

令和 3 年 6 月 28 日現在

機関番号：38005

研究種目：基盤研究(B) (一般)

研究期間：2018～2020

課題番号：18H02216

研究課題名(和文)Origins, spread and evolution of novel honey bee parasites and diseases

研究課題名(英文)Origins, spread and evolution of novel honey bee parasites and diseases

研究代表者

ミケエエヴ アレクサンダー (Mikheyev, Alexander)

沖縄科学技術大学院大学・生態・進化学ユニット・准教授

研究者番号：90601162

交付決定額(研究期間全体)：(直接経費) 13,000,000円

研究成果の概要(和文)：寄生生物によるホストスイッチの成功は、新たな資源を獲得し種分化を起こす進化上の出来事である。観察は困難で世界的なパンデミックの要因である。我々は、外部寄生虫として世界的にミツバチ減少をもたらしているVarroa属の二種のダニについて、ホストスイッチの動態の変遷を再現した。このダニがクローン様に均質とする従来の考えと、世界的に広まる現状には遺伝学的な矛盾がある。我々は数百個体に相当する遺伝的多様性がホストスイッチに関与することを発見し、ダニが多様なミツバチ集団や殺虫剤に適應する根拠を見出した。これにより、ダニの動態に関わる変数のうち特に遺伝的多様性がホストスイッチに重要なことが明らかとなった。

研究成果の学術的意義や社会的意義

Our results highlight the importance of demographic parameters, particularly genetic diversity, for parasitic host switches

研究成果の概要(英文)：Successful host switches by parasites are evolutionary events that enable them to access new resources, and can lead to eventual speciation. Host switch events can be difficult to observe, yet they can lead to worldwide pandemics. We reconstructed the demographic history of host switches by two species of ectoparasites, Varroa mites, which are the principal drivers of worldwide honey bee declines. Varroa mites are believed to be “quasi-clonal”, making their worldwide success a genetic paradox. However, we found that the host switch involved the genetic equivalent of hundreds of individuals, explaining the remarkable adaptation of the parasites to both diverse bee populations and pesticides. These results highlight the importance of demographic parameters, particularly genetic diversity, for parasitic host switches.

研究分野：evolution

キーワード：evolution parasites honey bees

様式 C - 19、F - 19 - 1、Z - 19 (共通)

1. 研究開始当初の背景

Arms races between parasites and their hosts drive evolutionary innovation. Novel parasites can decimate host populations or drive them extinct, unless counter-adaptations evolve. Similarly, parasite evolution accompanies the very act of host switching, since it requires adaptations to novel host physiology in order to persist and to spread. Because parasite adaptations tend to be host-specific, host switches are often associated with host-associated genetic differentiation and eventual speciation. However, only the endpoint of this process is typically observed, as host switches tend to occur rapidly, and the original host is often unknown. As a result, many unanswered questions remain about how parasites acquire new hosts. For instance, if host switches are accompanied by a bottleneck due to reduced gene flow from the ancestral host, how does the parasite have sufficient genetic diversity to adapt? Does gene flow cease completely, or does it continue at a low level, potentially providing additional genetic material for adaptations?

2. 研究の目的

One of the major limiting factors for host switching is the geographic separation between parasites and potential hosts. Globalization has eased these barriers, sometimes giving rise to pandemics (Hatcher, Dick, and Dunn 2012). As a result, host switches are easier to observe and to study in something approaching real time. One of the most dramatic and economically important switches involved the two ectoparasitic mite species, *Varroa destructor* and *Varroa jacobsoni*, which acquired the western honey bee (*Apis mellifera*) as a new host, ~70 and ~12 years ago, respectively (Anderson and Trueman 2000; Roberts, Anderson, and Tay 2015). *V. destructor*, in particular, spread worldwide, causing extensive honey bee population collapses, whereas *V. jacobsoni* has so far remained in Oceania (Traynor et al. 2020; Noël, Le Conte, and Mondet 2020). Both mites were originally found on the sister species, *Apis cerana*, and came into contact with *A. mellifera*, which was brought in for purposes of beekeeping (Crane 1968; Chantawannakul et al. 2016). These two host switches occurred in parallel and relatively recently, allowing the reconstruction of how the host switches took place, using genomic tools.

Both switches have been investigated using microsatellite markers and relatively short mitochondrial markers, which revealed that in both species, populations parasitizing *A. mellifera* were strongly differentiated and genetically depauperate (Solignac et al. 2005; Warrit, Smith, and Lekprayoon 2006; Navajas et al. 2010; Beaufort et al. 2015; Roberts, Anderson, and Tay 2015; Dietemann et al. 2019). While *V. destructor*, in particular, was described as “quasi-clonal” (Solignac et al. 2005), it successfully spread worldwide, and has shown a remarkable ability to parasitize genetically diverse *A. mellifera* populations, as well as to evolve resistance to human counter-measures, such as pesticides (González-Cabrera et al. 2016). How does a bottlenecked species achieve such a level of success? Increasing evidence from population genomic analysis of fungal pathogens suggests that the success of many pathogens appears to rely on maintaining some level of adaptive diversity despite the presence of bottlenecks during host switches (Fry 2016; McMullan et al. 2018), but similar work is lacking in animal systems.

3. 研究の方法

Using whole-genome sequencing on 63 mites collected in their native ranges from both the ancestral and novel hosts, we were able to reconstruct the known temporal dynamics of the switch using a combination of whole genome sequencing, both nuclear and mitochondrial.

4. 研究成果

In order to answer this question and to gain broader insight into how host switches happen, we sequenced genomes from sympatric populations of the two mites across Asia

and Oceania, collected on both novel and introduced hosts. This allowed us far greater power to examine how the host switch took place with much greater precision than was possible previously. We found strikingly parallel dynamics at play in both host switches, which were characterized by a surprisingly large effective population size at the time of the switch and ongoing gene flow with cryptic population genetic processes that may have helped *Varroa* succeed.

References

- Anderson, D. L., and J. W. Trueman. 2000. "Varroa Jacobsoni (Acari: Varroidae) Is More than One Species." *Experimental & Applied Acarology* 24 (3): 165-89.
- Beaurepaire, Alexis L., Tuan A. Truong, Alejandro C. Fajardo, Tam Q. Dinh, Cleofas Cervancia, and Robin F. A. Moritz. 2015. "Host Specificity in the Honeybee Parasitic Mite, Varroa Spp. in Apis Mellifera and Apis Cerana." *PLoS One* 10 (8): e0135103.
- Chantawannakul, Panuwan, Lilia I. de Guzman, Jilian Li, and Geoffrey R. Williams. 2016. "Parasites, Pathogens, and Pests of Honeybees in Asia." *Apidologie* 47 (3): 301-24.
- Crane, Eva. 1968. "Beekeeping Round the World." *Bee World* 49 (3): 113-14.
- Dietemann, Vincent, Alexis Beaurepaire, Paul Page, Orlando Yañez, Ninat Buawangpong, Panuwan Chantawannakul, and Peter Neumann. 2019. "Population Genetics of Ectoparasitic Mites Varroa Spp. in Eastern and Western Honey Bees." *Parasitology* 146 (11): 1429-39.
- Fry, William E. 2016. "Phytophthora Infestans: New Tools (and Old Ones) Lead to New Understanding and Precision Management." *Annual Review of Phytopathology* 54 (August): 529-47.
- González-Cabrera, Joel, Sonia Rodríguez-Vargas, T. G. Emyr Davies, Linda M. Field, Daniel Schmehl, James D. Ellis, Klemens Krieger, and Martin S. Williamson. 2016. "Novel Mutations in the Voltage-Gated Sodium Channel of Pyrethroid-Resistant Varroa Destructor Populations from the Southeastern USA." *PLoS One* 11 (5): e0155332.
- Hatcher, Melanie J., Jaimie T. A. Dick, and Alison M. Dunn. 2012. "Disease Emergence and Invasions." *Functional Ecology* 26 (6): 1275-87.
- McMullan, Mark, Maryam Rafiqi, Gemy Kaithakottil, Bernardo J. Clavijo, Lorelei Bilham, Elizabeth Orton, Lawrence Percival-Alwyn, et al. 2018. "The Ash Dieback Invasion of Europe Was Founded by Two Genetically Divergent Individuals." *Nature Ecology & Evolution* 2 (6): 1000-1008.
- Navajas, Maria, Denis L. Anderson, Lilia I. de Guzman, Zachary Y. Huang, Jeremy Clement, Ting Zhou, and Yves Le Conte. 2010. "New Asian Types of Varroa Destructor: A Potential New Threat for World Apiculture." *Apidologie* 41 (2): 181-93.
- Noël, Amélie, Yves Le Conte, and Fanny Mondet. 2020. "Varroa Destructor: How Does It Harm Apis Mellifera Honey Bees and What Can Be Done about It?" *Emerging Topics in Life Sciences* 4 (1): 45-57.
- Roberts, J. M. K., D. L. Anderson, and W. T. Tay. 2015. "Multiple Host Shifts by the Emerging Honeybee Parasite, Varroa Jacobsoni." *Molecular Ecology* 24 (10): 2379-91.
- Solignac, Michel, Jean-Marie Cornuet, Dominique Vautrin, Yves Le Conte, Denis Anderson, Jay Evans, Sandrine Cros-Arteil, and Maria Navajas. 2005. "The Invasive Korea and Japan Types of Varroa Destructor, Ectoparasitic Mites of the Western Honeybee (Apis Mellifera), Are Two Partly Isolated Clones." *Proceedings. Biological Sciences / The Royal Society* 272 (1561): 411-19.
- Traynor, Kirsten, Fanny Mondet, Joachim de Miranda, Maeva Techer, Vienna Kowalik, Melissa Oddie, Panuwan Chantawannakul, and Alison McAfee. 2020. "Varroa Destructor: A Complex Parasite, Crippling Honeybees Worldwide." *BIOLOGY*. <https://doi.org/10.20944/preprints202002.0374.v1>.
- Warrit, Natapot, Deborah Roan Smith, and Chariya Lekprayoon. 2006. "Genetic Subpopulations of Varroa Mites and Their Apis Cerana Hosts in Thailand." *Apidologie* 37 (1): 19-30.

5. 主な発表論文等

〔雑誌論文〕 計2件（うち査読付論文 2件/うち国際共著 2件/うちオープンアクセス 2件）

1. 著者名 Maeva A. Techer, Rahul V. Rane, Miguel L. Grau, John M.K. Roberts, Shawn T. Sullivan, Ivan Liachko, Anna K. Childers, Jay D. Evans, Alexander S. Mikheyev	4. 巻 2
2. 論文標題 Divergent evolutionary trajectories following speciation in two ectoparasitic honey bee mites	5. 発行年 2019年
3. 雑誌名 Communications Biology	6. 最初と最後の頁 357
掲載論文のDOI（デジタルオブジェクト識別子） 10.1038/s42003-019-0606-0	査読の有無 有
オープンアクセス オープンアクセスとしている（また、その予定である）	国際共著 該当する

1. 著者名 Nurit Eliash, Alexander S. Mikheyev	4. 巻 39
2. 論文標題 Varroa mite evolution: a neglected aspect of worldwide bee collapses?	5. 発行年 2020年
3. 雑誌名 Current Opinion in Insect Science	6. 最初と最後の頁 21-26
掲載論文のDOI（デジタルオブジェクト識別子） 10.1016/j.cois.2019.11.004	査読の有無 有
オープンアクセス オープンアクセスとしている（また、その予定である）	国際共著 該当する

〔学会発表〕 計1件（うち招待講演 1件/うち国際学会 0件）

1. 発表者名 Alexander Sasha Mikheyev
2. 発表標題 Coevolution while you wait: the arms race between honey bees and ectoparasitic Varroa mites
3. 学会等名 University Seminar（招待講演）
4. 発表年 2018年

〔図書〕 計0件

〔産業財産権〕

〔その他〕

6. 研究組織

氏名 （ローマ字氏名） （研究者番号）	所属研究機関・部局・職 （機関番号）	備考
---------------------------	-----------------------	----

7. 科研費を使用して開催した国際研究集会

〔国際研究集会〕 計0件

8 . 本研究に関連して実施した国際共同研究の実施状況

共同研究相手国	相手方研究機関
---------	---------