The Essex Beekeeper

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The Healthy Brood Box
Dysentery and Nosema

By Katy Langley and Salma Attan, Essex Bee Health Officers

Dysentery occurs when bees feed on ‘unsuitable’ stores, such as honey or sugar syrup with unusually high moisture contents. Bees are unable to retain the large accumulation of water in their bowels, resulting in diarrhoea. Fermented stores may also stimulate dysentery.

Nosemosis is caused by either of the two species of Nosema: N. apis and an Asian variant, N. ceranae. Both Nosema species are highly specialised ‘microsporidial’ parasites that multiply within living cells of the gut and both are widely distributed in the UK. Adult workers, drones and queens are all susceptible. Nosema spp. invade the digestive cells lining the mid-gut (epithelium) of adult bees where they multiply rapidly, eventually producing new mature spores (endospores), which infect neighbouring host cells. Nosema spores are shed into the gut when the host cell ruptures, where they either infect more epithelial cells or are later excreted by the bees. Under optimal conditions Nosema completes its development in 48 - 60 hours.

Heavily infected bees generate many millions of spores, which remain viable for at least a year on contaminated hive material, thus acting as a potential source of further infection. Nosema may spread most rapidly in the spring when the brood nest is expanding, particularly if normal comb cleaning behaviour coincides with confinement of foraging bees. Cell cleaning prior to storing autumn-fed sugar syrup (when little natural forage is available) may also result in the spread of Nosema infection. Infection is easily spread by beekeepers placing combs contaminated with Nosema spores into healthy colonies. Do not transfer soiled combs between hives. As always, good husbandry and apiary management practices are vital in maintaining vigorous, healthy stocks, which are more able to withstand infection.

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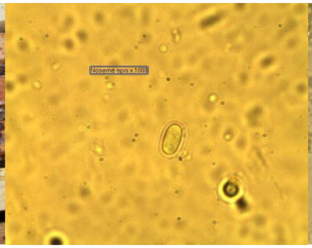
Infection with N. apis is often associated with symptoms of dysentery: dark brown faecal matter splattered onto the hive entrance or across the frames. Dysentery then helps to spread Nosema throughout the colony. Nosema infection shortens the life span of bees and makes colonies less productive. Infected bees have under-developed fat bodies and brood-food glands. Queens that contract the disease lay fewer eggs (because their ovaries degenerate more quickly than uninfected ones) and are likely to be superseded. A high level of infection results in reduced brood rearing and a reduction in honey production. Serious damage to colonies infected with Nosema is uncommon in the UK, but does occur in Spain and other Mediterranean countries.

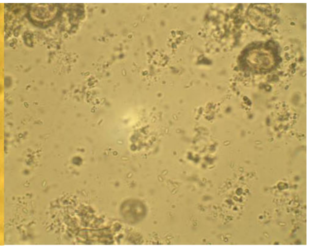
A simple method to detect Nosema uses a light microscope to confirm presence of spores, as follows:

1 Using a pestle and mortar, crush a sample of 30 adult bees in a little water. 2. Place a small drop of the resulting suspension onto a microscope slide and cover with a glass cover slip; the amount of liquid used should be just sufficient to fill the area under the cover slip. 3. Examine the suspension under the light microscope, magnification x400. 4. The spores of both N. apis and N. ceranae appear as translucent, greenish, rice shaped bodies 5. Spores of N. ceranae are more variable in shape and size than those of N. apis. They tend to be thinner, with a slight concave appearance. Both species are virtually identical in size and shape when viewed using conventional microscopy. There are no recommended treatments available, but avoid using fermented syrup to feed bees.

Dysentery on frames



N. apis



N. ceranae

EBKA Extraordinary General Meeting (EGM) held at 6.30pm on Tuesday 5th January 2021

As set out in the Notice in last month's edition you were advised that the meeting is to be held virtually via Zoom.

Details of the meeting ID and passcode code are as follows:-

You are invited to a scheduled Zoom meeting.

Topic: EBKA EGM 5th Jan 2021

Time: Jan 5, 2021 07:30 PM London

Join Zoom Meeting

https://us02web.zoom.us/j/7917024931?pwd=RXhmYnFkSXBCUHYzUzlBUUUyNFgvUT09

Meeting ID: 791 702 4931

Passcode: chelmsford

The meeting has been called to approve an update to the Rules of the EBKA.

Details of the proposed changes to the Rules can be found on the EBKA Website.

For members intending to join the meeting, please let me know in advance by emailing chairscebka1@virginmedia.com

Michael Webb

EBKA Acting Secretary

10 December 2020

Meetings in January 2021

Members are more than welcome to attend another Division's Zoom meeting. Just contact the Division and talk to the relevant co-ordinator.

Please note that all of these meetings are subject to Government COVID-19 rules that may be in place. Please check with the Division, too, to ensure that the event is running.

January 2021

07 **20:00 – 22:00 - tbc, Harlow Division**

Address: tba

19 **19:30 – 21:00 - AGM followed by Jane Ridler on Bees Abroad, Chelmsford Division**

Zoom meeting

22 **19:30 – 21:30 - Divisional AGM and Film, Saffron Walden Division**

Address: tba

27 **19:30 – 21:30 - tbc, Southend Division**

Address: WI Hall, Bellingham Lane, Rayleigh SS6 7ED

February 2021

04 **20:00 – 22:00 - tbc, Harlow Division**

Address: tba

16 **19:30 - 21:00 - Monthly Meeting - Swarming and use of Nucs, Chelmsford Division**

Address: Margaretting Village Hall, Wantz Rd, Margaretting, Ingatestone CM4 0EP

24 **19:30 – 21:30 - tbc, Southend Division**

Address: tba

chemicals in modern agriculture and beekeeping and the arrival of new diseases and parasites. These adaptations have left traces in the genomes of honey bees, allowing us to observe a small step in evolution."

Overall, the results of the study should be reassuring to bee lovers, as they suggest that Western honey bees maintain sufficient adaptive potential to face future anthropogenic and environmental changes. The authors caution however that high levels of genetic diversity do not necessarily preclude the loss of specific locally adapted genetic variants, which may jeopardize colony survival. In fact, there is a recent trend toward focusing conservation efforts on "functional" diversity, rather than total genetic diversity. Toward this end, genomic analysis of museum specimens may be of further use, enabling the identification of beneficial genetic variants at specific loci that should be targeted for conservation.

To ensure inclusion within the diary of county-wide events would Divisions provide the editor with details of local meetings by the 4th of the previous month.

Robert Silver – robert.silver@outlook.com

A Date for your 2021 Diary

The Central Executive Committee (CEC) has chosen,

Saturday 20 March at 2pm

as the date and time for the 2021 EBKA AGM.

As with the Divisional AGMs it is likely that, for the first time, it will have to be a virtual meeting using the Zoom App.

However, with the roll out of the Covid 19 vaccination programme across the country in the early part of this year, if it is at all possible, then it would be preferable to hold a meeting in a venue where our members can meet and socialise with members of other Divisions. In order to achieve that aim, a provisional booking has been made with Writtle College at Chelmsford to hold the meeting on that day in the Northumberland Room.

Further information about our 2021 AGM will be published when the possibility of holding meetings indoors is made clearer with an announcement by the Government.

Highlight: Museum Specimens Reveal the Secret Diversity of Bees

By Casey McGrath publication: Genome Biology and Evolution, publisher: Oxford University Press and date: 2020-12-04

The past several decades have been hard on Apis mellifera, the Western honey bee. Originally native to Europe, Africa, and the Middle East, Western honey bees have spread worldwide thanks to the nutritional and medicinal value of their honey, pollen, royal jelly, beeswax, propolis, and venom. Even more recently, the rise of the mobile hive and increased demand for pollination services have resulted in an army of bees being unleashed on crops each year, most notably almonds, which require several million bee visits per acre. At the same time, the last 50 years have seen dramatic declines in honey bee populations due to pesticide use, climate change, and habitat destruction. Most notably, the spread of the parasitic mite Varroa destructor from Asia to Western Europe and North America in the 1970s decimated A. mellifera colonies, making it nearly impossible for honey bees to survive without human intervention and resulting in the loss of the vast majority of wild and feral honey bee colonies. Given this decline, scientists have speculated that loss of genetic diversity among honey bees may be contributing to further losses in bee populations. A new study in Genome Biology and Evolution, titled "Digging into the genomic past of Swiss honey bees by whole-genome sequencing museum specimens," provides evidence that disputes this theory (Parejo et al. 2020), suggesting that loss of genetic diversity may not be among the long list of threats to bee survival.

The study, led by Melanie Parejo, a postdoctoral researcher at the University of the Basque Country in Spain, involved the genomic sequencing of 22 bee specimens—some nearly 150 years old—from the Natural History Museum in Bern, Switzerland (fig. 1). The study represents the first whole-genome analysis of museum bee specimens, an accomplishment made possible by recent advances in high-throughput sequencing that overcome the challenges of working with historic DNA, which is often highly fragmented. By comparing the genome sequences of the historic bee samples to those of modern bees collected across Switzerland, the authors sought to uncover how changes in agricultural practices over the last 50 years had influenced the evolution of the Western honey bee.

Bee specimens from the Natural History Museum in Bern, Switzerland, were sequenced to provide insight into the recent evolution of the Western honey bee. Credit: Melanie Parejo.

Due to recent declines in wild bee populations and increased breeding efforts, the researchers expected to see a reduction in the genetic diversity of the modern bees compared to that of the historic specimens. However, Parejo et al. actually observed higher genetic diversity in the modern honey bees. "This finding was particularly surprising to us," notes Parejo. "It was quite the opposite of what we expected and of the general narrative regarding honey bee diversity in the scientific literature, which points toward loss of genetic diversity as one of the many threats facing honey bees today."

To explain their unexpected findings, the authors suggest that A. mellifera's unique mating system, long-distance mating flights, or high recombination rate may help the Western honey bee maintain intrinsically high levels of variation. Moreover, the movement of hives and the introduction of bees from different regions may be promoting increased levels of genetic diversity in modern hives. Whatever the mechanism, this is good news for honey bees, as high levels of diversity have been shown to be crucial for colony fitness. Indeed, intracolony genetic diversity is associated with lower pathogen loads and a better chance of survival, perhaps owing to an enhanced ability to adapt to local environmental conditions.

The researchers also used the genomic data to identify signatures of selection between historic and modern Western honey bee populations. In modern bees, they found evidence for selection in immune-related genes, which may reflect the recent emergence or increasing prevalence of parasites and pathogens like Varroa and its associated viruses, the gut parasite Nosema ceranea, and the bacterium Melissococcus plutonius, which causes European foulbrood disease. Other genes with evidence for selection encoded nervous system proteins like ion channels and neurotransmitters, which are the targets of several widely used pesticides, including neonicotinoids and organochlorides. According to Parejo, these results "suggest that bees have had to adapt quickly to new challenges, particularly the increased use of