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Impact of managed honey bee viruses on wild bees Anja Tehel^{1,2}, Mark JF Brown³ and Robert J Paxton^{1,2}



Several viruses found in the Western honey bee (*Apis mellifera*) have recently been detected in other bee species, raising the possibility of spill-over from managed to wild bee species. Alternatively, these viruses may be shared generalists across flower-visiting insects. Here we explore the former hypothesis, pointing out weaknesses in the current evidence, particularly in relation to deformed wing virus (DWV), and highlighting research areas that may help test it. Data so far suggest that DWV spills over from managed to wild bee species and has the potential to cause population decline. That DWV and other viruses of *A. mellifera* are found in other bee species needs to be considered for the sustainable management of bee populations.

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Introduction: EIDs and viral pathogens of the Western honey bee (*Apis mellifera*)

We, our domestic animals, and wildlife are increasing challenged by a range of emerging infectious diseases (EIDs [1,2]) that threaten respectively our health, our farming and the ecosystem services we derive from the natural world. After cattle and pigs and before poultry, the Western honey bee (*A. mellifera*) has been considered the third most important domestic animal [3,4]; pollination by insects, including by the Western honey bee, is an important ecosystem service that contributes over US \$ 200 billion to global agricultural output at today's prices and, directly and indirectly, to one in every three mouthfuls of food [5]. Wild bee species also make a major contribution to crop pollination [6]. Elevated losses of

Western honey bees have been reported across northern temperate regions of the world over the past decade [7], with EIDs considered a primary cause of mortality [8], possibly because of increased viral virulence [9]. Wild bee species are also in decline in northern temperate regions of the world concomitant with a decline in the wild flowers they visit and pollinate [10], though causes of population decline, range contraction and wild bee species loss are diverse [11,12]. Given the importance of bees for pollination, these are serious concerns that could affect food security and the functioning of terrestrial ecosystems [13].

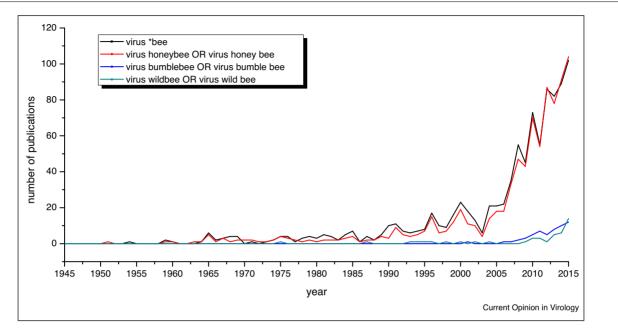
To date, 24 viruses have been associated with the Western honey bee [14], many of which are positive sense single strand (+) RNA viruses. One of these in particular, Deformed wing virus (DWV), has risen to prominence because of its association with the honey bee exotic ectoparasitic mite Varroa destructor [15[•]], a possibly synergistic association for virus and mite [16]. Varroa destructor (henceforth varroa mite) was originally an ectoparasite of the Asiatic Eastern honey bee (Apis cerana), but jumped to the Western honey bee and is nowadays widespread across most of the world with its new host, the Western honey bee, on which it vectors DWV and many other viruses [8,14]. Introduction of varroa mites to a naïve population of Western honey bees leads to a tremendous rise in DWV prevalence and titer per individual host [17,18], and DWV is the leading contender as the causal agent of colony decline [14].

Prominent among EIDs of a diverse range of animals are RNA viruses that exhibit high mutation (and substitution) rates [19] and cross species barriers to emerge (i.e. become more prevalent) in novel hosts, including humans [20], for example, Ebola and Zika. DWV and other (+) RNA viruses of the Western honey bee have now been detected in wild bee species [21^{••}], though knowledge of their impact on wild bee hosts remains limited (Figure 1; Table 1). That a virus is found across two or more host species, be they managed or wild bees, is important because it dictates the epidemiology and evolutionary trajectory of that pathogen [22,23[•]]. Here we bring together recent literature to explore the hypothesis that viral spill-over from managed Western honey bees negatively impacts wild bee species.

DWV prevalence and impact

Before the introduction of the varroa mite to the Western honey bee in Europe ca. half a century ago, serological (antibody-based) detection of DWV suggested it was at extremely low prevalence [24]. Varroa mites are now found in most, if not all, Western honey bee colonies





Increase in the number of publications on viruses across bee species over the past 70 years, showing that most relate to managed honey bees (the Western honey bee, *Apis mellifera*, or other Asiatic honey bee species that all belong to the genus *Apis*), and relatively few to bumble bees (genus *Bombus*) or other wild bees (species in the family Apidae other than honey bees and bumble bees, plus all species in the families: Halictidae, Megachilidae, Andrenidae, Colletidae, Melittidae and Stenotritidae); Web of Science search (accessed on March 18th, 2016) using terms in the box.

across all of Europe (except isolated offshore islands and in extreme northern latitudes) and, using PCR-based screening, DWV is the most commonly detected virus, often found at high titer [25]. Careful screening of Western honey bee colonies on the archipelagos of Hawaii and New Zealand has clearly demonstrated that DWV rose to 100% prevalence of colonies after the introduction of varroa mites [17,18]. It is arguably present in all Western honey bee colonies that harbor varroa mites, and phylogenetic analysis of viral gene sequences suggest it has likely followed the introduction of varroa mites to North America and elsewhere to become an EID of Western honey bees worldwide [15°]. Australia remains the only large land mass that, to date, has not reported varroa mites in its managed Western honey bee colonies.

Concomitant with its rise in prevalence across Western honey bee colonies and in titer in individual honey bees, DWV is the most commonly reported virus detected by PCR in a range of other bee species (Figure 2). It has been found in three Asiatic honey bee (*Apis*) species in Asia [25,26]. Across Europe and North America, DWV has also been detected in bumble bees (*Bombus* spp.) [27^{••},28– 30,31^{••},32–34], other wild bee species [27^{••},29,35–37] and even taxonomically more distant hosts such as ants, wasps and cockroaches [28,29,38]. These represent an eclectic mix of host species, and the field would benefit from more systematic surveying of the prevalence of DWV, both in terms of geographic and taxonomic (host species) coverage.

Whether these increases in host range of DWV beyond Western honey bees are a consequence of pathogen spill-over of this EID of the Western honey bee are equivocal because most studies merely report PCRbased detection of DWV. For the Asiatic honey bees that also host varroa mites, phylogenetic analysis of DWV isolates from these different host species supports the suggestion of EID spill-over from introduced, managed Western honey bees harboring varroa mites and DWV [25]. Given the mechanistic link between varroa mites and DWV transmission, EID spill-over into Asiatic honey bee species is a plausible interpretation of the phylogenetic data.

As only honey bees (*Apis* spp.) host varroa mites that can vector DWV, it is assumed that bumble bees and other wild bee species acquire DWV though robbing of DWV-infected colonies of Western honey bees for honey or, more likely, by collection and ingestion of DWV with pollen or nectar from flowers that are also visited by DWV-infected Western honey bee workers [27^{••},39,40]. Given this assumption, we highlight two issues that confound the interpretation of data on DWV prevalence in wild bee species in terms of impact on hosts.

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