

# Summary of an experiment – The Genome Sequence and Evolution of Baculoviruses

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## I. setting of the experiment where? How?

Before there were dinosaurs, there were a humongous insect's that when compared to the insect of today variety are on the similar scale to dinosaurs as birds. They were trying to find a way of knowing what viruses could have infected these insects by classifying a common ancestor from evolutionary equivalent. Here an impractical use of time and a time-machine. So instead we would like to try and find a possible work around. One possible way is to look at the viral genes and then compare them all at a relative frequency of their at that site at which it pops up at a virus's genome. Where their gene should be placed and compared that to the other four groupings of this distinctive virus. In this study, they found that they had already had the thirty distinct genes and were just introducing more genomes into the tree. They already had the set of core genes to go about and compare to the other the newly acquired genomes in order for them to do analysis of their phylogenetic tree.

For some of them they tried to do a one-on-one comparison to the viral genes in which that made did not lead to a consistent look tree. They made several different types of trees, some in which had different functions in order for them to see how many distinctive changes had occurred, between the first graph and the final graphs organization.

Where do I want to go with this statement? When we look at a certain population of Baculoviruses, we are looking for population control of insect, so when the virus that infects these insects populations such as mosquitoes why? Is the classification of baculovirus with specific genes

## II. what is the knowledge that I am seeking for summarizing the experiment

## III