



EurBee 8

8th Congress of Apidology

18-20 SEPTEMBER 2018
Ghent, Belgium
Program & Abstract Book



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Mite adaptations in European *Apis mellifera* populations surviving *Varroa destructor* by means of natural selection?Moro A.¹, Le Conte Y.², Neumann P.¹, de Miranda J.R.³, Locke-Grandér B.³, Dahle B.^{4,5}, Blacquièrre T.⁶, Beaufrepaire A.²¹ Institute of Bee Health, University of Bern, Bern, Switzerland; ² INRA, Unité 406 - Abeilles et Environnement, Avignon, France; ³ Swedish University of Agricultural Sciences, Uppsala, Sweden; ⁴ Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway; ⁵ Norwegian Beekeepers Association, Kløfta, Norway; ⁶ Wageningen University & Research, Wageningen, Netherlands

The ectoparasitic mite *Varroa destructor* is a key factor driving colony losses of Western honey bees, *Apis mellifera*. However, some populations of European *A. mellifera* subspecies have survived by means of natural selection >10 years without mite treatments. This could result from adaptations for host resistance and/or adaptations of the parasite. Given that mites have adapted one would expect genetic differentiation between mites from local surviving and susceptible host colonies. Here, we estimated possible genetic differentiation among mites from four surviving and local susceptible populations (Norway, Sweden, France and the Netherlands) using 9 polymorphic DNA microsatellite markers (N=1270 mites from 44 colonies). Significant but low levels of genetic differentiation between mites infesting surviving and susceptible colonies were detected in the Netherlands, France and Norway. In addition, the comparison of mites from the four countries revealed genetic differences reflecting the geographical location of the apiaries. Our results suggest that colonies from these surviving populations do not survive because of parasite adaptations. However, the levels of genetic differentiation among the four locations indicate that *V. destructor* is more diversified than previously recognized in Europe. This finding suggests that surviving honey bee populations may be locally adapted to their sympatric mite populations. Altogether, this work is of strong relevance for the utilization of surviving honey bee colonies in their non-natural environment.

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Investigations into unmanaged honey bee colonies in IrelandBrowne K.A.¹, Henriques D.^{2,3}, Hassett J.⁴, Geary M.⁴, Moore E.⁴, Pinto M.A.², McCormack G.P.¹¹ Department of zoology, National University of Ireland, Galway, Ireland; ² Mountain Research Centre (CIMO), Polytechnic Institute of Bragança, Bragança, Portugal; ³ Centre of Molecular and Environmental Biology (CBMA), University of Minho, Braga, Portugal; ⁴ Department of Applied Science, Limerick Institute of Technology, Limerick, Ireland

Unmanaged honey bee colonies of local ecotype surviving without human intervention are likely to form a valuable genetic resource for the sustainability of managed apiaries as well conservation of threatened subspecies. In Ireland, following the Isle of Wight disease (which devastated honey bee colonies at the beginning of the 20th century) and subsequent hybridisation with C lineage bees, there has been a general acceptance by government agencies, scientists, and many beekeepers that no *Apis mellifera mellifera* (*Amm*) colonies persisted in the wild.

However, sporadic reports were received in 2014/2015 of the existence of unmanaged honey bee colonies. Given that Ireland's human population is low in density with only 32 persons per square km in some rural areas and only approximately 3000 registered beekeepers, many of whom are reported to not favour purchasing imported bees, it is feasible that honeybees could have naturally adapted to introduced pathogens such as *Varroa destructor*. We initiated an investigation into the state of unmanaged honey bee colonies and in 2016 we launched a nationwide request through press and social media seeking locations of unmanaged colonies which realised over 170 replies in a short time period.

We found that unmanaged colonies have utilised a wide variety of both natural and artificial cavities and survived unaided for periods reported to be from three to over 20 years. Given the difficulty in confirming the authenticity of these timings the survival of individual colonies has been monitored since 2016. Sixty-two of the colonies were sampled and a combined approach using mitochondrial, microsatellite and single nucleotide polymorphism (SNP) genotyping has shown the majority to be pure *Apis mellifera mellifera* and forming an integral part of the previously described pure *Amm* population in Ireland. This data, along with survival records for >2 years, and details of surrounding habitat and health of the unmanaged colonies, will be presented.