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Rough Draft

Competence levels of Very Short Dispersed Repeats

 Natural transformation refers to bacteria’s ability to uptake exogenous DNA from another bacteria, across its own cell wall. The cells ability to take up this exogenous DNA is known as competence. The first cases of natural transformation and DNA uptake were first observed over 80 years ago in bacteria species such as Bacillus, Neisseria, and Staphylococcus. Since then these types of bacteria have been the focus of many experiments that study this phenomenon.

 For my study, I would like to look at the well-known bacteria uptake sequence in Haemophilus influence (5’-AAGTGCGGT-‘3) and by using online genomic tools, look at other bacterial genomes that share this sequence and other similarities they have with H. influenza to try to understand the significance of this highly conserved sequence.

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| --- | --- | --- | --- |
| Bacteria | Uptake Occurrence | Randomness | Length |
| H. influenza 86028NP | 734 |  | 1,913,428 |
| Mannheimia succiniciproducens | 730 |  | 2,314,078 |
| Haemophilus somnus 2336 | 694 |  | 2,263,857 |
| Actinobacillus-succinogenes-130Z | 838 |  | 2,319,663 |
| Actinobacillus-pleuropneumoniae-L20 | 33 |  | 2,274,482 |

H. influenza belongs to the bacteria family of Pasteurellaceae, which account for gram-negative bacteria with similar metabolic functions. The Pasteurellaceae family is commonly known for its pathogenic members.

 I looked to see if other bacteria in this family shared this sequence and found that some did and others did not. The bacteria that stuck out the most to me was Mannheimia-succiniciproducens because this had the most occurrence of this sequence next to H. influenza and it made me curious why it has been conserved so highly. When I tried to learn more about this bacterium, I found close to nothing, which made me even more curious as to why this bacteria does not have prevalence in literature. The next most striking occurrence I found was in the bacteria [*Actinobacillus succinogenes*](http://en.wikipedia.org/wiki/Actinobacillus_succinogenes), and I was able to find a little more information on this bacterium than I was for M. succiniciproducens.

 Further exploration of the uptake sequences is to be worked on in the upcoming days to determine how unique that these sequences appear in the genomes above and potentially what genes are regulating these as well if these sequences appear in non-coding regions of the genome. The exact algorithm is still being worked on.

**Works Cited**

More info on A. succinogenes

[**http://genome.jgi-psf.org/actsu/actsu.home.html**](http://genome.jgi-psf.org/actsu/actsu.home.html)

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