# A novel virus surveillance strategy for colony collapse disorder based on host specific features of invertebrate iridescent virus

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## Abstract

Honey bees are crucial pollinators for more than 1000 crops, hence they are closely associated with agriculture economics and human life. Recent studies indicate that colony collapse disorder (CCD) induced by iridovirus severely reduces honey bee population, yet valid detection for virus surveillance is not available. The *Iridoviridae* family is classified into invertebrate iridescent viruses (IIVs) and vertebrate iridescent viruses (VIVs). The IIVs of different genus are reported to affect host-specific insect growth and reproduction, and may lead to cell apoptosis of economically important honey bees. However, the major capsid protein represents approximately 40 percent of the total particle polypeptide is highly conserved among different IIVs, and true receptor for viral infection is still unknown. Here we collect clustered subfamilies of vertebrate and capsid proteins for exclusive feature analyses and epitope prediction. A voting mechanism based on five renowned linear epitope (LE) prediction systems was proposed for clustered pathogen groups under the constraint of non-cross-infectious between vertebrate and invertebrate host species. All predicted LE candidates for invertebrate iridovirus could be identified and virtually re-confirmed through predicted structural alignment analysis. In this study, all predicted conserved and unique LEs for bee infected invertebrate iridovirus were *in silico* analyzed comprehensively. Whether the predicted LEs possessing high antigenicity responses would be further experimentally verified. We demonstrated that a combination of multiple LE prediction systems incorporating multiple sequence/structural alignment analysis could provide an effective approach *in silico* LE prediction, especially for honey bee specific pathogens.

## Image

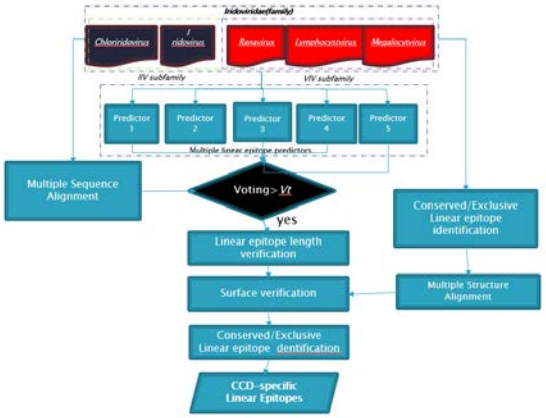



Figure 1. The proposed system for identifying host specific linear epitopes of IIVs and applied for CCD surveillance applications.

## Recent Publications

1.Bromenshenk JJ, Henderson CB, Wick CH, Stanford MF, Zulich AW, Jabbour RE, et al. (2010) Iridovirus and microsporidian linked to honey bee colony decline. PLoS ONE 5(10): e13181.

2. Chinchar VG,Waltzek TB, Subramaniam K. (2017) *Ranaviruses* and other members of the family *Iridoviridae*: Their place in the virosphere. Virology. 2017 Nov;511:259-271

3. Price SJ, Ariel E,Maclaine A, Rosa GM, et al. (2017) From fish to frogs and beyond: Impact and host range of emergent *ranaviruses*. Virology. 2017 Nov;511:272-279.

4. Camazine, S. & T.P. Liu. (1998) A putative iridovirus from the honey bee mite varroa jacobsoni oudemans. J. Invertebr. Pathol. 71: 177-178.

5. L. Bailey, Brenda V. Ball, R. D. Woods (1976) An iridovirus from bees. Journal of general virology 31: 459-461



## Biography

Shiuan-Yu Pai, a senior student of Department of Veterinary Medicine at National Taiwan University, Taipei, Taiwan. He is a member of International Veterinary Student Association and has served as vice president of Taiwan Veterinary Medicine Student Association. He also held 2016 IVSA symposium in Taiwan. His expertise is wildlife rescue, rehabilitation and research. He is interested in wild animal no matter vertebrate or invertebrate, and travels a lot to observe those gorgeous creatures. He has participated in rescue action in Taichung Wildlife Conservation Association during intern, saw many species suffering from illness. Thus, he is learning to use bioinformatics method to analyze and solve problems, aiming at integration of *in silico* and *in vitro* data as a novel strategy for virus detection.

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**Notes/Comments:**