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### **Evaluation of the doctoral thesis of Benjamin Guinet, University of Lyon.**

In his thesis, “Etude globale de la domestication virale chez les guêpes parasitoïdes”, Benjamin Guinet used different comparative genomic analyses to identify genes of viral origin that are integrated in the genomes of a diversity of hymenopteran species, and sometimes acquired key functions in the species’ life cycles. He also discovered and described a new family of viruses and was able to date different key endogenization events in the evolutionary history of a group of wasps.

In the first of three studies, the different conducted analyses and newly developed pipelines revealed numerous endogenization and domestication events of viruses in hymenopteran genomes, and an enrichment of these events in species with endoparasitic lifestyles. I enjoyed reading this study very much and expect it to trigger new research directions on virus domestication. I was wondering whether it would be possible to provide information on the ability to detect pseudogenized viral genes in the host genomes; a priori the detection of recent or domesticated endogenization events will be more likely than non domesticated cases, as the latter will have a faster rate of divergence. This would be important for assessing the rate of domestication among endogenized viruses among species with different lifestyles as well as for the conclusion that IVSPER genes in the Campopleginae and Banchinae subfamilies were indeed independently acquired. The study also reports that dsDNA viruses are more frequently endogenized than expected, given their representation in the databases; however, databases likely provide some information on diversity of viruses, but not their relative abundances (i.e., proportion of individuals infected with one or another type of virus in the database), which is what would matter for exposure probability. Perhaps the frequency of different free-living viruses sequenced along with their hosts during the generation of reference genomes could give more biologically relevant information for assessing “infection risk” with specific virus categories?

Given the additional detection of endogenization events in the *P. orseoliae* assembly when using a new “free-living” virus for homology searches, it might also be useful to systematically add all the free-living viruses sequenced along with the hosts when screening for endogenization?

Finally, since the pipeline to conduct large scale screens for virus endogenization was newly developed, it would have been useful to provide some parallels to the widely used pipelines

for detecting horizontal gene transfers in eukaryote genomes where for example the simultaneous presence of a viral gene BLAST hit and eukaryotic gene hit on the same contig is key for HGT inference (i.e., similar classification strategies as the ones used here).

The second study describes morphological and genomic features of a new viral family, the “Filamentoviridae”. This family appears to be particularly abundant among Hymenoptera with parasitoid lifestyle. The discovery of this family and its association with parasitoids of course raises the question of whether the viruses play a particular role for the biology of parasitoids, which will be an interesting avenue for future research.

The third study then focuses on dating different endogenization events of Filamentoviridae. It shows that Filamentoviridae and Hymenoptera likely co-existed and co-evolved for a long time (one event dated to 75 Mya!), which may help explain the acquisition of specific functions associated with virus domestications over evolutionary time.

The three studies are introduced by a broad general overview on viruses, their endogenization and domestication, with different specific examples illustrating each topic. There is also a general description on the biology, diversity and phylogeny of parasitoid wasps which nicely introduces the specific foci of the three studies.

In summary, I have no hesitation in recommending this work for the award of a PhD. The work presented in this thesis provides new insights into the dynamics of virus domestication in parasitoid wasps and the potential factors promoting this domestication, topics for which we currently have very little understanding overall. The results developed during the thesis will not only serve as a useful tool for further analyses but should also go on to inspire new work on virus endogenization and domestication in general.

Yours sincerely,



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