



**CALIFORNIA STATE SCIENCE FAIR
2002 PROJECT SUMMARY**

Name(s) H. Cindy Ko	Project Number S1314
Project Title Genomic Comparison Between Pathogenic <i>A. actinomycetemcomitans</i> and Non-Pathogenic <i>H. aphrophilus</i>	
<p style="text-align: center;">Abstract</p> <p>Objectives/Goals The objective of my project was to find the fragments of DNA that were present in <i>A.actinomycetemcomitans</i> (A.a.) and not present in <i>H.aphrophilus</i> (H.a.). A.a. is the bacteria associated with juvenile periodontitis and H.a. is its harmless, phylogenetic cousin.</p> <p>Methods/Materials The method of Representational Difference Analysis (RDA) was employed to reveal the differences between <i>A. actinomycetemcomitans</i> and <i>H. aphrophilus</i>. It is essentially a subtraction method that allows only the DNA fragments unique to A.a. to be replicated by Polymerase Chain Reaction (PCR).</p> <p>Results Eight fragments of DNA from <i>A. actinomycetemcomitans</i> were found, cloned into competent cells, and sequenced. Those sequences were later compared to other genomes decoded online on such websites as NCBI and Oklahoma University. Homologues to four of these fragments were found and compared, the four others found no homology to either sites' databases. Therefore, these fragments are deemed to be unique to A.a. (concluded from the information on the database) and some of them are even unique to the particular strain used, D-7.</p> <p>Conclusions/Discussion These fragments were matched to other pathogenic bacteria (such as: <i>Multocida tuberculosis</i>, and <i>Escherichia coli</i>, for example), leading to the possibility that several of these pathogenic bacteria share similar genes that allow them to be pathogenic. The fragments coded for such things as sensory kinases, methionine aminopeptidases, etc. These functions could be the reason why A.a. causes juvenile periodontitis and H.a. is completely commensal. For example, the sensory kinase could help A.a. sense other bacteria in the mouth, competing for a similar ecological niche.</p>	
Summary Statement The project focuses on finding the genomic differences between <i>A. actinomycetemcomitans</i> and <i>H. aphrophilus</i> in hopes of finding the genes responsible for making <i>A. actinomycetemcomitans</i> pathogenic and <i>H. aphrophilus</i> merely commensal.	
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