

# Review of: "Empirical estimates of the mutation rate for an alphabaculovirus"

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This article is small and precise, focuses to answer one question, that is, the mutation rate of AcMNPV. The experimental design skillfully regarded the bacterial sequence in AcBAC as a neutral selection region (similar to a housekeeper gene), and constructed a recombinant virus with POLH. Through continuous passaging for 5 generations, SNV mutation was analyzed to estimate the mutation rate of the whole AcMNPV genome, so as to provide a theoretical basis for calculating the evolution time of other baculoviruses. The highlight lies in its algorithm calculation, and the calculated mutation rate is similar to that of other DNA/RNA (representative strain enterobacteria phage T2, Escherichia virus  $\lambda$ ), thus the mutation rate is persuasive.

There are concerns with this study which include the following:

1. The effect of the 11.6 KB bacterial sequence region inserted into AcBAC on the mutation rate of the whole virus genome is unknown, it is only a neutral mutation region in theory. It is more convincing if the wild-type AcMNPV passing through 5 generations alone is set as control, and there was no significant difference between the mutation rate of AcBAC and wild-type AcMNPV passing through 5 generations.
2. In the background part, there is little introduction to the background related to mutation. For those without relevant professional knowledge, it is a little abstruse and difficult to understand.