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Testing Bacterial Antibiotic Production under Carbohydrate and Protein Starvation

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SENIOR THESIS APPROVAL

This Honors thesis entitled

"Testing Bacterial Antibiotic Production under Carbohydrate and Protein Starvation"

written by

Briley Baird

and submitted in partial fulfillment of the requirements for completion of the Carl Goodson Honors Program meets the criteria for acceptance and has been approved by the undersigned readers.

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Testing bacterial antibiotic production under carbohydrate and protein starvation

An honors thesis by Briley Baird

Ouachita Baptist University

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Summary

Bacteria produce antibiotics when they are under stress, including starvation stress. Bacteria were tested under carbohydrate and protein starvation against Bacillus subtilis and Escherichia *coli* (due to the respective Gram positivity and negativity), in order to check for antibiotic production. The bacteria being tested were isolated by past Microbiology classes and stored in a -80°C freezer in the basement of Jones Science Center at Ouachita Baptist University. These test bacteria were grown on tryptic soy agar (TSA) to produce isolated bacterial colonies. Samples of isolated test colonies were then grown under conditions of carbohydrate starvation (M9 salts agar with 0.1% glucose and 1% peptone) or protein starvation (M9 salts agar with 1% glucose and no peptone) in the presence of Bacillus subtilis and Escherichia coli. After five days of incubation at 28°C, antibiotic production by test bacteria was determined by measuring growth inhibition of B. subtilis or E. coli. Of the 27 bacteria tested, 10 were found to consistently produce the zones of inhibition. Three produced zones of inhibition under all conditions, two did so only under carbohydrate starvation conditions, and none only under protein starvation. Also, two bacteria only responded when grown in the presence of *B. subtilis*, while no bacteria responded when grown solely in the presence of E. coli.

Introduction

Bacteria are evolving. Every day, these tiny prokaryotes fight for survival against the multitudes of antibiotics specifically designed to kill them. Many lose the battle and die off. A lucky few, however, possess a genetic mutation that makes them resistant to the antibiotic. As the regular bacteria are killed by the antibiotics, this mutation allows the resistant bacteria to survive and thrive. Over time, the bacterial population changes to become resistant to antibiotics (Baym et al., 2016). Unfortunately for us, this process has created bacteria that are no longer affected by what we have always used to combat them. In keeping ourselves healthy, we have created antibiotic-resistant bacteria.

In August of 2016, a woman checked into a Reno, Nevada, hospital shortly after returning from India (Dall, 2017). Doctors discovered she was infected with a bacterium best known for causing urinary tract infections, *Klebsiella pneumoniae* (Branswell, 2017). In September of 2016, the woman died (Dall, 2017). The was due to the fact that the specific strain of *Klebsiella pneumoniae* was resistant to every single antibiotic available (Dall, 2017). Around the same time as the woman's death, the UN expressed an unprecedented amount of interest in combatting the global antibiotic resistance problem (Napolitano, 2016). Although this woman's infection may seem unique in being resistant to every available antibiotic, antibiotic resistant infections—bacterial infections untreatable by one or more antibiotics are isolated that can comhat this growing issue, different species of bacteria will continue to become more resistant to our existing medicines until incidences like the Nevadan woman's death become commonplace.

For my thesis, I have contributed to a solution for this rising problem. Bacteria secrete antibiotics to inhibit the growth of other species of bacteria when they are starved (Cordero et al.,

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2012). I have used this competition mechanism to my advantage to test the previously isolated antibiotic-producing bacteria for the ability to kill off known bacteria, specifically *Bacillus subtilis* and *Escherichia coli*. These bacteria were selected because they are common examples of the Gram + and Gram - bacteria, respectively. They were also selected because they are safe to handle.

Over the course of these experiments, I grew the test bacteria under carbohydrate and protein starvation. Some bacteria produced antibiotics to starvation of carbohydrates, while others respond to the starvation of proteins (Ochi and Ohsawa, 1984), (Gallo and Katz, 1972). To ensure the production of their antibiotics, I starved them of both nutrients, separately, to make sure they are affected. These bacteria wore tested against *B. subtilis* and *E. coli* because they are examples of the two most common types of bacteria. *B. subtilis* is Gram positive, whereas *E. coli* is Gram negative. Gram positive and Gram negative bacteria have different cell wall structures, and, resultantly, have different susceptibilities to antibiotics. If the antibiotics killed either, or both, of these bacteria, then the antibiotics could potentially work against antibiotic-resistant bacteria of the same type (Gram + vs Gram -).

In addition to this, I also used my thesis to discuss the effects of bacteria and biofilm formation on contact lenses. Biofilms are groups of bacteria surrounded by a mucus-like matrix . If biofilms form on contacts, that could easily lead to bacterial infections in the eyes (Bruinsma et al., 2001).

Materials and Methods

Bacteria

Twenty-seven test bacteria were obtained from the -80⁻⁻ freezer located in the basement of Jones Science Center. These 27 bacteria had been isolated from soil samples by previous microbiology classes at Ouachita Baptist University, and had all been found to successfully produce antibiotics under certain conditions. However, they had not ever been tested under the set of conditions used in these experiments. These bacteria were: Hall, Feather, JLM, Red, Compton, Jackson, Hargis, Lewis, Small, Ach!, Run!, Bubbles, Janet, Smith, Darquez, Ewok, Lafawnduh, Blaneece, Games, LEO, Jamison, HegiBarfield, Archer, HolcombRubin, S2B1, S4B1, and S6B3.

<u>Media</u>

There were four different kinds of media used in these experiments. Tryptic Soy Agar (TSA) was used. Tryptic Soy Broth (TSB) was used. These were used for routine upkeep of the test bacteria. For the actual swab patches, M9 salts salts 1% Glucose – 0% Peptone Agar and M9 salts 0.1% Glucose – 1% Peptone Agar were used.

Growing Test Bacteria from Frozen Samples

Samples of all the needed bacteria were preserved in a $-80\Box$ freezer since their original isolation. From these samples, the bacterial colonies needed for testing purposes were grown. Small amounts the frozen bacteria were streaked onto individual TSA plates. This was done in a sterile environment, created by the updraft of a flame from a Bunsen burner. They were streaked in the pattern depicted in Figure 1. The streak plates were incubated for five days at $25\Box$.

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Afterwards, the freshly grown colonies were used to grow two other TSA streak plates labeled "primary" and "back-up." All of the plates were then stored in a $4\sqcap$ refrigerator.



Swab patches

Following the growth of the streak plates, swab patches were made. In order to plate the background bacterium on the agar, *B. subtilis* and *E. coli* were grown in TSB for 24 hours at 37°C before making the swab patches. After the 24 hours, sterile cotton swabs were used to cover the entire surface of the agar with the desired bacterium. The agar plates were then allowed to sit for 15 minutes at room temperature to allow the bacteria to anchor themselves to the agar.

After the waiting period, the test bacteria were plated in a small square approximately 5mm in diameter with a sterilized loop on each of the four variations of medium-background bacteria combinations. Six bacteria were plated on each medium-background bacterium combination on each plate, creating the swab patches. They were plated in the pattern shown in Figure 2, with each test bacterial patch not being in direct contact with any other test bacterial

patch. This entire process was also done beneath a Bunsen burner updraft to increase sterility. The swab-patch plates were then incubated for five days at $25\square$. After incubation, the swab-patch plates were examined for zones of inhibition around the different test bacteria. The diameters of each bacterial patch were measured as well as the diameters of each zone of inhibition plus bacterial patch, when applicable. All results were recorded, and each test bacterium was tested under all medium-background bacterium combinations three times for triplicate results.

The test bacteria were plated on two types of agar (M9 salts 1% Glucose – 0% Peptone and M9 salts 0.1% Glucose – 1% Peptone) in the presence of two types of background bacteria (*Bacillus subtilis* and *Escherichia coli*) for a total of four different kinds of swab patches: M9 salts 1% Glucose – 0% Peptone agar with *B. subtilis* background bacteria M9 salts 1% Glucose – 0% Peptone agar with *E. coli* background bacteria, M9 salts 0.1% Glucose – 1% Peptone with *B. subtilis* background bacteria, and M9 salts 0.1% Glucose – 1% Peptone with *E. coli* background bacteria.



Figure 2. This figure is a photograph of an incubated spread patch. As seen in the photo, three horizontal lines and three vertical lines are drawn on the casing to create twelve separate areas. Six different bacteria are plated with a sterile ring on each spread patch, making sure to place the diagonal from each other so that none of the bacterial squares are bordering each other. As shown in the photo, the bacteria are plated in a square shape. When the bacteria produce zones of inhibition, the fan out from the bacteria in circular shape, as seen with the bacterium labeled Compton.

Each of the 27 test bacteria were assayed using swah-patch assays on each of the four medium-background hacterium combinations: M9 salts 1% Glucose – 0% Peptone agar with *B. subtilis* background, M9 salts 1% Glucose – 0% Peptone agar with *E. coli* hackground, M9 salts 0.1% Glucose – 1% Peptone with *B. subtilis* background, and M9 salts 0.1% Glucose – 1% Peptone with *E. coli* background. All of these tests were performed in triplicate.

Of the 27 bacteria, 17 did not produce antibiotics under any of the four mediumbackground bacterium combinations. The 17 that did not produce antibiotics are: Hall, Feather, JLM, Lewis, Ach!, Run!, Bubbles, Janet, Smith, Darquez, Ewok, Lafawduh, Games, LEO, HegiBarfield, HolcombRuhin, S2B1, and S6B3. The 10 bacteria that produced antibiotics under one or more sets of test conditions are: Red, Compton, Jackson, Hargis, Small, Blaneece, Jamison, Archer, S2B1, and S6B3. The results from Trials 1, 2, and 3 are depicted in Tables 1, 2, and 3, respectively.

By averaging the results from the three trials, mean values for the antibiotic production zones created by the 10 bacteria were calculated. These values are depicted in Figure 3. Of the 10 bacteria that produced zones of inhibition, Compton, Jackson, Jamison, S2B1, and S6B3 produced antibiotics that inhibited both B. subtilis and E. coli under both peptide and carbohydrate starvation conditions. Red and Small both inhibited B. subtilis under carbohydrate and protein starvation, but only inhibited E. coli under peptide starvation. Hargis and Archer inhibited the growth of the *B. subtilis* under protein starvation and peptide starvation. Blaneece responded to two of the test conditions, inhibiting growth of both *E. coli* and *B. subtilis* when starved of peptides but not when starved of carbohydrates.

| | 0.1% Glucose - 1% Peptone | | | | | 1% (| <u> Slucose – (</u> | 0% Peptone | |
|----------|----------------------------|------|-----------------|------|----------|---------------------|---------------------|-----------------|-----|
| | B. subtilis bckgrnd | | E. coli bckgrnd | | 100 | B. subtilis bckgrnd | | E. coli bckgrnd | |
| Name | <u>Bacteria</u> | Zone | Bacteria | Zone | Name | Bacteria | <u>Zone</u> | <u>Bacteria</u> | Zo |
| Red | 9mm | 15mm | 10mm | none | Red | 7mm | 14mm | 10mm | 28 |
| Comptor | n 4mm | none | 6mm | none | Compton | 6mm | 14mm | 7mm | 14 |
| Jackson | 8mm | 11mm | 10mm | 13mm | Jackson | 6mm | 9mm | 9mm | 201 |
| Hargis | 5mm | none | 11mm | none | Hargis | 8mm | 9mm | 7mm | no |
| Small | 7mm | none | 8mm | none | Small | 5mm | none | 9mm | 13 |
| Blaneece | e Smm | none | 6mm | none | Blaneece | 8mm | 10mm | 10mm | no |
| Jamison | 8m m | 23mm | 7mm | 19mm | Jamison | 4mm | 11mm | 7mm | 10 |
| Archer | 8mm | 16mm | 5mm | none | Archer | 5mm | 10mm | 12mm | noi |
| S2B1 | 5mm | none | 5mm | none | S2B1 | 4mm | 6mm | 5mm | 25r |
| CCD2 | 11000 | 10 | 0.000 | 12mm | S6B3 | 5mm | 9mm | 10mm | 25r |

Table 1. This table depicts the Trial 1 results of the 10 bacteria that produced antibiotics under any of the four sets of test conditions. The measurements listed refer to the diameter of the bacterial growth on the swab patches (denoted "Bacteria"), and, when applicable, the diameters of the bacterial growth on the swab patches plus the zone of inhibition (denoted "Zone"). "Glucose Starvation Conditions" refers the swab patches with M9 salts0.1%G-1%P Agar. "Protein Starvation Conditions" refers to the swab patches with M9 salts 1%G-0%P Agar. Bacteria are arranged in the order that they were tested.

| | | | | | | | | | _ |
|---------------------------|---------------------|------|-----------------|-------------|-------------------------------|---------------------|--------------|-----------------|-----|
| 0.1% Glucose - 1% Peptone | | | | | Protein Starvation Conditions | | | | |
| | B. subtilis bckgrnd | | E. coli bckgrnd | | | B. subtilis bckgrnd | | E. coli bckgrnd | |
| <u>Name</u> | Bacteria | Zone | Bacteria | <u>Zone</u> | <u>Name</u> | Bacteria | Zone | Bacteria | Zon |
| Red | 8mm | 10mm | 10mm | none | Red | 8mm | 11mm | 9mm | 28n |
| Compton | 8mm | 10mm | 11mm | none | Compton | 8 mm | none | 1 1 mm | 22n |
| Jackson | 8mm | 16mm | 15mm | 17mm | Jackson | 7mm | 8mm | 10mm | 25m |
| Hargis | 8mm | 12mm | 10mm | none | Hargis | 8mm | 14mm | 7mm | non |
| Small | 13mm | 19mm | 10mm | none | Small | 9mm | 13mm | 8mm | 15m |
| Blaneece | 7mm | none | 8mm | none | Blaneece | 11mm | 13mm | 20mm | 43m |
| Jamison | 8mm | 20mm | 7mm | 16mm | Jamison | 9mm | 17mm | 7mm | 8mr |
| Archer | 7mm | 21mm | 9mm | none | Archer | 9mm | 19m m | 1 2 mm | non |
| S2B1 | 7mm | 17mm | 11mm | 25mm | S2B1 | 9mm | 20mm | 11mm | 33m |
| 56B3 | 12mm | 28mm | 11mm | 18mm | S6B3 | 11mm | 2 1mm | 1 2 mm | 26m |
| | | | | | | | | | |

Table 2. This table depicts the Trial 2 results of the 10 bacteria that produced antibiotics under any of the four sets of test conditions. The measurements listed refer to the diameter of the bacterial growth on the swab patches (denoted "Bacteria"), and, when applicable, the diameters of the bacterial growth on the swab patches plus the zone of inhibition (denoted "Zone"). "Glucose Starvation Conditions" refers the swab patches with M9 salts0.1%G-1%P Agar. "Protein Starvation Conditions" refers to the swab patches with M9 salts 1%G-0%P Agar. Bacteria are arranged in the order that they were tested.

| 0.1% Glucose - 1% Peptone | | | | | Protein Starvation Conditions | | | | |
|---------------------------|---------------------|-------------|-----------------|------|-------------------------------|---------------------|--------------|-----------------|------|
| | B. subtilis bckgrnd | | E. coli bckgrnd | | | B. subtilis bckgrnd | | E. coli bckgrnd | |
| Name | Bacteria | <u>Zone</u> | Bacteria | Zone | <u>Name</u> | Bacteria | Zone | Bacteria | Zone |
| Red | 12mm | 18mm | 9mm | none | Red | 9mm | 16mm | 12mm | 32mm |
| Compton | 10mm | 13mm | 12mm | 13mm | Compton | 9mm | none | 9mm | 22mm |
| Jackson | 12mm | 19mm | 1 3mm | 16mm | Jackson | 8mm | 1 4mm | 12mm | 29mm |
| Hargis | 9mm | 21mm | 10mm | none | Hargis | 9mm | 21mm | 7mm | none |
| Small | 10mm | 16mm | 10 m m | none | Small | 10mm | 14mm | 13mm | 20mm |
| Blaneece | 1 1 mm | none | 8mm | none | Blaneece | 8mm | 10mm | 17mm | 40mm |
| Jamison | 1 0mm | 33mm | 9mm | 18mm | Jamison | 9mm | 17mm | 7mm | none |
| Archer | 8mm | none | 9mm | none | Archer | 8mm | 11mm | 7mm | none |
| S2B1 | 10mm | 20mm | 10mm | 25mm | S2B1 | 9mm | 21mm | 11mm | 35mm |
| S6B3 | 14mm | 24mm | 13mm | 15mm | S6B3 | 13mm | 22mm | 14mm | 24mm |

Table 3. This table depicts the Trial 3 results of the 10 bacteria that produced antibiotics under any of the four sets of test conditions. The measurements listed refer to the diameter of the bacterial growth on the swab patches (denoted "Bacteria"), and, when applicable, the diameters of the bacterial growth on the swab patches plus the zone of inhibition (denoted "Zone"). "Glucose Starvation Conditions" refers the swab patches with M9 salts0.1%G-1%P Agar. "Protein Starvation Conditions" refers to the swab patches with M9 salts 1%G-0%P Agar. Bacteria are arranged in the order that they were tested.



Figure 3. The average diameters of the bacterial patches combined with the zones of inhibition over the three trials were calculated for all four sets of conditions (M9 salts0.1% Glucose – 1% Peptone with B. subtilis background bacteria [BsCarbStrv], M9 salts 1% Glucose – 0% Peptone agar with B. subtilis background bacteria [BsPepStrv], M9 salts0.1% Glucose – 1% Peptone with E. coli background bacteria [EcCarbStrv], and M9 salts 1% Glucose – 0% Peptone agar with E. coli background bacteria [EcCarbStrv], and M9 salts 1% Glucose – 0% Peptone agar with E. coli background bacteria [EcCarbStrv], and graphed in this figure. Standard Error is accounted for and depicted in the graph as well.

Discussion

This research began with 27 test bacteria that had been deemed strong candidates to produce antibiotics under starvation conditions by previous microbiology classes. In the end, only 10 of these actually did so. By no means, however, does that make this research a failure. Quite the opposite is true. Because of this research, these 10 bacteria are now known to definitively produce antibiotics under at least one of the four sets of medium-background bacterium conditions tested. Of the two kinds of starvation tested, all 10 of the bacteria produced antibiotics when starved for proteins. Nine out of the 10 responded to carbohydrate starvation. Out of these nine, four (Red, Compton, Jackson, and S2B1) consistently produced larger zones of inhibition when starved of protein starvation than when starved of carbohydrates. Because of this, it can be concluded that protein starvation is a slightly more effective method to induce antibiotic production in most bacteria than carbohydrate starvation. This suggests that proteins may be more significant for bacterial survival than carbohydrates. Bacterial cells combat protein starvation using the stringent response. This data suggest that the stringent response might be more effective than the catabolite repression, bacterial cells' mechanism to combatting carbohydrate starvation.

Overall, the bacteria inhibited the growth of the *B. subtilis* more effectively than *E. coli*, with two of the bacteria not producing zones of inhibition against *E. coli* under either starvation condition and three bacteria (Small, Red, and Blaneece) only producing zones of inhibition against *E. coli* when starved of proteins instead of carbohydrates. This was to be expected, as *E. coli* is a Gram negative bacterium. The presence of the extra outer membrane that causes it to be Gram negative increases the bacterium's resistance to antibiotics. On the other hand, *B. subtilis* is Gram positive, making it more susceptible to antibiotics than *E. coli*.

All 10 of the bacteria that proved to be effective antibiotic producers under some or all sets of starvation/background combination conditions could, after further experimentation, potentially be used to fight the rising problem that is antibiotic-resistant bacteria. The antibiotics that the 10 test bacteria produced to inhibit the growth of *E. coli* and/or *B. subtilis* could be harvested and used against antibiotic-resistant bacteria. Before this could be done, however, more experimentation needs to be done. The next immediate step will be to test these newfound antibiotics for eukaryotic toxicity. This will be done by growing the test bacteria in the presence of eukaryotic cells in order to see if the eukaryotes remain viable. If the test bacteria prove toxic, testing with them will cease. If the bacteria prove safe for eukaryotic cells, then bacterial genome sequencing will follow. This will be done by RNA sequencing. Since these test bacteria were simply harvested from soil, it's possible that some or all of the bacteria have already been discovered. Sequencing is needed to determine if this is the case.



Biofilms and Contact Lenses

Have you ever stepped on a rock in a rushing river and noted its slippery surface? Have you ever run your tongue over your teeth after going a little too long between brushes and felt an extra layer of slickness? Have you ever looked out over a small pool of water only to see a layer of green pond scum covering patches of the surface? If your answer to any of these is yes, then you're familiar with biofilms. Caused by the accumulation of certain kinds of bacteria, biofilms are found all throughout life (Watnick and Kolter, 2000). Biofilms, which act as anchoring mechanism with added bonus of increased antibiotic resistance, are a coalition of bacteria embedded in a secreted polymeric matrix (Watnick and Kolter, 2000). Because of this protection, bacteria that form into biofilms are often more of a threat to humans than bacteria that do not form biofilms, and one particular facet of life where biofilms can cause major damage is contact lenses.

Biofilms are protective coverings that some kinds of bacteria produce in order to help them stay anchored in place, trap food, and surround themselves with other species of bacteria that they can benefit from being in close proximity with. While not the main focus of biofilms, an added bonus is their increased resistance to antibiotics. In order for hiofilm formation to commence, large amounts bacteria must become densely packed on a surface (Donlan, 2002).

Once enough bacteria grow or migrate to one spot, quorum signaling will initiate the biofilm formation (Miller and Bassler, 2001). Quorum signaling is a group behavior signaling mechanism that bacteria can use to communicate with each other (Miller and Bassler, 2001). Biofilms begin as a single species, but over time, other species are incorporated into the biofilm. Because many biofilms contain multiple kinds of bacteria, it's imperative for the biofilm synthesis stimuli to be capable of interspecies communication (Watnick and Kolter, 2000). While quorum signaling is mainly used between bacteria of the same species, intraspecies communication is still possible. Once stimulated, gene regulation is altered, and the bacteria begin to secrete a matrix composed of mainly polysaccharide materials (Donlan, 2002). The matrices secreted from each individual bacterium combine with each other to form a larger, all-encompassing matrix that draws in nearby fungi, protozoa, inorganic objects, and everything it touches (Donlan, 2002). Figure 1 is a close-up photo of a biofilm.

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Figure 1. This figure shows a photograph taken of individual bacterial cells anchored to a surface and each other. The matrix visible around the individual cells is the secreted biofilm components that have merged from each bacterium to form a larger biofilm.

Many different conditions determine if biofilms can form. Perhaps the most necessary condition is the presence of an aqueous environment (Donlan, 2002). The solid-liquid interphase provides the ideal parameters for biofilm attachment and formation (Donlan, 2002). Other factors that affect the attachment of microbes, and, consequently, the formation of biofilms include temperature, levels of nutrients present, pH, and ionic strength (Donlan, 2002). If any of these factors vary outside of what certain species of bacteria can survive in, no microbes will anchor there in the first place.

The biofilms themselves create a largely self-sufficient environment for bacteria (Donlan, 2002). Because the biofilms are often composed of multiple species of bacteria, nutrients can be recycled between the species to maintain life (Donlan, 2002). That being said, it would not be safe to assume that the bacteria never face any internal threats. It's not uncommon that the bacteria will multiply too rapidly and deplete the nutrients from the area (Watnick and Kolter, 2000). When this happens, it becomes necessary for some of the bacteria to migrate to a new, nutrient-rich area. When this overcrowding occurs, quorum signaling will cause some of the bacteria to shift into a mobile form and leave the biofilm in search of a new home (Donlan, 2002). This is the most common ideal life cycle of bacteria inside a biofilm, which is depicted in

Figure 2. However, sometimes the bacteria arc spread to new areas in different ways. Sometimes, outside forces will break off a piece of the biofilm. When this happens, the bacteria can reattach themselves and start over, growing a fresh biofilm at a new location (Donlan, 2002). One environment that biofilms particularly thrive in is the semi-aqueous surface of modern day soft contact lenses (Bruinsma et al., 2001).

The concept of contact lenses has been around for many years. Leonardo da Vinci is credited with coining the idea for contacts way back in 1508 ("A Brief History", 2015). Despite the early schematics, the first contact lenses, which were made from glass and covered the entire eye, were not actually created until 1887 ("A Brief History," 2015). In 1939, contacts shifted to be made from plastic, but it wasn't until 1948 that the lens design changed to only cover the cornea instead of the entire sclera ("A Brief History," 2015).



Figure 2. This figure depicts the life cycle of a biofilm. The upper images are representations of the different steps while the lower images are actual photographs of biofilms at the various stages. Step one is the bacteria anchoring themselves to the surface. Step two is the individual colonies secreting their biofilms. Step three is the biofilms growing and spreading. Step four is the once the biofilms have combined and grown into one massive biofilm. Finally, step five shows some of the bacteria being sent out to colonize new areas once the current biofilm has reached maximum capacity.

In 1987, disposable soft contacts finally became available, and contacts remained relatively unchanged until 2002, when the first silicone hydrogel contacts became commercially available ("A Brief History," 2015). The silicone hydrogel contact lenses are the most common kind of contacts in today's society. Unfortunately, they are also the type of contacts that biofilms most easily form on.

Contact lens cases are ideal environments for biofilm formation since they often hold contact solution, creating a solid-liquid interphase (McLaughlin-Borlace et al., 1997). From that point, it is as easy as the biofilm bacteria shifting into their mobile form to travel from the lens case to the actual contact lens itself (McLaughlin-Borlace et al., 1997). The common soft contact is made of a hydrogel material (Kacker, et al, 2017). According to the Merriam Webster dictionary, a hydrogel is "a gel composed of usually one or more polymers suspended in water" (2017). This watery solid is the ideal environment for biofilms, so once they are introduced to a contact lens, the biofilm bacteria thrive.

If immediate care isn't taken, these biofilms can infect the eye when the contact lens user puts in their contacts. This can lead to a bacterial infection in the cornea of the eye (Bruinsma et al., 2001). Common ocular infections caused by biofilms are microbial keratitis, infiltrative keratitis, acute red-eye, and contact lens peripheral ulcers (Kacker et al., 2017). In the case of microbial keratitis, as many as 66% of cases can be linked to biofilm formation on contact lenses (Kacker et al., 2017). If not treated, bacterial infections of the eye can lead to corneal scarring, vision loss, or even permanent blindness (Kacker et al., 2017).

According to McLaughlin-Borlace et al., the best way to prevent contact lens contamination is to minimize handling of contacts (1997). Every time a user takes contacts in and out of their eyes and stores them in a lens case, the risk for some sort of contamination goes

up. The safest route would be for contact lens users to wear single-use contacts. This allows for a fresh, sterile pair every time they put in their contacts. If the user prefers some other kind of contact lens, then the kind of lens solution can make a big difference (Kacker et al., 2017). It's a common misconception that water can be used in place of lens solution. This is completely false, as even purified water does not contain the chemicals needed to break down bacteria and other things that may be adhering to the contacts (Heiting, 2017). According to Kacker et al., lens solutions that contain hydroxyalkylphosphonate, boric acid, edetate disodium poloxamine, and sodium borate are fairly effective for preventing the growth of biofilms on the lenses. Other lens solutions, such as those containing a cocktail of purified water, HPMC, CMC, EDTA and borax in sodium chloride base, are not as useful against biofilm formation, but they are still a much better alternative to using pure water as lens solution (Kacker et al., 2017).

Despite all of this, the best way to treat contact lenses or lens cases that form biofilms is disposal. Once biofilms form, they can be tricky to remove due to their sticky matrix and difficulty to penetrate (Kacker et al., 2017). It's always the safest route to throw away that case and pair of contacts for a new pair. When it comes to your vision, it's always better to be safe than sorry.

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