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Data from: Patterns of Widespread Decline in North American Bumble Bees

Bumble bees (*Bombus*) are vitally important pollinators of wild plants and agricultural crops worldwide. Fragmentary observations, however, have suggested population declines in several North American species. Despite rising concern over these observations in the United States, highlighted in a recent National Academy of Sciences report, a national assessment of the geographic scope and possible causal factors of bumble bee decline is lacking. Here, we report results of a 3-y interdisciplinary study of changing distributions, population genetic structure, and levels of pathogen infection in bumble bee populations across the United States. We compare current and historical distributions of eight species, compiling a database of >73,000 museum records for comparison with data from intensive nationwide surveys of >16,000 specimens. We show that the relative abundances of four species have declined by up to 96% and that their surveyed geographic ranges have contracted by 23–87%, some within the last 20 y. We also show that declining populations have significantly higher infection levels of the microsporidian pathogen *Nosema bombi* and lower genetic diversity compared with co-occurring populations of the stable (nondeclining) species. Higher pathogen prevalence and reduced genetic diversity are, thus, realistic predictors of these alarming patterns of decline in North America, although cause and effect remain uncertain.

Bumble bees (*Bombus*) are integral wild pollinators within native plant communities throughout temperate ecosystems, and recent domestication has boosted their economic importance in crop pollination to a level surpassed only by the honey bee. Their robust size, long tongues, and buzz-pollination behavior (high-frequency buzzing to release pollen from flowers) significantly increase the efficiency of pollen transfer in multibillion dollar crops such as tomatoes and berries. Disturbing reports of bumble bee population declines in Europe have recently spilled over into North America, fueling environmental and economic concerns of global decline. However, the evidence for large-scale range reductions across North America is lacking. Many reports of decline are unpublished, and the few published studies are limited to independent local surveys in northern California/southern Oregon, Ontario, Canada, and Illinois.

Furthermore, causal factors leading to the alleged decline of bumble bee populations in North America remain speculative. One compelling but untested hypothesis for the cause of decline in the United States entails the spread of a putatively introduced pathogen, *Nosema bombi*, which is an obligate intracellular microsporidian parasite found commonly in bumble bees throughout Europe but largely unstudied in North America. Pathogenic effects of *N. bombi* may vary depending on the host species and reproductive caste and include reductions in colony growth and individual life span and fitness. Population genetic factors could also play a role in *Bombus* population decline. For instance, small effective population sizes and reduced gene flow among fragmented habitats can result in losses of genetic diversity with negative consequences, and the detrimental impacts of

these genetic factors can be especially intensified in bees. Population genetic studies of *Bombus* are rare worldwide. A single study in the United States identified lower genetic diversity and elevated genetic differentiation (FST) among Illinois populations of the putatively declining *B. pensylvanicus* relative to those of a codistributed stable species. Similar patterns have been observed in comparative studies of some European species, but most investigations have been geographically restricted and based on limited sampling within and among populations.

Although the investigations to date have provided important information on the increasing rarity of some bumble bee species in local populations, the different survey protocols and limited geographic scope of these studies cannot fully capture the general patterns necessary to evaluate the underlying processes or overall gravity of declines. Furthermore, valid tests of the *N. bombi* hypothesis and its risk to populations across North America call for data on its geographic distribution and infection prevalence among species. Likewise, testing the general importance of population genetic factors in bumble bee decline requires genetic comparisons derived from sampling of multiple stable and declining populations on a large geographic scale. From such range-wide comparisons, we provide incontrovertible evidence that multiple *Bombus* species have experienced sharp population declines at the national level. We also show that declining populations are associated with both high *N. bombi* infection levels and low genetic diversity.

This data was used in the paper "Patterns of widespread decline in North American bumble bees" published in the Proceedings of the National Academy of United States of America.



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Nosema bombi isolate Bom.pen.Ark1 18S ribosomal RNA gene [\(/dataset/data-patterns-widespread-decline-north-american-bumble-bees/resource/1fb2b96a-5993-4707-af24-77d8d495c22d\)](#)

Nosema bombi isolate Bom.pen.Ark1 18S ribosomal RNA gene, partial sequence;...

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Nosema bombi isolate 1 small subunit ribosomal RNA gene ([/dataset/data-patterns-widespread-decline-north-american-bumble-bees/resource/7c963643-3696-4ec3-a6e3-3430cd174c4e](#))

Nosema bombi isolate 1 small subunit ribosomal RNA gene, partial sequence;...

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