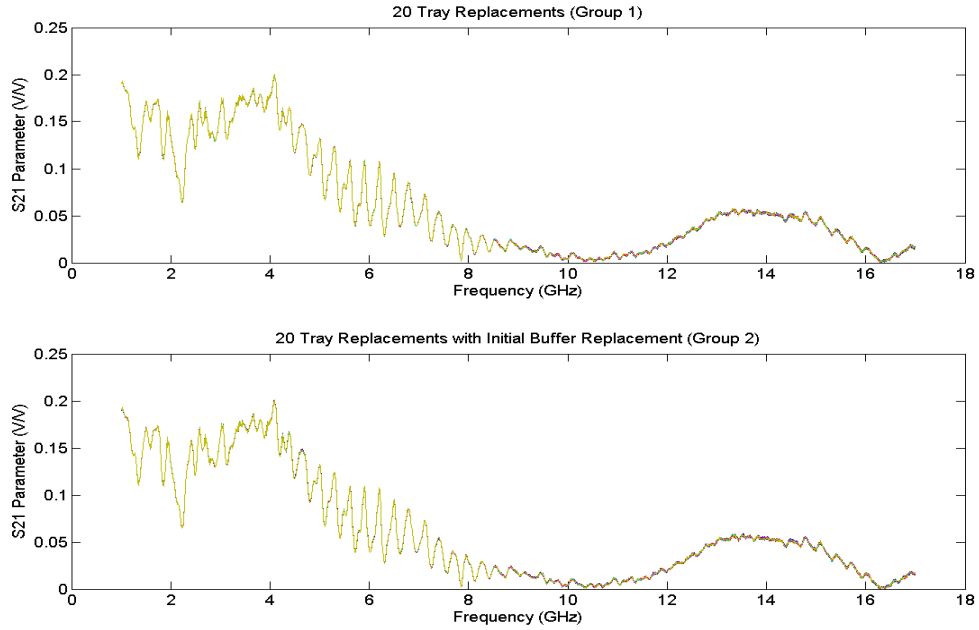


Figure 5. The top picture shows the first set of 20 tray replacements. After each run, the tray was taken out of the permanent test fixture and then immediately placed back into the test fixture. The bottom set is after initial buffer replacement and 20 sweeps with tray replacement in between each sweep.

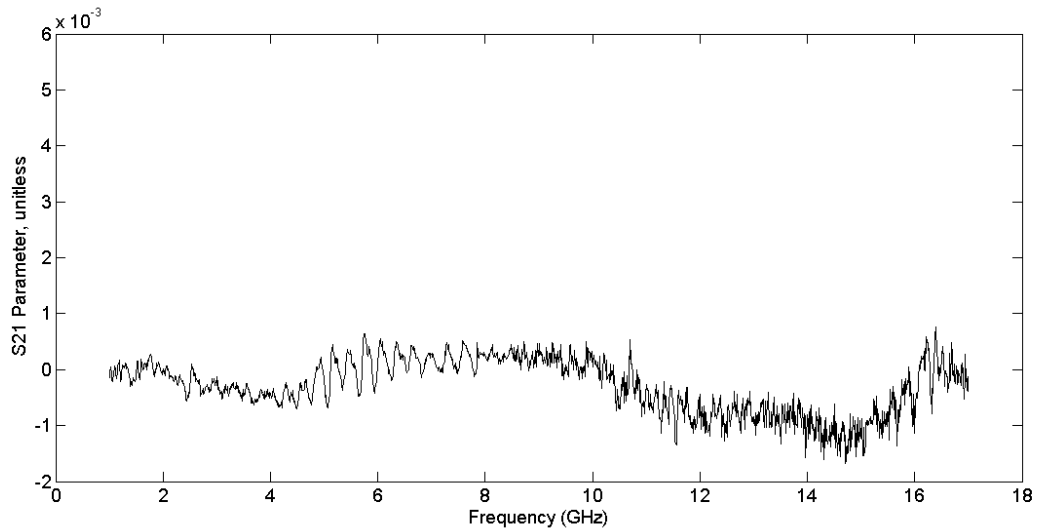


Figure 6. The difference of the means of the two populations (Figure 5) to find greatest error. A difference of the means centered on 0 concludes that the two groups of 20 runs were similar.

Figure 7 shows the calculated standard deviation of physically taking out and replacing the cell culturing tray into the permanent test fixture 20 times for group 1. Then group 2 calculates the standard deviation of replacing buffer into the tray and replacing the cell-culturing tray another 20 times.

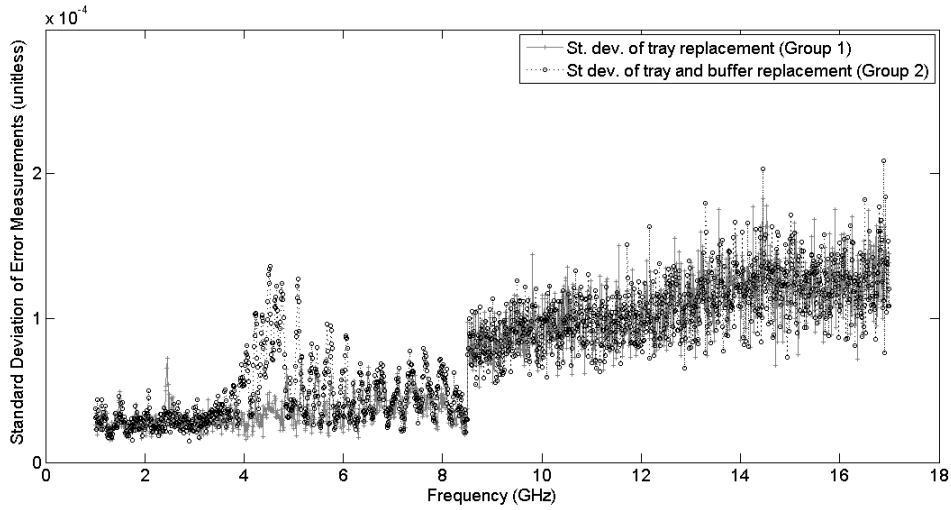


Figure 7. The standard deviation calculated from the tray replacement experiments that measured the amount of change due to replacement of the tray into the test fixture and the refilling of buffer within the tray.

4.3. Revised Experiment Results

These experimental results are from a 1.0-17.0 GHz sweep.

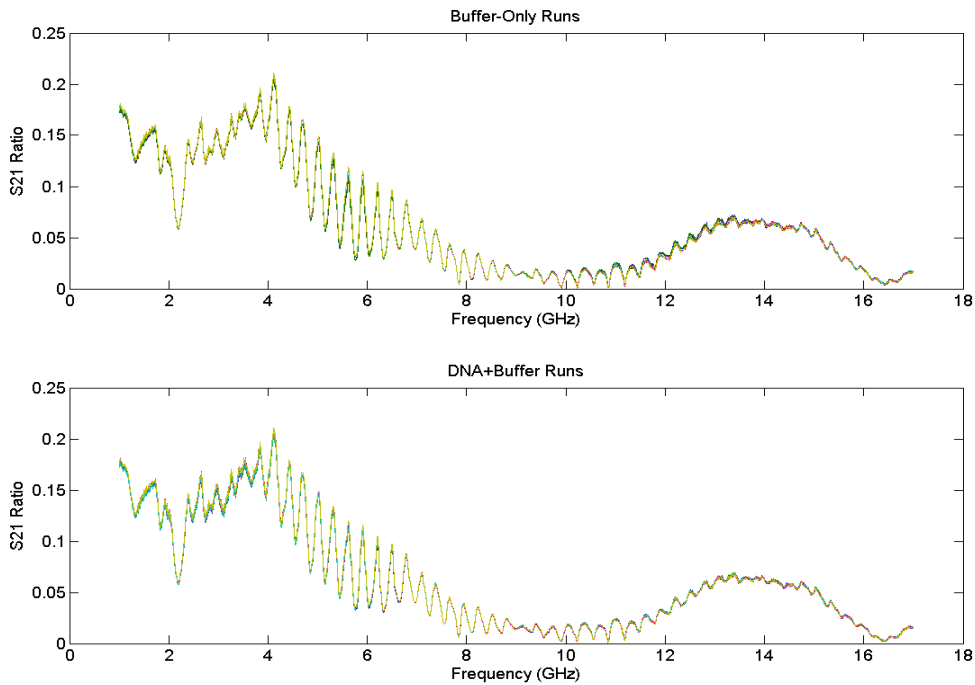


Figure 8. The top group is 20 sweeps with the tray containing only buffer. The bottom group is the 20 sweeps with the tray containing a mixture of DNA and buffer.

The top graph shows the 20 sweeps from 1.0-17.0 GHz while the tray contained 200 μ L of 1X TE buffer only. The bottom graph shows the raw data from the 20 runs of the tray containing DNA and buffer. All the runs are very similar in waveform and amplitude. Separations in the runs can be seen in the 2.0-4.0 GHz range and the 12.0-14.0 GHz range in both sets of data. Since these calculations are a magnitude smaller than even at maximum error, a DNA signal could not have been produced by any introduced systematic error.

To better understand where the DNA and buffer sweeps were different from the buffer only sweeps, a difference of the means was calculated. First, the point-by-point mean of both sets of 20 sweeps was calculated. Next, the mean of the DNA and buffer minus the mean of the buffer only was taken and represented in Figure 9. If there was no change between the two sets of data, then the difference of the means would be 0.

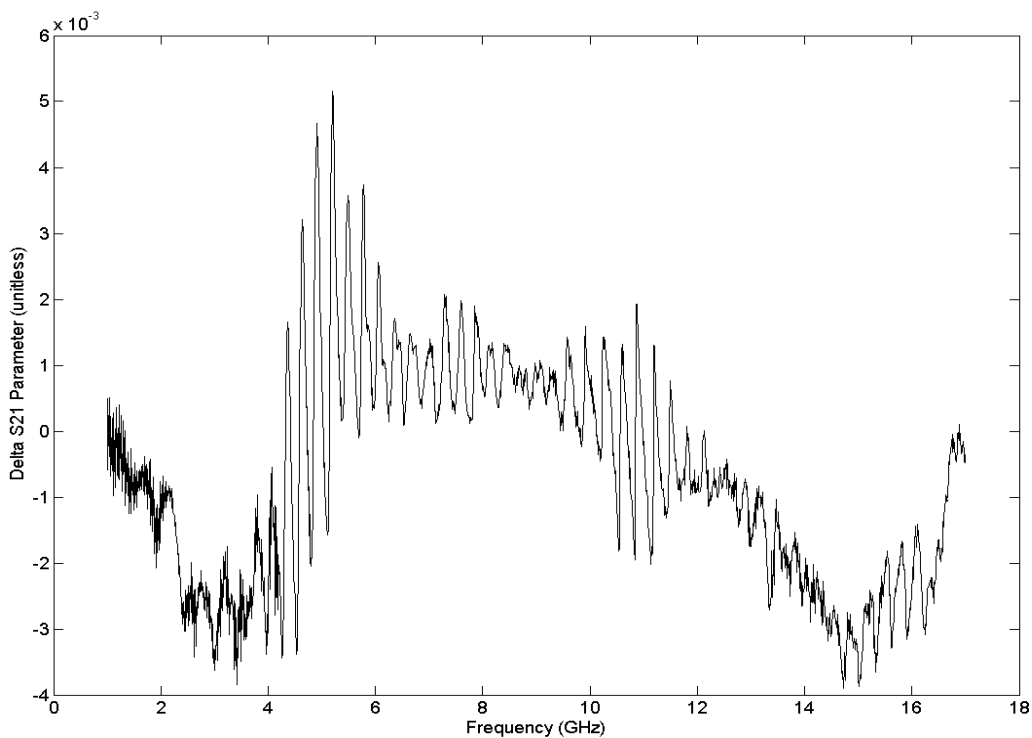


Figure 9. Above shows the means of the DNA plus buffer sweeps (20 sweeps) and subtracting the mean of the sweeps that contained buffer only (20 sweeps).

Finally, to determine if any frequencies had an increased rate of interaction with Lambda DNA, a two-tailed t test was run using MATLAB. An array of p-values was calculated by the t-test. If the p-value

was less than 0.05 it was determined to be a frequency of interest. Figure 10 shows all p-values that were less than 0.05 and where the p-value occurred with respect to frequency.

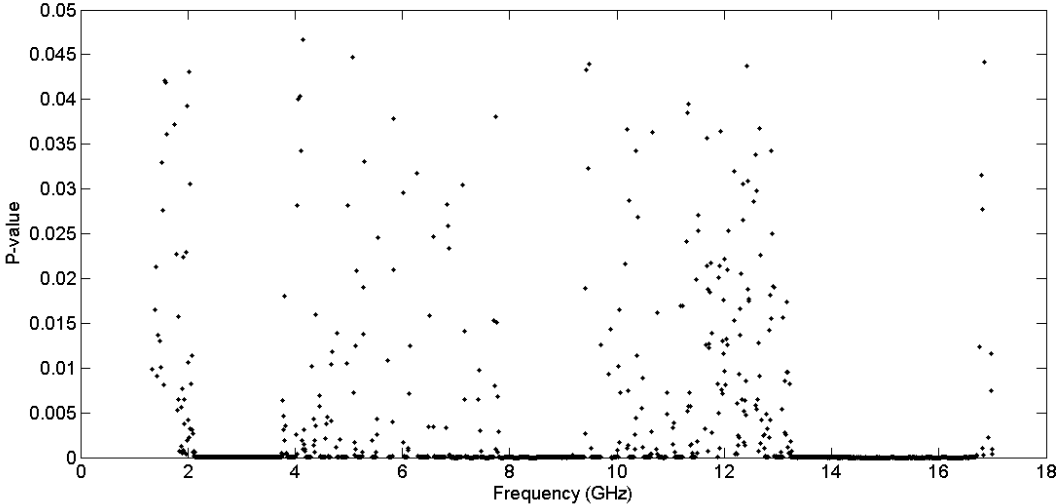


Figure 10. Above is a plot of p-values that meet the criteria of being less than 0.05. Any p-value that was less than 0.05 was plotted with respect to its frequency location.

5. DISCUSSION

Based on the experiments that were run, the results suggest areas of interaction between Lambda DNA and RF energy have been observed. Even at the low power level of 0 dBm, interaction of certain RF energy with Lambda DNA were detected. Since the RF energy was kept at a very low power level, heating of the DNA molecule was not the cause of the interaction. Also, the implementation of the permanent test fixture made it possible to create reproducible results with minimal error. Since the maximum amount of error seen due to the system and human error was along the magnitude of 10^{-4} , the signal due to Lambda DNA cannot be attributed to this error. Certain regions, between 14.0-16.0 GHz, measured the greatest error and therefore the resulting DNA signal may be affected. Based on the calculated p-values, the frequencies of greatest interaction with Lambda DNA occurred between: 2.15-3.72 GHz, 7.82-9.37 GHz, and 13.29-16.68 GHz.

An interesting phenomenon that occurs in the data sets is the wave oscillations. Although it is not certain what causes these oscillations, it was concluded that they may be a result of RF energy hitting the partial resonance modes of the Lambda DNA.

There is a strong possibility that more significant data points could be found if the full power of statistical tests were used because of the data having a repeatable waveform and structure. A bootstrapping method would be able to account for individual differences in each sweep and create tighter confidence intervals around the observed data.

A limitation of this work is the fact that a pre-experimental DNA structure was not determined. If the structure of the Lambda DNA had been recorded before experimentation began, then a post-experimental structure could have been compared. This would have given graphical results if the structure of the DNA had changed.

Any future experimentation on this research will involve a more extensive look into how the DNA molecule changes. This will include observing the Lambda DNA's structure pre and post experiment. Also, more information about the physical and chemical changes of the Lambda DNA could be observed by performing assays to measure degradation rates and DNA viability after RF exposure. These findings could give quantitative results about the scale on which DNA is being affected by the RF energy exposure.

Since there are multiple variables in this research procedure, some of the specifications could be changed and results could be compared to the present findings. One factor that could be changed when repeating this experiment would be to increase the transmit power of the top horn to 10 dBm. Since 0 dBm is the lowest amount of power that can be transmitted by the horn, a different signal may be observed if a greater amount of power is being transmitted through the DNA solution. Another change could be to use a 12 well cell-culturing tray instead of a 96 well tray. It may be observed that the 96 wells introduce a certain oscillations of noise due to reflections or scattering in the received wave due to the concavity of the wells in the tray, and the 12 well tray may introduce different noise oscillations in the signal.

Finally, being able to perform a repeated experiment using genomic DNA instead of Lambda DNA would lead to answering fundamental questions about technology affecting DNA. This would be insightful because the exact human genes affected by RF energy exposure would be measured through analysis, such as gene sequencing. This would lead to answering whether RF energy positively or negatively affects DNA. In all future work a more rigorous method of statistical analysis will be used. Using a more powerful statistical method will improve the accuracy of locating frequencies of interest.

6. CONCLUSION

Overall, some frequencies in the GHz range have been tested and were proven to fall outside that maximum error range by having a p-value less than 0.05. This leads to the conclusion that Lambda DNA does interact with RF energy between the frequencies of 1.0-17.0 GHz. By taking frequency sweeps over a range of RF energy, this research was able to observe changes of absorption/reflection patterns on a wider spectrum than previous studies that only targeted one frequency. Specific regions have been identified where the Lambda DNA and buffer solution have a greater tendency to absorb RF energy.

This shows that the experimental protocol was repeatable and strengthens the case for reproducibility of the results. Even when testing instruments were changed, similar resulting waveforms were observed. Since the results could be replicated, this gives assurance that the experimental protocol is a sound framework in which future experiments can expand on.

This research has built a framework that a wide variety of research fields can expand on. The future work of this research has many possibilities because there are many unknowns about how RF energy interacts with all biological organisms on a molecular level. It will be important to identify any negative effects that RF energy can cause to molecules such as DNA. If RF energy can be harnessed to create a positive change of molecular function on DNA, this would revolutionize health care.

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