A Further Exploration of Bacterial Divisional Factors with Regards to Genome Size

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This year we continued in the exploration of the correlation between prokaryotic genome size and the rate at which the bacteria is able to undergo binary division. The specific goal being, to create a model that could predict how large the genome of a prokaryotic bacteria is, using materials available to the average high-school student with a calculated error percentage of less than 2 % percent in every case. We tested our method on 11 different prokaryotes that together we believe are representative of the broad spectrum of the prokaryotic kingdom. We were successful in our original goal of achieving an error percentage of less than 2% in every case that we studied. We believe that this method could have implications in the field of microbiology as an accurate measurement of an unknown prokaryotes genome, which is extremely helpful in the identification process of an unknown pathogen, especially in areas without access to more expensive and advanced equipment.

Awards Won: