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Pathogens of common wasps in their native and invaded range.

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The common wasp (Vespula vulgaris) is native to Eurasia but has invaded and attained high densities in Argentina, Australia and New Zealand. The first aim in this study was to define the native range of invasive populations. The second aim was to examine pathogens and parasites of these wasps within the introduced and specific native ranges. Using variation in two mitochondrial genes, the likely home range of invasive populations of these wasps was found to be the United Kingdom, Ireland or nearby countries in Western Europe. Populations within the invaded range appear to have arisen from a small number of introductions, limiting the likelihood of the co-introduction of wasp parasite and pathogens. Using proteomic methods, the presence and diversity of pathogens and parasites was examined in wasps from the native (Belgium and England) and invaded range (New Zealand and Argentina). Contrary to expectations, no evidence of 'enemy release' was observed, as the number of pathogen taxa observed in the native range was similar in both the introduced and native range. The pathogens observed in wasps were similar to a variety of taxa found in honeybees. Given the importance of Nosema spp. as pathogens in honeybees, wasps were examined for microsporidian infection prevalence. Rates of microsporidian infection were similar in the native and introduced ranges. Wasps appear to carry Nosema spp. observed in honeybees and bumblebees. Perhaps many of the pathogens and parasites affecting wasps are 'generalist' species affecting bees and wasps, which has major implications for wasp and bee disease management.