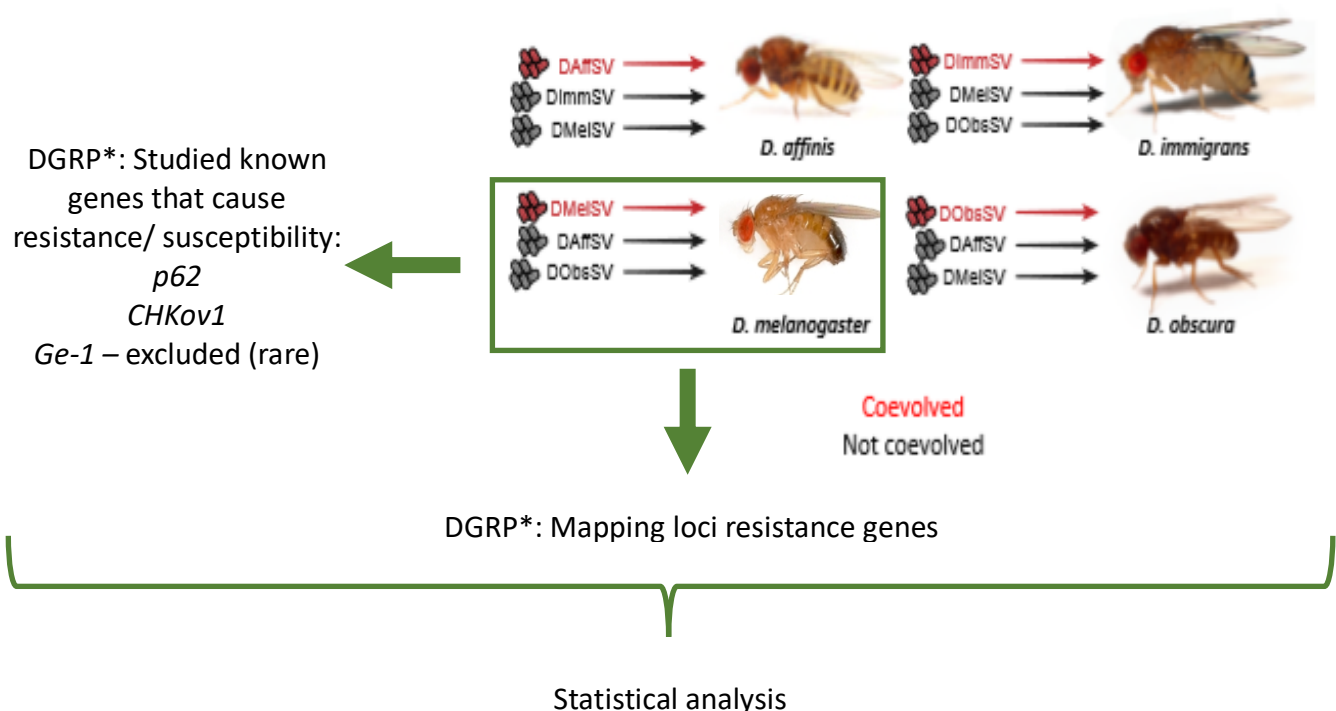


Paper: Host-pathogen coevolution increases genetic variation in susceptibility to infection

Main question: Is there genetic variation responsible for coevolution resistance in host-pathogen infections?

Work importance: The study of natural host-pathogen systems and genetic variation associated with resistance or susceptibility to disease will allow to make associations on how the host and pathogen genetics adapt due to coevolution.

Methods: To examine how selection by pathogens affects levels of genetic variation it was used a natural host-pathogen system: *Drosophila* and sigma viruses.



Conclusions: The authors found that there is more genetic variation in naturally coevolved host-pathogens by measuring the viral load and comparing the genetic variance between viruses within the same host. However, the genes that cause protection to DMeISV are not protective against the other viruses. This was shown by studying flies homozygous or heterozygous for the alleles from known resistance genes (*p62* and *CHKov1*), concluding that carrying the resistant allele for *CHKov1* is enough to increase resistance to viral infection. Finally, it was also found more major-effect variants in natural coevolved host-virus associations compared to non-coevolved, it was identified 7 QTLs that explain most of the genetic variance to coevolved virus and 2 QTLs that confer resistance to more than one virus.

Overall, pathogen selection of host can increase the amount of genetic variation in host susceptibility and lead to resistance that is majorly controlled by major effect resistance loci.