Iron acquisition by the dental pathogen aggregatibacter actinomycetemcomitans.

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University of Louisville

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IRON AQUISITION BY THE DENTAL PATHOGEN AGGREGATIBACTER ACTINOMYCETEMCOMITANS.

By

Porscha LaRai Jefferson
B.A., D.M.D, University of Louisville, 2012

A Thesis
Submitted to the Faculty of the
School of Dentistry of the University of Louisville
in Partial Fulfillment of the Requirement for the Degree of

Master of Science

Department of Oral Health and Rehabilitation
University of Louisville, School of Dentistry
Louisville, Ky

December 2012
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A Dissertation approved on

July 25, 2012

by the following Dissertation Committee:

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David Scott (Co-mentor)

Douglas Darling
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I am not the smartest, the fastest, or the best at anything but what I lack in natural ability I make up with hard work, and dedication. And it has been nothing short of hard work and dedication that has led me to accomplish my Masters degree. However due to the vast amount of work and time, dedication and perseverance were not enough. If it were not for my mentor, faculty, family, friends, and other fellow students this degree would have not been possible for me. It would still be just a dream. I would like to thank everyone involved in this accomplishment, whether it was just words of encouragement, being a listening ear, or showing me the same procedure for the 100th time because I lost focus once again. All of your actions were appreciated and I couldn’t have done this without everyone.

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Dr. Scott, and Dr. Darling thank for taking a chance on me. Thank you for pushing me while always being supportive. Thank you for this opportunity. Carlo what can I say. Thank you so much for all your help with this project. You were truly a big help in the lab and this wouldn’t have been possible without you either. You sparked my interest in research and helped me obtain a goal. Thank you. Blair, Whitney, Sri, Emily, Henri, Acesion, and Dolores thank you guys for all your support. Thank you for helping me out in anyway that you could. Your hardwork and help never went unappreciated. Thank you so much. Potempa lab thank you so much for giving me the original opportunity to participate in summer research. I will never forget the smell of *P. gingivalis*. Barbara, thank you for always pushing me to do more. John Houston, thank you for always being encouraging and uplifting in this never ending battle.
Dr. Lee Mayer thank you for always believing me and trying to make sure I did not over extend myself. You have been such an amazing inspiration to my dental and research career. You are truly a Grandpa to me and I am so thankful to have you in my life. Mrs. Jackie Williams, I couldn’t imagine doing this without you. Thank you for always making sure that I had everything I needed, helping me in anyway you can. Thank you for always being there for me. But most of all thank you for always being friend to me. I appreciate it more than you will ever know.

To my Dad, Carl Jefferson, and my Mom, Tina Phillips, thank you for always supporting me and believing me. Thank you for helping me in anyway you can. Thank you for always encouraging me and always telling me that there wasn’t anything that I couldn’t do. I love you guys. Thank you for all your support.

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ABSTRACT

IRON ACQUISITION IN THE DENTAL PATHOGEN AGGERGATIBACTER ACTINOMYCETEMCOMITANS

By

Porscha LaRai Jefferson

July 25, 2012

The dental pathogen *A. actinomycetemcomitans*, a Gram- negative organism, has been associated with aggressive forms of periodontitis. *A. actinomycetemcomitans* requires iron to grow. In the host, iron-binding proteins such as transferrin, lactoferrin, hemoglobin, and ferritin, maintain a low free-iron concentration. Microorganisms, however, have evolved complex systems to efficiently harvest iron.

The iron acquisition systems encoded in the genome of *A. actinomycetemcomitans* are likely tailored towards the specific survival strategies needed to survive in the oral biofilm. The objectives of this project were to determine the growth of *A. actinomycetemcomitans* in different iron sources and to examine the expression of the various iron uptake systems encoded by this organism under these conditions.

*A. actinomycetemcomitans* was grown in chemically defined media (CDM) with or without an iron chelator (dipyridyl (DIP), and supplemented with various iron forms to determine growth.
The growth of \textit{A. actinomycetemcomitans} was decreased in a dose-dependent manner when cultured in CDM without exogenous ferrous sulfate supplemented with DIP (CD/DIP). Growth of \textit{A. actinomycetemcomitans} was restored most efficiently when CDM/DIP was supplemented with hemin, less so with ferric citrate, and ferric chloride, and not with ferrous sulfate. Using these growth conditions, we examined the differential regulation of the numerous iron uptake systems encoded in the \textit{A. actinomycetemcomitans} genome.
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INTRODUCTION

Periodontal Disease

Periodontal disease is a chronic progressive disease that affects various structures of the periodontal tissues including the alveolar bone and periodontal ligament. Periodontal disease has been divided into two separate categories: Gingivitis and Periodontitis. Both diseases are inflammatory conditions that are encompassed in the term periodontal disease, however the affects of both diseases are quite different. Gingivitis, the initial stage of periodontal disease, is an inflammation of the gingival tissue characterized by swelling, redness, and bleeding upon probing of the gingiva (3). Although gingivitis is reversible following proper oral hygiene, if left untreated, it can progress into the more severe, chronic inflammatory condition, periodontitis. Periodontitis always develops from gingivitis however not all gingivitis will progress into periodontitis.

Periodontitis is defined as a condition in which there is an inflammatory reaction that occurs in the periodontium resulting in the destruction of the supporting soft tissues surrounding the teeth, loss of gingival fibers of the periodontal ligament, and resorption of the alveolar bone. Periodontitis has also been further categorized into mild, moderate, and severe periodontitis based on the patients clinical attachment loss (39,40). Mild periodontitis presents with 1-2 mm of attachment loss, moderate periodontitis
presents with 3-4 mm of attachment loss, and severe periodontitis displays attachment loss greater than 4 mm. Periodontitis is even further divided into chronic or acute forms and generalized (presenting in greater than 30% of the oral cavity) or localized (less than 30% of the oral cavity is involved).

Due to the progressive nature of this condition, if periodontitis is left untreated, loosening and/or tooth loss is usually the result. Due to the destructive nature of periodontal disease, it has been a frequent interest in many research projects. It has been concluded that periodontal disease is the clinical result of a complex interaction between the host and plaque bacteria. Destruction of periodontal supporting tissues happens as a response to very intricate host-parasite interactions. The net result of this host-parasite interaction, which in an unpredictable moment, accumulate and exceed the threshold of tissue integrity thus causing tissue destruction and ultimate bone loss.

Periodontal disease is the most prevalent of bone diseases in humans and has long been implicated as a risk factor in impairment of oral functions and tooth loss. 10-15% of adults that have periodontal disease have it severely enough that it results in tooth loss, ultimately leading to mastication malfunction and ageusia. While periodontal disease is prevalent worldwide, it has had a significant impact on the United States population (9, 18, 52). Brown et al estimate that about 21.8% of adults (22.6 million) exhibit signs of mild periodontitis, 9.5% (9.9 million) display signs of moderate periodontitis, and about 3.1% (about 3.2 million) exhibit signs of advanced periodontitis (9). The total amount expended for periodontal preventive procedures as well as the treatment of periodontal diseases in the U.S. was $14.3 billion in 1999 (9). Undoubtedly, innovative methods for
the prevention and treatment of periodontal disease would have a major impact on healthcare costs.

Past research has suggested periodontal disease can be complicated by certain systemic diseases, however more recently, studies suggest that the reverse may also be true (13, 28, 29, 32, 44, 46, 50). Current research, however controversial, proposes that periodontal disease has important systemic implications, and can influence other diseases such as cardiovascular disease (28, 29, 36, 39), pulmonary disease (44, 55) diabetes (23, 32, 50), and adverse pregnancy outcomes (11, 46, 47). Thus, a better understanding of the factors that contribute to periodontal disease can be used to develop measures to improve not only oral health of the patient, but also overall health of individuals.

The onset and progression of periodontal disease is associated with several risk factors, including but not limited to gender, age, socio-economic status, nutrition, stress, genetic makeup, and tobacco smoke. Though there are several risk factors, tobacco smoke has been considered one of the most important risk factors associated with periodontal disease (54). It is theorized that there is a positive correlation between increased tobacco usage in the population and increased numbers of periodontal infections (33, 52). A dose-dependent correlation has been demonstrated between the frequency of an individual smoker and the severity of the deteriorating periodontal health of that individual (6). Smokers are extremely more susceptible to periodontitis, with increased alveolar bone resorption (24), attachment loss, percentage of oral sites with significant attachment loss (25), tooth mobility, and tooth loss (42) than non smokers. Additionally, patients who smoke are more often refractory to treatment than non-smokers (49). Despite conflicting data that tobacco smoke may not influence the sub-
gingival microflora (22, 10), recent data strongly indicates that tobacco-induced susceptibility to periodontitis is correlated with populational shifts in the microbial composition of the oral biofilm (15, 19, 26). For example, Umeda et al showed that there is an increased risk of *Treponema denticola* inhabiting the oral cavity of smokers (61); while Zambon et al reported a higher prevalence of *Aggregatibacter actinomycetemcomitans*, *Tannerella forsythia* and *Porphyromonas gingivalis* in smokers (66).

While all of these factors play a role in the progression and severity of the disease, there is clear evidence that the inflammatory response in the periodontum is initiated against the resident microbial biofilm within the subgingival pocket (1). It is this inflammatory reaction caused by the host innate immune response to the bacterial pathogen that dictates the severity and progression of the periodontal infection (5).

The oral biofilm consists of several hundred bacterial species, but periodontal disease is often associated with a progressive succession of the predominant bacterial species in dental plaque from Gram-positive to Gram-negative (1, 4). In order for bacteria to colonize and persist in a host, bacterial pathogens must be able to counteract the innate and adaptive immune system of the host. Bacteria are able to evade the host immune system by maintaining a plethora of virulence factors. Many bacteria produce numerous virulence factors that have been well-characterized, including adherence proteins, cytotoxic factors, biofilm polysaccharides, chemotactic inhibitor, collagenases, LPS, and toxins to counteract the host immune system. It is these different bacterial behaviors and the resulting immune response to these pathogens that combine to promote inflammatory tissue destruction in periodontitis (5). The production by various proinflammatory
cytokines (i.e. IL-1B, IL-6, TNFα, IL-8, and RANKL) in response to specific Gram-negative bacteria within the oral cavity leads to the activation of osteoclasts (37). Activation of the bone-resorbing osteoclasts eventually results in bone resorption and alveolar bone loss—clinical symptoms of periodontitis (41, 45, 51).

**Microbial Induction of Periodontal Disease**

Dental plaque is the single most important risk factor associated with the onset and progression of periodontal disease (1). The formation of dental plaque begins with adsorption of early colonizing bacteria onto an acquired pellicle, a layer of salivary proteins that is mainly composed of glycoproteins that forms shortly after a dental cleaning or tooth eruption. Once an acquired pellicle is formed, early colonizers are able to manipulate the environment in order for other bacteria to be able to colonize and adhere, thus forming dental plaque. It is this dental plaque that initiates the host inflammatory reaction (5).
Figure 1. Anatomy of the periodontium (as reviewed by Baker, P.J. (12)).

A) In health, gingival fibers connect the gingival soft tissue to the root of the tooth, and the alveolar bone and cementum are connected by periodontal ligament fibers. B) In periodontal disease, subgingival infection by Gram-negative bacteria results in soft tissue damage, producing attachment loss and deepening the sulcus into the periodontal pocket. Alveolar bone resorption moves the bone surface away from the tooth root (vertical bone loss) and reduces the height of the alveolar bone crest (horizontal bone loss). Copyright permission to reproduce figure granted by Elsevier and (5).
As mentioned previously, bacteria are able to adhere to the acquired pellicle on hard tissue to form a biofilm. The ability of bacteria to adhere tightly to underlying substrata impedes the efficient removal of biofilms by physical or chemical means. In the oral cavity, biofilms form on the surfaces of both hard and soft tissues, and the development of the biofilm depends on interactions between both bacterial cell-surface adhesions and host receptors and bacteria-bacteria interactions (12). Without the ability to adhere to surfaces in the oral cavity, bacteria are swallowed with the saliva and enter the digestive tract, where they may not survive.

The last stage of bacterial colonization in the oral cavity involves late colonizers, whose presence is often associated with periodontal disease progression. A hallmark of inflammatory periodontal disease is the increased subgingival colonization by several Gram-negative species, including *A. actinomycetemcomitans*, *Prevotella intermedia*, *Campylobacter rectus*, and a group of three other bacteria designated 'the red complex' bacteria (*T. denticola*, *T. forsythia*, and *P. gingivalis*) (40). It is the bacteria previously mentioned that are considered the late colonizers or the anaerobic bacteria that cause this inflammatory reaction in the gingival tissues. The red complex is a group of microorganisms that are most intimately associated with adult periodontal disease. *A. actinomycetemcomitans*, another late colonizer, is associated with an aggressive form of periodontitis primarily found in juveniles, however this bacterial speices can also be found in chronic periodontitis as well (58).
Aggregatibacter actinomycetemcomitans

*A. actinomycetemcomitans* (formerly *Actinobacillus actinomycetemcomitans*) is a small, fastidious, CO₂-requiring coccobacillus (34). It is a capnophilic, facultative anaerobic Gram-negative bacterium that belongs to the family Pasteurellaceae (34). *A. actinomycetemcomitans* was initially isolated from actinomycotic oral lesions along with *Actinomyces israelii*, leading to its species name (30). *A. actinomycetemcomitans* was first isolated in 1912 (38), however it was never recognized as a member of the oral microbial environment until 1975 (35). *A. actinomycetemcomitans* has been associated with several systemic infections including chronic periodontitis, but the pathogen is most known for its strong association with localized aggressive periodontitis, an extremely destructive form of periodontal disease that is most common in adolescents and young adults (58). The fact that *A. actinomycetemcomitans* has also been recovered from subgingival microflora of periodontally healthy patients suggest that *A. actinomycetemcomitans* may also represent an opportunistic pathogen. Due to *A. actinomycetemcomitans* strong association with localized aggressive periodontitis, most studies of *A. actinomycetemcomitans* have focused on its role in this disease. If the disease is left untreated, localized aggressive periodontitis results in rapid destruction of the alveolar bone and all supporting structures ultimately causing tooth loss. The disease specifically targets the mandibular incisors and first molars (65).

*A. actinomycetemcomitans*, like other bacterial pathogens, utilizes a plethora of virulence factors to cause disease and evade the host immune response. *A. actinomycetemcomitans* produces numerous virulence factors that have been well-characterized, including adherence proteins, cytotoxic factors, biofilm polysaccharides,
chemotactic inhibitor, collagenases, LPS, and toxins. There is also strong evidence that leukotoxin (LtxA), a 116-kDa protein that belongs to the repeats-in-toxin (RTX) family of pore forming toxins, expression affects disease progression (8, 31). Studies have shown that the target of LtxA is quite specific, which is unusual among RTX toxins, killing only polymorphonuclear leukocytes, monocytes and T-cells, all cells responsible for the innate immune response, in humans, apes, and Old World monkeys (60). Previous studies have also demonstrated the ability of \textit{A. actinomycetemcomitans} to bind and invade epithelial (43) and endothelial cells (56), which may be an important mechanism for evading the host immune system and disseminating beyond the initial site of infection (17). Furthermore, fresh clinical isolates of \textit{A. actinomycetemcomitans} express fimbriae (Figure 2), which allow them to form tenacious biofilms on a variety of solid surfaces, such as hydroxyapatite, glass, and plastic (53). Fimbriae expression may be important in biofilm pathogenesis \textit{in vivo}, however it is not the sole determinant in biofilm formation, as isogenic smooth strains are capable of forming biofilms (57). However fimbriae are thought to enable \textit{A. actinomycetemcomitans} to colonize the tooth surface, persist in the oral cavity, and initiate infection in the presence of salivary flow, thus classifying them as a virulence factor.
Figure 2. Characteristics of clinical isolates of *A. actinomycesitumcomitans* (16). A) When *A. actinomycesitumcomitans* is initially isolated from the oral cavity and cultured on solid medium, it grows as a 'rough' colony with a characteristic star-like structure in the center. B) As the bacterium is passaged in liquid broth, it loses its ability to express fimbriae due to a spontaneous mutation in the *flp* promoter region, and the broth becomes turbid with the growth of isogenic non-adherent variants. When plated on solid medium, these variants form large, smooth colonies (16). Copyright permission to reproduce figure granted by Society for General Microbiology and (16).
Necessity of Iron

Iron is the most abundant metal in nature, and as such, plays a major role in the life processes of all organisms (62). Iron is the central atom of the heme group in hemoglobin, which is necessary for oxygen transport in blood. Iron is also present in myoglobin which allows oxygen to diffuse through muscle cell), cytochromes (proteins involved in the electron transport chain), proteins involved with DNA synthesis and cell division. Furthermore, iron is used to help produce the connective tissues in the human body, it is incorporated in the production of neurotransmitters, as well as playing an integral role in the maintenance of human immune system. Due to the fact that iron plays such a integral role in life processes it is tightly regulated. Too little iron can lead to iron deficiency anemia and present with symptoms of constant fatigue, palor, and severe weakness. Too much iron is known as hemochromatosis and can present as abdominal pain, fatigue, and generalized darkening of the skin.

The paucity of free iron in mucous membranes, tissues, or body fluids acts as a host defense mechanism against bacterial infections by creating a bacteriostatic environment, because iron is an essential nutrient for all life (22). Host iron binding proteins such as transferrin, lactoferrin, hemoglobin, ferritin all act collectively to maintain a low free iron concentration, thus inhibiting bacterial growth (63). As mentioned before all organisms require iron to survive. A critical component of bacterial virulence is the ability to obtain iron from their host. Several bacteria have evolved iron-sequestering mechanisms such as the secretion of siderophores, which compete with host
iron binding molecules for iron. Previous research has shown that *A. actinomycetemcomitans* is not capable of binding transferrin (22, 64). In addition, this dental pathogen is not known to excrete siderophores (64). However, it has been shown that *A. actinomycetemcomitans* is capable of binding both lactoferrin and hemoglobin (2, 21), two iron-containing compounds that serve as iron sources for other bacteria (48). The exact sources that *A. actinomycetemcomitans* utilizes in the oral cavity are not known.

Research to date has shown that *A. actinomycetemcomitans* has at least 15 iron acquisition genes encoded in its genome (54). The amount of *A. actinomycetemcomitans*’ genome involved in iron acquisition suggests the importance of iron availability to the survival of this organism. With all of this capability that *A. actinomycetemcomitans* has to obtain iron, there must be some discretion or priority in the specific type of iron that *A. actinomycetemcomitans* prefers to utilize. The iron acquisition systems encoded in the genome of *A. actinomycetemcomitans* are tailored towards the specific survival strategies needed to survive in the oral biofilm. Due to *A. actinomycetemcomitans* genome and the fact that *A. actinomycetemcomitans* is a facultative anaerobe, *A. actinomycetemcomitans* is expected to be able to utilize inorganic and organic as well as ferric and ferrous iron sources both in planktonic culture and biofilms. The most common iron transport systems utilized by bacteria seem to be the ferric iron transport complexes such as ABC transporters. However other bacteria such as *H. pylori*, *E coli*, *P. gingivalis* and *V. cholera* also employ ferrous iron transport through *Feo* (Ferrous Iron Transport) systems. Due to relatively soluble nature of ferrous iron (0.1 M for Fe2+ cf 10^-18 M for Fe3+ at pH 7), it would seem that ferrous iron would be the preferred iron source for
most bacteria (68). However only under anaerobic conditions, or low pH environments
does ferrous iron transport seem predominant. This fact lead us to believe that A.
actinomycetemcomitans is able utilize ferrous iron as well as ferric iron transport in the
oral cavity (68, 69, 70). Our hypothesis is that A. actinomycetemcomitans primarily
utilizes ferric iron and hemin as iron sources in the oral biofilm due to the nature of A.
actinomycetemcomitans genome. In this study, we investigate the planktonic growth of A.
actinomycetemcomitans in an iron-limited and iron-chelated environment as well as
analyze the ability of A. actinomycetemcomitans to grow in an iron-chelated environment
supplemented with different iron sources and investigate what particular iron aquisition
genes are being upregulated in each particular iron environment.
<table>
<thead>
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<th>Gene Name</th>
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<th>Definition</th>
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<tr>
<td>hmsHf</td>
<td>AA00490,00491</td>
<td>hemin transport and storage</td>
</tr>
<tr>
<td>afuABC</td>
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<td>iron(III) ABC transporter</td>
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<tr>
<td>hgpA</td>
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<td>hemoglobin binding protein A</td>
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<tr>
<td>fecBCDE</td>
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<td>AA01048-01051</td>
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<tr>
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<td>Outer membrane hemophore receptor</td>
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Table 1. Iron Uptake Operons in *A. actinomycetemcomitans*. Iron acquisition operons encoded in *A. actinomycetemcomitans* genome (54). There is a redundancy of ferric iron transporters (ABC transporters), hemin and hemoglobin transporters. *A. actinomycetemcomitans* even seems to be able to utilize sideophore like molecules secreted from other bacteria through utilization of it’s enterochelin transport system.
Bacterial strains and culture conditions. *A. actinomycetemcomitans* bacterial strain employed in this study was *A. actinomycetemcomitans* 652. *A. actinomycetemcomitans* 652 is an afimbriated, smooth colony morphotype strain and was grown at 37°C under microaerophilic conditions in Chemically Defined Media (CDM; Sigma-Aldrich, St. Louis, MO) and CDM supplemented with 150 μM of dipyridyl (DIP; Sigma-Aldrich, St. Louis, MO) per liter. Ferric Chloride, Ferric Citrate, Ferrous Sulfate, Hemin (Sigma-Aldrich, St. Louis, MO) were added to CDM with DIP at a 250 μM concentration per liter.
<table>
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<th>Size (kbp)</th>
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</tr>
<tr>
<td>5' 01642</td>
<td>GCGCGCGATCTGGCGGTACCTACT</td>
<td>afuA 01642</td>
<td>0.191</td>
</tr>
<tr>
<td>3' 01642</td>
<td>GCGCGATCTGGCGGTACCTACT</td>
<td>afuA 01642</td>
<td>0.191</td>
</tr>
<tr>
<td>5' AA02120</td>
<td>GCAAGGTTATGAAGGTGCTGCGGC</td>
<td>ftnA/rsgA 02120</td>
<td>0.351</td>
</tr>
<tr>
<td>3' AA02120</td>
<td>GCAAGGTTATGAAGGTGCTGCGGC</td>
<td>ftnA/rsgA 02120</td>
<td>0.351</td>
</tr>
<tr>
<td>5' AA00762</td>
<td>CCATGGGAATTGAGACAAACAAGCAACGTTAG</td>
<td>hgpA AA00762</td>
<td>0.263</td>
</tr>
<tr>
<td>3' AA00762</td>
<td>TCTAGATAGTCCATTCCTGCGGTAACAA</td>
<td>hgpA AA00762</td>
<td>0.263</td>
</tr>
</tbody>
</table>
Achievement of an Iron Limited Environment. *A. actinomycetemcomitans* was grown in a chemically defined media (CDM) in order to regulate the amount and type of iron that the bacteria could use for growth. *A. actinomycetemcomitans* was grown in CDM that contained FeS04 (CDM regular), and was then passaged into CDM that lacked an iron source (FeS04), creating an iron limited environment.

**Chemically Defined Media (CDM)**

<table>
<thead>
<tr>
<th>Amino Acids</th>
<th>1L of 20x (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>L-Glutamic Acid HCl</td>
<td>27.2 mM</td>
</tr>
<tr>
<td>Glycine</td>
<td>26.6 mM</td>
</tr>
<tr>
<td>L-Threonine</td>
<td>16.79 mM</td>
</tr>
<tr>
<td>L-Serine</td>
<td>19.03 mM</td>
</tr>
<tr>
<td>L-Lysine HCl</td>
<td>10.95 mM</td>
</tr>
<tr>
<td>L-Arginine HCl</td>
<td>11.49 mM</td>
</tr>
<tr>
<td>L-Histidine HCl H2O</td>
<td>14.09 mM</td>
</tr>
<tr>
<td>L-Glutamine</td>
<td>8.38 mM</td>
</tr>
<tr>
<td>L-Asparagine H2O</td>
<td>15.12 mM</td>
</tr>
<tr>
<td>L-Proline</td>
<td>13.23 mM</td>
</tr>
<tr>
<td>L-Asparatic Acid</td>
<td>15.03 mM</td>
</tr>
<tr>
<td>L-Ornithine HCl</td>
<td>2.37 mM</td>
</tr>
<tr>
<td>L-Hydroxyproline</td>
<td>3.05 mM</td>
</tr>
<tr>
<td>Amino acids (Hydrophobic)</td>
<td>1L of 20x (g)</td>
</tr>
<tr>
<td>--------------------------</td>
<td>---------------</td>
</tr>
<tr>
<td>L-Alanine</td>
<td>22.45 mM</td>
</tr>
<tr>
<td>D-Alanine</td>
<td>22.45 mM</td>
</tr>
<tr>
<td>L-Leucine</td>
<td>15.25 mM</td>
</tr>
<tr>
<td>L-Valine</td>
<td>17.07 mM</td>
</tr>
<tr>
<td>L-Tryptophan</td>
<td>9.79 mM</td>
</tr>
<tr>
<td>L-Methionine</td>
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<td>L-Isoleucine</td>
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<td>L-Phenylalanine</td>
<td>12.11 mM</td>
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<tr>
<td>L-Tyrosine</td>
<td>2.21 mM</td>
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<tr>
<td>L- Cystine</td>
<td>416.2 μM</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Purines/Pyrimidines</th>
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</tr>
</thead>
<tbody>
<tr>
<td>Adenine</td>
<td>1.85 mM</td>
</tr>
<tr>
<td>Guanine</td>
<td>1.32 mM</td>
</tr>
<tr>
<td>Cytosine HCl</td>
<td>2.43 mM</td>
</tr>
<tr>
<td>Thymine</td>
<td>1.59 mM</td>
</tr>
<tr>
<td>Xanthine</td>
<td>1.31 mM</td>
</tr>
<tr>
<td>Hypoxanthine</td>
<td>1.47 mM</td>
</tr>
<tr>
<td>Uracil</td>
<td>1.78 mM</td>
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</table>
### Inorganic Salts

<table>
<thead>
<tr>
<th>Inorganic Salts</th>
<th>1L of 20x (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MnSO₄</td>
<td>830.8 μM</td>
</tr>
<tr>
<td>NaCl</td>
<td>34.2 mM</td>
</tr>
<tr>
<td>K₂HPO₄</td>
<td>22.9 mM</td>
</tr>
<tr>
<td>KH₂PO₄</td>
<td>146.9 mM</td>
</tr>
<tr>
<td>KNO₃</td>
<td>19.78 mM</td>
</tr>
<tr>
<td>KI</td>
<td>12.05 μM</td>
</tr>
<tr>
<td>CuSO₄·5H₂O</td>
<td>5.206 μM</td>
</tr>
<tr>
<td>Boric Acid</td>
<td>161.7 μM</td>
</tr>
<tr>
<td>ZnSO₄·7H₂O</td>
<td>56.8 μM</td>
</tr>
<tr>
<td>Sodium molybdate</td>
<td>48.6 μM</td>
</tr>
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</table>

### Vitamins/Factors

<table>
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<tbody>
<tr>
<td>Choline chloride</td>
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<tr>
<td>Beta-alanine</td>
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</tr>
<tr>
<td>Pyridoxal</td>
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</tr>
<tr>
<td>Pyridoxine HCl</td>
<td>5.91 mM</td>
</tr>
<tr>
<td>Pyridoxamine diHCl</td>
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</tr>
<tr>
<td>Compound</td>
<td>Concentration</td>
</tr>
<tr>
<td>--------------------------------</td>
<td>-----------------</td>
</tr>
<tr>
<td>Spermidine HCl</td>
<td>6.88 mM</td>
</tr>
<tr>
<td>Nicotinic acid</td>
<td>8.12 mM</td>
</tr>
<tr>
<td>Nicotinaminde</td>
<td>8.19 mM</td>
</tr>
<tr>
<td>Calcium pantothenate</td>
<td>4.56 mM</td>
</tr>
<tr>
<td>Spermine tetraHCl</td>
<td>2.87 mM</td>
</tr>
<tr>
<td>Thiamine HCl</td>
<td>3.32 mM</td>
</tr>
<tr>
<td>Myo-Inositol</td>
<td>55.5 mM</td>
</tr>
<tr>
<td>Nicotinamide adenine dinucleotide</td>
<td>1.51 mM</td>
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<tr>
<td>p- Aminobenzoic acid</td>
<td>729.2 μM</td>
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<tr>
<td>Vitamin B12</td>
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</table>

<table>
<thead>
<tr>
<th>Compound</th>
<th>Concentration</th>
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<tbody>
<tr>
<td>NaHCO3</td>
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<table>
<thead>
<tr>
<th>Compound</th>
<th>Concentration</th>
</tr>
</thead>
<tbody>
<tr>
<td>L- Cysteine HCl</td>
<td>10.7 mM</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Compound</th>
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</tr>
</thead>
<tbody>
<tr>
<td>MgSO4 7H2O</td>
<td>28.4 μM</td>
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<tr>
<td></td>
<td>1L of 1X (g)</td>
</tr>
<tr>
<td>-----------------</td>
<td>-----------------------------------</td>
</tr>
<tr>
<td>FeSO₄ 7H₂O</td>
<td>17.9 mM</td>
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</tbody>
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<table>
<thead>
<tr>
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</thead>
<tbody>
<tr>
<td>CaCl₂ 2H₂O</td>
<td>680.2 μM</td>
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</table>

<table>
<thead>
<tr>
<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td>Pimelic acid</td>
<td>624.2 nM</td>
</tr>
<tr>
<td>D- Biotin</td>
<td>409.3 nM</td>
</tr>
<tr>
<td>DL-6,8-thioctic</td>
<td>484.6 nM</td>
</tr>
<tr>
<td>Folic acid</td>
<td>2.265 μM</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>1L of 1X (mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Riboflavin</td>
<td>2.66 μM</td>
</tr>
</tbody>
</table>

**Table 6. A. actinomycetemcomitans Chemically Defined Media.** All chemicals used were from Sigma-Aldrich, St. Louis, MO.
Achievement of an Iron Chelated Environment. A.

*Actinomyces* growth was achieved by passaging the bacteria in an iron limited environment (a media in which no exogenous iron source was added) and an iron chelated environment (a media in which a chelator was added). On Day 1, *A. actinomyces* strain 652 was inoculated into regular CDM from a frozen stock. This culture was incubated at 37°C overnight under microaerophilic conditions. On Day 2, the bacteria from the overnight culture of regular CDM was inoculated into CDM with no iron plus 100 uM, 150 uM or 200 uM of dipyridyl (DIP) to achieve a 1st passage in an iron chelated environment. This 1st passage was incubated at 37°C overnight under microaerophilic conditions. On Day 3, the bacteria from the overnight culture of CDM no iron 1st passage plus 100 uM, 150 uM, or 200 uM of DIP was inoculated into fresh media of CDM no iron plus 100 uM, 150 uM, or 200 uM of DIP to achieve a 2nd passage in an iron chelated environment. CDM no iron is an iron-limited environment. CDM no iron supplemented with DIP (iron chelator) is an iron-chelated environment. Growth of *A. actinomyces* was accessed by measuring optical densities of the bacteria at 600 nM utilizing spectrophotometer. Figure 3 shows how this was accomplished.
Figure 3: Achievement of an iron limited and iron chelated environment.

Diagram shows how *A. actinomycetemcomitans* was passaged in order to achieve an iron limited environment. The same mechanism was utilized in order to obtain an iron chelated environment except in an iron chelated environment an iron chelator, dypridyl (DIP), was added to the CDM No Iron at 100 uM, 150 uM, and 200 uM concentrations respectively.
**RNA Isolation.** Overnight cultures of the appropriate *A. actinomycetemcomitans* incubated at 37°C until the mid-exponential growth phase (O.D. of .08 for 1st passage CDM No Iron with 150 uM DIP and .028 for 2nd passage CDM No Iron with 150 uM DIP) for RNA isolation. Total RNA was isolated from *A. actinomycetemcomitans* cells using the 5 Prime PerfectPure RNA Cell & Tissue kit (5 Prime Inc., Gaithersburg, MD) according to the manufacturer's instructions. To ensure that the samples were free of contaminating genomic DNA, the RNA preparation was digested with RQ RNase-free DNase I (Promega Corporation, Madison, WI). The concentration and purity of each RNA sample were measured via spectrophotometry (ND-1000 Spectrophotometer, NanoDrop Technologies, Inc, Wilmington, DE) and was also assessed by gel electrophoresis. Samples were checked for contamination of genomic DNA by real-time PCR using *A. actinomycetemcomitans* 5s rRNA primers (Table 2) RNA samples were considered free of significant genomic DNA if no amplification product was detected by real-time PCR after at least 30 cycles of amplification. RNA that was not immediately utilized for a reverse-transcription reaction was aliquoted into 1.5 ml Eppendorf tubes and stored at -80°C until future use.
cDNA synthesis and qPCR for iron acquisition gene expression. First-strand cDNA was prepared by using SuperScript III Reverse Transcriptase (Invitrogen, Carlsbad, CA) according to the manufacturer’s instructions. Quantitative PCR (qPCR) was performed with the Smart Cycler system (Cepheid, Sunnyvale, CA) in a final reaction volume of 25 μl that contained 100 ng of cDNA, appropriate iron acquisition primers (5’ Induction and 3’ Induction; ~71 μM final concentration), and 1x FastStart SYBER Green Master (Roche, Indianapolis, IN). The amplification conditions for qPCRs were as follows: denaturation at 95°C for 15 seconds, annealing at 55°C for 30 seconds, and elongation at 72°C for 30 seconds for 35 cycles. The threshold cycle for each qPCR was determined from a second derivative plot of total fluorescence as a function of cycle number by using the software package supplied with the Smart Cycler system. All gene-specific threshold values were normalized against threshold values from primers specific for the A. actinomycetemcomitans 5S rRNA gene (~60 μM final concentration). qPCR reactions were carried out in triplicate with consistent results. Each qPCR end-point amplification product was visualized by electrophoresis on 2% agarose gels. Primers utilized in this study included afuA 1642 (iron III ABC transporter), afuA 0696 (periplasmic iron-compund binding protein), hgpA 0696 (hemoglobin binding protein A), JeeR 0795 (iron III dicitrate-binding protein), and ftmA 2120 (nonheme ferritin) (54).
CHAPTER THREE: EXPRESSION OF IRON ACQUISITION GENES

Introduction:

Dental plaque forms on surfaces of teeth and is composed of a dynamic microbial community. As this microbial community matures, there is an increase in gram negative bacteria and decrease in gram positive bacteria. As gram negative bacteria proliferate in the oral biofilm, the host immune system reacts to the microbes, and eventually leads to periodontal disease. *A. actinomycetemcomitans*, is a gram negative coccibacillus, that is associated with the aggressive forms of periodontal disease. However in order for bacteria such as *A. actinomycetemcomitans*, to proliferate inside a human a host, iron is needed. Iron is an essential element needed for growth and normal metabolic functions in all organisms. Because the human host regulates iron, thus keeping a bacteriostatic environment, bacteria must overcome this iron sequesteration by encoding in its genome iron acquisition systems, in order to obtain iron from the host environment so that the bacteria may thrive and proliferate. Research to date has shown that *A. actinomycetemcomitans* has at least 15 iron aquistion genes encoded in its genome. The iron acquisition systems encoded in the genome of *A. actinomycetemcomitans* are tailored towards the specific survival strategies needed to survive in the oral biofilm. Due to all of the capability that *A. actinomycetemcomitans* has to obtain iron, there must be some dicression or priority in what type of iron *A. actinomycetemcomitans* prefers to utilize for
growth. Due to the redundancy of ferric iron transporters in *A. actinomycetemcomitans* genome and the major iron sources that *A. actinomycetemcomitans* will encounter in the oral cavity lead us to our hypothesis that *A. actinomycetemcomitans* primarily utilizes ferric iron, obtained from iron chelators or host proteins, and hemic as iron sources in the oral cavity.

**Results:**

*A. actinomycetemcomitans* is capable of growing in an iron-limited environment. In order for us to test *A. actinomycetemcomitans*’ ability to grow in an environment that lacked an iron source, *A. actinomycetemcomitans* was first grown in an iron rich media (CDM regular) overnight in an incubator at 37°C. One milliliter of overnight planktonic cultures of *A. actinomycetemcomitans* strain 652 grown in CDM regular was inoculated into fresh CDM 19 mL. Growth was analyzed for 12 hours by measuring the Optical Density at 600 nm every hour. The first passage with no iron culture was achieved by inoculating from an overnight culture of *A. actinomycetemcomitans* grown in CDM regular into fresh CDM with no added iron source (CDM No Iron). The second passage CDM No Iron culture was achieved by inoculating from an overnight culture of *A. actinomycetemcomitans* grown in the first passage of CDM No Iron. The third passage CDM No Iron culture was achieved by inoculating from an overnight culture of *A. actinomycetemcomitans* grown in the second passage of CDM No Iron. Results shown in Figure 4 are averages of O.D. ± standard deviations.
Figure 4. Growth of *A. actinomycetemcomitans* in an iron-limited environment. Growth of *A. actinomycetemcomitans* measured by spectrometry O.D. 600 nm. Growth was measured in triplicates, results of growth were averages ± standard deviations.

Results showed that *A. actinomycetemcomitans* was able to grow in an iron limited environment. Growth occurred similarly in all 3 passages of *A. actinomycetemcomitans* without an iron source. These results lead us to a couple of conclusions, either *A. actinomycetemcomitans* was capable of growing very well in an iron limited environment due to large internal iron storage system that lasted the bacteria well into the third passage or there were trace amounts of iron in media CDM No Iron, even though no exogenous iron source was added to the media. This lead us to our second experiment of obtaining an iron-chelated environment.
An iron-chelated environment reduces the growth of *A. actinomycetemcomitans*. Passages in an iron chelated environment were achieved as described above in Figure 4. However, the growth of *A. actinomycetemcomitans* was analyzed in an iron-chelated environment at different concentrations of dipyridyl (DIP). Growth was analyzed for 12 hours by measuring the Optical Density at 600 nm every hour, as above. Figure 5a. DIP was added to the 1st and 2nd passages at 100 µM. Figure 5b. DIP was added to the 1st and 2nd passages at 150 µM. and Figure 5c. DIP was added to the 1st and 2nd passages at 200 µM. Results are averages O.D. at 600 nm ± standard deviations.
Figure 5a. Achievement of an Iron Chelated Environment with 100 uM DIP.

Growth of *A. actinomycetemcomitans* measured by spectrometry O.D. 600 nm. Growth was measured in triplicates, results of growth were averages ± standard deviations.
Figure 5b. Achievement of an Iron Chelated Environment with 150 uM DIP.

Growth of *A. actinomycetemcomitans* measured by spectrometry O.D. 600 nm. Growth was measured in triplicates, results of growth were averages ± standard deviations.
Figure 5c. Achievement of an Iron Chelated Environment with 200 μM DIP.

Growth of *A. actinomycetemcomitans* measured by spectrometry O.D. 600 nm. Growth was measured in triplicates, results of growth were averages ± standard deviations.

Results from these growth analyses displayed that an iron-chelated environment reduces the growth of *A. actinomycetemcomitans*. It also proved that *A. actinomycetemcomitans* has an internal iron storage system that allows growth in an iron chelated environment well into the 1\textsuperscript{st} passage. However by the 2\textsuperscript{nd} passage of *A. actinomycetemcomitans* in an iron chelated environment the internal iron storage system had been depleted and *A. actinomycetemcomitans* growth was drastically reduced. It also proved that there were trace elements of iron in the No Iron CDM media that *A. actinomycetemcomitans* was able to utilize for growth. Now that an environment was created in which *A. actinomycetemcomitans* was depleted of all sources, we then decided
to add different sources of iron in order to see what types of iron that A. actinomycetemcomitans preferred to utilize for growth.

**Growth of A. actinomycetemcomitans utilizing different iron sources.** To determine A. actinomycetemcomitans' ability to utilize iron sources for growth, the 1st passage CDM No Iron with 150 μM DIP was inoculated into fresh CDM No Iron with 150 μM DIP medium supplemented with 250 μM of hemin, ferric chloride, ferric citrate, or ferrous sulfate. To prevent ferrous sulfate from oxidizing to ferric sulfate, the growth was analyzed under anaerobic conditions. The 1st passage was achieved as in Figure 3. Growth was analyzed for 12 hours by measuring the Optical Density at 600 nm every hour. Results are averages of O.D. at 600 nm ± standard deviations.
Figure 6. Growth of *A. actinomycetemcomitans* utilizing different iron sources with 150 uM DIP and 250 uM of appropriate iron sources. Growth of *A. actinomycetemcomitans* measured by spectrometry O.D. 600 nm. Growth was measured in triplicates, results of growth were averages ± standard deviations.

Hemin, Ferric Chloride, and Ferric Citrate are iron sources that *A. actinomycetemcomitans* is capable of utilizing for growth. Growth of *A. actinomycetemcomitans* in ferrous sulfate was similar to the amount of growth that was witnessed in the 2nd passage in an iron chelated environment leading us to the the conclusion that *A. actinomycetemcomitans* appears to not to be able to utilize ferrous sulfate as effectively for growth. Now that *A. actinomycetemcomitans* growth was analyzed under different iron conditions, we wanted to see what particular iron genes were up regulated or down regulated during these various iron conditons.
Expression of iron-uptake genes under an iron-chelated environment.

Cultures utilized in this experiment were achieved as described in Figure 2. RNA was extracted mid exponential phase (O.D. of .08 for the first passage in CDM no iron and O.D. of .025 for the second passage in CDM no iron). RNA was isolated and cDNA was synthesized as described in the previous methods. Real-time PCR was performed using primers specific for iron genes. Iron genes utilized in this study were chosen based on the genes association with qorum sensing, due to the fact that previous research has shown that iron acquisition in \emph{A. actinomycetemcomitans} is regulated by qorum sensing (72). Expression of genes are normalized to 1st passage expression. Results are averages of Delta T ± standard deviations. Delta T was calculated by subtracting the cycle threshold (Ct) determined for the each particular iron gene reaction from the Ct of the 5s rRNA control.

<table>
<thead>
<tr>
<th>Table 4a. afuA 1642 (iron (III) ABC transporter)</th>
</tr>
</thead>
<tbody>
<tr>
<td>delta T</td>
</tr>
<tr>
<td>2nd Passage in CDM No Iron with 150 uM DiP</td>
</tr>
<tr>
<td>1st Passage in CDM No Iron with 150 uM DIP</td>
</tr>
</tbody>
</table>

delta T was calculated by subtracting the cycle threshold (Ct) determined for the afuA 01642 reaction from the Ct of the 5s rRNA control. P value = 0.031
Table 4b. *afuA* 0696 (periplasmic iron-compound-binding protein)

<table>
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<tr>
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<th>delta (delta T)</th>
<th>Fold Change</th>
</tr>
</thead>
<tbody>
<tr>
<td>2&lt;sup&gt;nd&lt;/sup&gt; Passage in CDM No Iron with 150 uM DIP</td>
<td>13.68 ± 0.601</td>
<td>7.62E-5 ± 0.03E-3</td>
<td>9.52 ± .081</td>
</tr>
<tr>
<td>1&lt;sup&gt;st&lt;/sup&gt; Passage in CDM No Iron with 150 uM DIP</td>
<td>15.87 ± 0.467</td>
<td>8E-6 ± 0.002E-3</td>
<td>1</td>
</tr>
</tbody>
</table>

delta T was calculated by subtracting the cycle threshold (Ct) determined for the *afuA* 0696 reaction from the Ct of the 5s rRNA control. P value = 0.0150

Table 4c. *hgpA* 0762 (hemoglobin binding protein A)

<table>
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<th>delta (delta T)</th>
<th>Fold Change</th>
</tr>
</thead>
<tbody>
<tr>
<td>2&lt;sup&gt;nd&lt;/sup&gt; Passage in CDM No Iron with 150 uM DIP</td>
<td>9.133 ± 1.100</td>
<td>0.002 ± .001</td>
<td>.319 ± .241</td>
</tr>
<tr>
<td>1&lt;sup&gt;st&lt;/sup&gt; Passage in CDM No Iron with 150 uM DIP</td>
<td>7.486 ± 0.962</td>
<td>0.006 ± .004</td>
<td>1</td>
</tr>
</tbody>
</table>

delta T was calculated by subtracting the cycle threshold (Ct) determined for the *hgpA* 0762 reaction from the Ct of the 5s rRNA control. P value = 0.0978
Table 4d. fecB 0795 (iron(III) dicitrate-binding protein)

<table>
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<tbody>
<tr>
<td>2nd Passage in</td>
<td>2.06 ± .064</td>
<td>0.240 ± .011</td>
<td>2.02 ± .007</td>
</tr>
<tr>
<td>CDM No Iron with 150</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>uM DIP</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1st Passage in CDM</td>
<td>3.076 ± 0.050</td>
<td>0.119 ± .004</td>
<td>1</td>
</tr>
<tr>
<td>No Iron with 150 uM</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DIP</td>
<td></td>
<td></td>
<td></td>
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</table>

delta T was calculated by subtracting the cycle threshold (Ct) determined for the fecB 0795 reaction from the Ct of the 5s rRNA control. P value = 0.0003

Table 4e. ftmA 2120 (nonheme ferritin)

<table>
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<th>delta T</th>
<th>delta (delta T)</th>
<th>Fold Change</th>
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<td>2nd Passage in</td>
<td>8.009 ± .003</td>
<td>0.004 ± 0.004 E-3</td>
<td>.809 ± 0.286</td>
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<td>CDM No Iron with 150</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>uM DIP</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>1st Passage in CDM</td>
<td>7.704 ± .424</td>
<td>0.005 ± .001</td>
<td>1</td>
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<tr>
<td>No Iron with 150 uM</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DIP</td>
<td></td>
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</table>

delta T was calculated by subtracting the cycle threshold (Ct) determined for the fecB 0795 reaction from the Ct of the 5s rRNA control. P value = 0.0816
Discussion:

Target genes utilized in this study were chosen due to the fact that previous research has shown that iron acquisition in *A. actinomycetemcomitans* are regulated by quorum sensing (58). The target genes in this study were associated with quorum sensing. Results showed that in an iron chelated environment, iron uptake genes of *A. actinomycetemcomitans* are differentially regulated. Using the 1st passage as a starting point presented as a potential limitation. CDM regular, media containing an iron source, should have been baseline and as we started to starve the bacteria we could have witnessed differential regulation in gene expression. Real time PCR results were normalized to the 1st. *AfuA* 1642, an iron III ABC transporter, was ultimately turned down during the second passage in CDM No Iron with 150 uM DIP. *AfuA* 0696 showed an up regulation of the gene during the 2nd passage in CDM No Iron with 150 uM DIP. This was a very interesting result. *AfuA* 1642 showed down regulation during the 2nd passage and *AfuA* 0696 showed an up regulation during the 2nd passage. This suggest that there may be some distinction between these two ferric iron transporters. It may be possible that under very limiting iron conditions that *A. actinomycetemcomitans* is upregulating ferric iron transport that may be specific for iron coming from a particular source and the other ABC transporter may be down regulated because it is intended to transport iron obtained from a different source. While cells are starving, there seems to be an upregulation of *afuA* 0696 and *fecB* 0795, an iron (III) ABC transporter, and a iron (III) dicitrate binding protein (scavenging system) respectively. The gene regulation of *ftnA* 2120 essentially stayed the same in the first and the second passage. This makes sense that *ftnA* 2120 is not being regulated at all considering it is essentially an iron.
storage molecule. There was down regulation of the hemoglobin binding protein, hgpA 0762 and afuA 0696. What is interesting is that there are three different afuA annotated gene clusters in A. actinomycetemcomitans, and all three have different sequences. This may suggest that these genes may differentially expressed, may have different functions, and may be expressed under different conditions.

Due to the fact that A. actinomycetemcomitans possess a wide variety of potential mechanisms to obtain iron sources, of the iron acquisition genes encoded in A. actinomycetemcomitans genome, A. actinomycetemcomitans differentially expresses genes according to what environment it is in and what different iron sources it is exposed to.
CHAPTER FOUR: SUMMARY AND FUTURE DIRECTIONS

Iron is the most abundant metal in nature, and as such plays a major role in many life processes of all organisms. In the human host, iron is highly regulated, creating a bacteriostatic environment. However in order for organisms to survive they must be able to overcome this iron limitation by encoding in their genome iron acquisition systems. Research to date has revealed that *A. actinomycetemcomitans* has encoded in its genome at least 15 iron acquisition systems to overcome this bacteriostatic environment (67). The iron acquisition systems encoded in *A. actinomycetemcomitans* are tailored towards the specific survival strategies needed to survive in the oral biofilm. Thus *A. actinomycetemcomitans* is expected to be able to utilize inorganic and organic as well as ferric and ferrous iron sources both in planktonic culture and biofilms. These particular findings were expected due to the redundancy of ferric iron transporters in *A. actinomycetemcomitans* genome, and the particular iron sources that *A. actinomycetemcomitans* encounters in the oral cavity. In this study, we investigated the planktonic growth of *A. actinomycetemcomitans* in an iron-limited and iron-chelated environment as well as analyze the ability of *A. actinomycetemcomitans* to grow in an iron-chelated environment supplemented with different iron sources and investigate what particular iron acquisition genes are being upregulated in an iron chelated environment.
We discovered that *A. actinomycetemcomitans* is capable of growing in an iron limited environment, that though there wasn’t a external iron source added to the media that *A. actinomycetemcomitans* was able to scavage trace amounts of iron from other chemicals in the CDM, and efficiently use it for growth. However *A. actinomycetemcomitans* was not capable of growing in an iron chelated environment. By the second passage in an iron chelated environment *A. actinomycetemcomitans* growth was drastically reduced. This lead us to the conclusion that *A. actinomycetemcomitans* has an excellent internal iron storage system that the bacteria is capable of using for growth during the first passage of growth but is not large enough to use for growth during the second passage. The reduction of growth of the bacteria in an iron-chelated environment occurred in a dose dependent manner.

Growth of *A. actinomycetemcomitans* utilizing 250 μM of ferric citrate, ferric chloride, and hemin respectively with 150 μM DIP restored growth to the levels above the 1st passage in an iron chelated environment. Growth of *A. actinomycetemcomitans* was higher in an hemin iron environment, suggesting that *A. actinomycetemcomitans* prefers hemin as an iron source. However *A. actinomycetemcomitans* growth in a ferrous sulfate iron source was very low. It was very similar to the amount of growth that was witnessed in the 2nd passage in an iron-chelated environment leading us to the conclusion that *A. actinomycetemcomitans* appears to not to be able to utilize ferrous sulfate as effectively for growth. This was not suprising considering the analysis of *A. actinomycetemcomitans* genome did not reveal in iron acquisition genes for ferrous iron sources. However we thought that because *A. actinomycetemcomitans* is an anaerobic
bacteria, that in an anaerobic environment that *A. actinomycetemcomitans* may be able to utilize the non oxidized ferrous iron source.

Results from Realtime PCR showed that in an iron chelated environment, iron uptake genes of *A. actinomycetemcomitans* are differentially regulated. Using the 1st passage as a starting point presented as a potential limitation. CDM regular, media containing an iron source, should have been baseline and as we started to starve the bacteria we could have witnessed differential regulation in gene expression. Real time PCR results were normalized to the 2nd passage and what was seen was afuA 1642 showed a 7 fold increase than in the 1st passage compared to the 2nd passage. AfuA 0696 showed a 10 fold higher increase than in the 2nd passage that in the 1st passage. While cells are starving, there seems to be an upregulation of afuA 0696 and fecB 0795, and iron (III) ABC transporter, and a iron (III) dicitrate binding protein (scavenging system) respectively. The gene regulation of ftnA2120 essentially stayed the same in the first and the second passage. This makes sense that ftnA2120 is not being regulated at all considering it is essentially and iron storage molecule. There was a down regulation of the hemoglobin binding protein and afuABC 0696. What is interesting is that there are three different afuA annotated gene clusters in *A. actinomycetemcomitans*, and all three have different sequences. This may suggests that these genes may differentially expressed may have different functions, and may be expressed under different conditions.

Though many questions have had some light shed on them during my research, more research still needs to be done. Ultimately the original idea of my research was to first look at the expression of a couple of these iron acquisition systems under the initial iron conditions used, in other words the 1st and 2nd passages in CDM No Iron with 150
uM DIP. After the expression of the iron acquisition genes were established under the iron chelated conditions, our goal then was to add back specific iron sources and see what happened to gene expression with the different iron operons under these different iron conditions. The first part of our goal we accomplished, however the second part is a project that a future student will carry on. I also only focused on a limited numbers of operons, in the future more iron acquisition genes should be included. Also to make my research show more validity, mutant strains of *A. actinomycetemcomitans* should be formulated, knocking out specific iron operons and testing the growth and gene regulation under the different iron conditions. Because past and current research all describe *A. actinomycetemcomitans* as growing in a biofilm, more studies on iron acquisition genes with *A. actinomycetemcomitans* grown in a biofilm formation are needed if there are any hopes in formulating a chelator that is strong enough to chelate the preferred iron source of *A. actinomycetemcomitans*, that the human host is also able to tolerate.
REFERENCES


CURRICULUM VITAE  

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Higher Education

2000-2004  
Holmes High School  
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-Work Ethic Diploma  
-Holmes High School Diploma  
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2004-2008  
University of Louisville  
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2008-2012  
University of Louisville School of Dentistry  
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D.M.D.

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M.S.

2012-current  
University of Louisville School of Dentistry  
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Pediatric Speciality Certificate
Academic Appointments:

2011-2012  Biochemistry Academic Tutor  
            University of Louisville School of Dentistry

2011-2012  Aesthetics Academic Tutor  
            University of Louisville School of Dentistry

2011-2012  Oral Diagnosis and Oral Pharmacology Academic Tutor  
            University of Louisville School of Dentistry

2009-2012  Research Student  
            University of Louisville School of Dentistry

2009-2012  Head and Neck Anatomy Academic Tutor  
            University of Louisville School of Dentistry

2009-2010  Microbiology Academic Tutor  
            University of Louisville School of Dentistry

2007-2008  Upward Bound Academic Tutor  
            University of Louisville  
            Louisville, KY

Honors and Academic Achievements

2012  Oral Health and Systemic Research Award

2012  American Academy of Pediatric Dentistry Award

2012  Pierre Fauchard Award

2012  Karen Andrus Award

2012  Kentucky Off-site Clinical Community Service Scholar

2012  Hispanic Dental Association U of L Chapter Award

2011  The Hinman Research Symposium- Louisville Representative

2011-2012  Clinical Outreach Scholarship
2011  SNDA National Convention Delegate (Baltimore, Maryland)
2011  Indiana University Research Participant
2011  SNDA Leadership Conference Delegate
2011  3rd Place in Research Louisville
2010-2012  Student Representative on ULSD Admissions Committee
2010  Student Representative for Outreach Scholar Committee
2010  Research Louisville Participant
2010  2nd Place in Research Louisville
2010  2nd Place in Research at SNDA National Research Competition
2009  4th Place in Research at Student Convention
2010  SNDA National Convention Delegate (Hawaii)
2008-2010  University of Louisville School of Dentistry Dean’s List
2008-2012  General Dentistry Scholarship (Full Tuition)
2007  MCAT/DAT Summer Program Participant
2006-2008  Alpha Epsilon Delta Health Honor Society
2006-2008  University of Louisville Dean’s List
2004-2008  Woodford Porter Senior Scholarship (Full Tuition & Room and Board)
2004  Salutatorian
2004  Louisville Book Award
2004  Advanced Placement Social Studies Award
2004  Key to the City of Covington for Academic Achievement
2004  Northern Kentucky Coaches Association Cheerleading Scholarship
2003 Advanced Placement Math Award
2003 Northern Kentucky University Spanish Award
2002-2003 Governor School for the Arts Participant
2002-2003 Governor Scholar Program Recipient

**Academic Positions**

2011 Cultural Competency Seminar- Student Panel Member
2010-2011 Student National Dental Association- President
2010-2011 American Association of Women Dentist- Secretary
2010-2011 Dental Class Secretary
2009-2010 Student National Dental Association- Social Chair
2008-2012 American Student Dental Association- General Member
2008-2010 American Dental Education Association- General Member
2008-2012 Psi Omega Dental Fraternity
2004-2008 Kappa Delta Sorority General Member
2004-2008 Alpha Epsilon Delta Pre Health Honor Society
2003-2004 Holmes High School Class President
2003-2004 National Honor Society President

**Work Experiences**

2012-current Pediatric Dental Resident
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Louisville Ky, 40208

2012-current Dentist
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2011  Dental Student  
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   Louisville Ky, 40217

2008  Library Student Assistant  
   Kornhaeuser Library  
   Louisville Ky, 40208

2007-2008  Upward Bound Academic Tutor  
   University of Louisville  
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2005  Brand Representative  
   Abercrombie & Fitch  
   Louisville Ky, 40208

2005  Sales Associate  
   Charolette Russe  
   Louisville Ky, 40208

2004-2006  Lifeguard  
   City of Covington Recreation Parks  
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2003-2006  Veterinarian Assistant  
   Ft. Wright Pet Care  
   Ft. Wright, Ky 40214

**Community Service**

2009-2011  Rural America Missions (Pikeville) Volunteer

2008-2012  Whitney Young Foundation Volunteer

2008-2012  Black Achievers Volunteer

2008-2012  Lincoln Foundation Volunteer

2008-2012  University of Louisville School of Dentistry Impressions Program

2008-2012  Wayside Christian Services Soup Kitchen Volunteer

2008-2012  Angel Tree Volunteer
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