Tracking Honey Bee Disease

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What is the problem?

The National Bee Unit (NBU) at the Food and Environment Research Agency (Fera) is charged with controlling the notifiable brood diseases American and European foul brood (AFB and EFB; Figure 1).

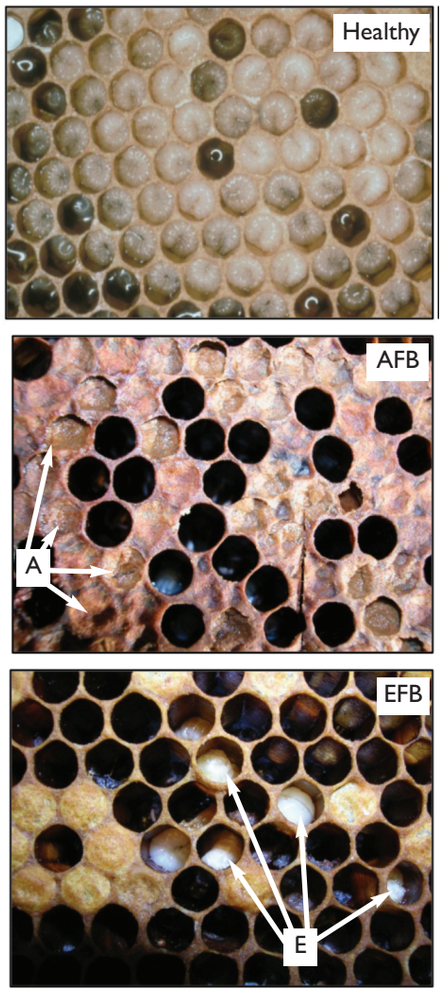

Figure 1. Images showing healthy brood (top panel); brood affected with AFB (middle) and EFB (bottom). Note EFB tends to affect the larval stages pre-capping (E for Early) and AFB tends to affect pupae after capping (A for After). All photos are courtesy of The Food and Environment Research Agency (Fera), Crown Copyright; images supplied by the National Bee Unit at Fera.

For more details please see the Advisory leaflet *Foulbrood disease of honey bees and other common brood disorders*, which can be downloaded from BeeBase (www.nationalbeeunit.com).

AFB and EFB are diseases that can lead to the death of infected honey bee colonies, and are caused by the bacteria *Paenibacillus larvae* and *Melissococcus plutonius*, respectively. EFB is believed to be more common than AFB but both diseases occur across England and Wales (Figure 2). AFB and EFB are statutory notifiable diseases which means you are legally obliged to report any suspected diseased colonies immediately to the NBU (01904 462510).

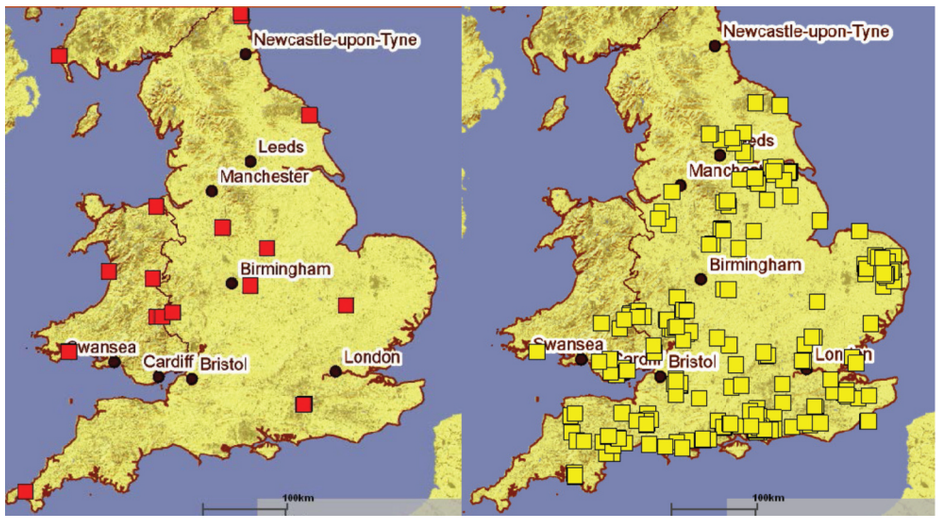

Figure 2. Distribution of AFB (left) and EFB (right) across England and Wales in 2013.

Foul brood disease can be spread by the movement of bees, equipment and honey; by sharing equipment or honey extraction facilities; by collecting swarms and, of course, by the actions of the bees themselves. Such a broad range of possible transmission routes means that it is sometimes difficult to appreciate where new infections may have originated from. Imagine being a Bee Inspector and finding a new disease outbreak (just pick any square from Figure 2). You will need to ask yourself and provide answers to questions such as: 'which square did the disease originate in?' and: 'which of the other hundreds of previous disease findings are related to the new outbreak?' Until recently, this was an insurmountable challenge for successfully tracking honey bee diseases. Fortunately, advances in science provide us with a greater understanding in how bee disease moves across the landscape.

Following in the footsteps of medical research, our laboratory designed typing schemes for *P. larvae* (Morrissey *et al.*, 2014) and *M. plutonius* (Haynes *et al.*, 2013), which allow us to discriminate between different strains of each bacterium. Those with sharp eyes will notice that these methods were developed by NBU PhD students (Ed Haynes and Barbara Morrissey) who were part-funded by Bee Diseases Insurance (BDI). The development of methods capable of discriminating between bacteria began by identifying regions of genetic material (genes) which differed across the pathogen population. The genetic sequences of these variable genes were then compared between diseased samples collected across England and Wales. Genetically similar isolates were grouped into Sequence Types (STs) based on their unique pattern across all the variable genes studied. STs within each bacterial species were then grouped into family lineages known as clonal complexes.

This year we published our findings from a two-year survey of EFB across England and Wales, funded under the Insect Pollinators Initiative (IPI; Budge *et al.*, 2014). Using our methods, we found that there were at least fifteen different types of *M. plutonius* causing EFB across England and Wales. Two bacterial families (CC12 and CC13) were rare and highly localised, suggesting they may only have recently been introduced into our country. The third family (CC3) was far more common with a broad geographical distribution, suggesting this family may be long-established and endemic to England and Wales (Figure 3). Now look at Figure 3 and again imagine being a Bee Inspector in mid-Wales wanting to understand the origin of an outbreak of Sequence Type 20 from Clonal Complex 13 (blue square). Now that all outbreaks across England and Wales are no longer the same colour and shape, it becomes easier to link disease outbreaks and visualise possible transmission routes.

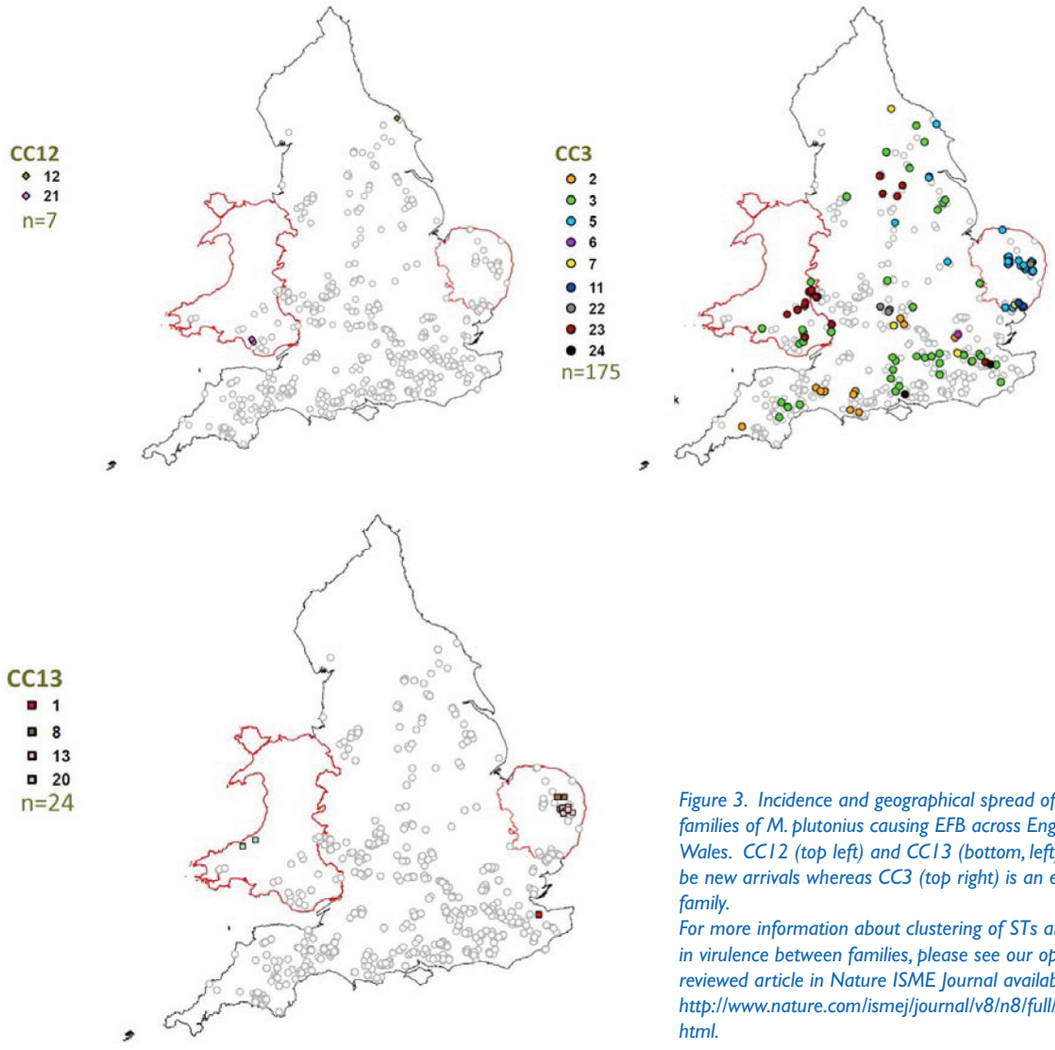

Figure 3. Incidence and geographical spread of three bacterial families of M. plutonius causing EFB across England and Wales. CC12 (top left) and CC13 (bottom, left) are likely to be new arrivals whereas CC3 (top right) is an established family.
For more information about clustering of STs and differences in virulence between families, please see our open access peer-reviewed article in Nature ISME Journal available at: http://www.nature.com/ismej/journal/v8/n8/full/ismej201420a.html.

Now we have established methods to track and trace foul brood diseases, we are looking for the international community to embrace these tools and begin to use them to characterise the foul brood pathogens in their countries. We created international databases hosted by the pubMLST website, kindly managed by Keith Jolley from the Department of Zoology at the University of Oxford. Scientists from Switzerland, Germany and Japan have already begun to use these facilities to record information about the genetic types present in their countries. For example, a recent study in Japan found new versions of *M. plutonius* that had not previously been identified in Europe. Interestingly, some types were circulating between countries and common types were even shared between different honey bee species (Takamatsu *et al.,* 2014). In assisting the international community to understand disease movements and control foul brood, we are providing a better understanding of global pathogen diversity that will ultimately help to protect our borders.

References

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