

昆虫病理学研究ワークショップ

Workshop on insect pathology and evolution of insect viruses

2009年11月18日（水）午後1時～5時

東京農工大学府中キャンパス2号館 4階 401室

18th November, 2009, 1:00pm Tokyo University of Agriculture and Technology (TUAT), Fuchu-campus
2 gokan building 4th floor, room no. 401

招待講演 エリザベス ヘルニヨ博士

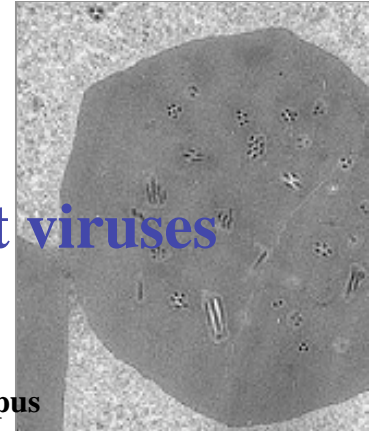
ツール大学昆虫生物研究所 主任研究員

Invited speaker: Dr Elisabeth A. Herniou

Institut de Recherche sur la Biologie de l'Insecte,
Université de Tours, Tours, France

「分子系統解析によるブラコウイルスの進化的起源の解明」

Phylogenomic approaches unravel the origin and tempo of bracovirus evolution



昆虫ウイルスの分子系統解析の専門家であるHerniou博士をフランスより招きポリドナウイルス研究の最新トピックとバキュロウイルスの進化について講演していただきます（講演要旨参照）。また、応用遺伝生態学研究室の修士課程学生による研究紹介を行います（プログラム参照）。

学科や専攻に関係なく学生・職員の参加をお待ちしています。農工大学外からの参加も歓迎します。参加費無料。
All students and staff are invited to attend. Overseas students are especially welcome. The talks will be in English. Attendance is free.

問い合わせ先：

応用生物科学科 仲井まどか 内線5695

Contact: Madoka Nakai madoka@cc.tuat.ac.jp

昆虫病理学研究ワークショップ

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Workshop Program

Organizer: Madoka Nakai (TUAT)

13:00-13:15 Naoya Akizuki (M1 student, TUAT)

Manipulation of reproduction of *Homona magnanima* by the symbiont *Wolbachia*.

13:15-13:30 Keisuke Ushiki (M1 student, TUAT)

Does immunosuppression by *Chelonus inanitus* (Braconidae) increase host susceptibility to baculoviruses?

13:30-13:45 Kaoru Teduka (M1 student, TUAT)

Construction of recombinant viruses without using cell cultures.

-Tea Break-

14:15-14:30 Kentaro Kurumaji (M2 student, TUAT)

Endocrinological regulation by *Xestia c-nigrum* granulovirus, which does not encode ecdysteroid UDP-glucosyltransferase.

14:30-14:45 Shohei Hikiyama (M2 student, TUAT)

Comparative genome analyses of *Adoxophyes orana* granulovirus and an occlusion body shape/size mutant.

14:45-15:00 Kaoru Tanaka (M2 student, TUAT)

Resistant development of insect against *Adoxophyes honmai* nucleopolyhedrovirus.

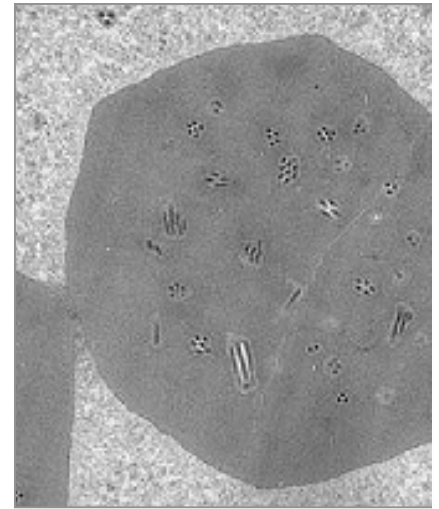
-Tea Break-

15:30-16:30 Elisabeth Herniou (Université de Tours)

Phylogenomic approaches unravel the origin and tempo of bracovirus evolution.

16:30-17:00 Discussion

17:00 close



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Phylogenomic approaches unravel the origin and tempo of bracovirus evolution

Elisabeth Herniou (Université de Tours)

Recent genomic data revealed the nudiviral origin of the polydnviruses of braconid wasps. Here we assembled all the viral genomic data available for bracoviruses to perform detailed phylogenetic analyses of the relationships between bracoviruses, nudiviruses, baculoviruses and salivary gland hypertrophy viruses. We performed multiple alignments of the 19 bracovirus genes of viral origin. We verified the phylogenetic signal congruence between all the genes, before concatenating the alignments for the phylogenetic reconstruction of the evolutionary history of bracoviruses. The tree showed that nudiviruses are paraphyletic with the inclusion of bracoviruses within the clade. Bracoviruses indeed derive from nudiviruses.

The analyses of evolutionary rates revealed that the transition from free living to obligatory symbiotic virus has led to changes in the selection pressure put upon the viral genes. Lastly, since this phylogeny is connecting virus with braconid wasp evolution, we were able to use fossil data to date the virus tree.

