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CHAPTER 2

HOUSE FINCH (*CARPODACUS MEXICANUS*) POPULATION- AND GROUP-LEVEL RESPONSES TO A BACTERIAL DISEASE

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Abstract.—We examined changes in group sizes of House Finches (*Carpodacus mexicanus*; hereafter "finches"), at feeders over the course of establishment of a novel disease caused by the bacterium *Mycoplasma gallisepticum*. Our goal was to identify factors linked with the severity of decline in sizes of finch groups, with the aim of inferring causes of variation in rates of disease transmission and disease-induced mortality. We found that only site-specific density-dependence consistently predicted the sizes of declines in finch group sizes. By contrast, there were no differences in declines among habitats known to differ in finch abundance, or among regions with different overall abundances of finches. We also failed to find differences in declines along a gradient of winter temperature. Our results suggest that the effects of disease on host populations in this system are primarily determined by interactions among finches at individual sites, with little consistent influence of factors extrinsic to these local groups.
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Resumen.—Examinamos los cambios en el tamaño de grupos de *Carpodacus mexicanus* en los alimentaderos durante el establecimiento de una enfermedad nueva causada por la bacteria *Mycoplasma gallisepticum*. Nuestra meta fue el identificar los factores asociados con la severa reducción en el tamaño de los grupos de *C. mexicanus*, con el objetivo de inferir causas en la tasa de transmisión de la enfermedad y de mortalidad debido a la enfermedad. Encontramos que solamente factores denso-dependientes y específicos a un sitio, predijeron constantemente las dimensiones de las reducciones en el tamaño de los grupos de *C. mexicanus*. En contraste, no hubo diferencias en las reducciones entre los habitats que se sabia que se diferenciaban en cuanto a abundancia de *C. mexicanus*, o entre regiones con diferentes abundancias de *C. mexicanus*. No pudimos encontrar diferencias en las reducciones a lo largo de un gradiente de temperaturas invernales. Nuestros resultados sugieren que los efectos de la enfermedad en la población hospedera en este sistema están principalmente determinados por interacciones entre *C. mexicanus* en sitios únicos, con poca influencia de factores extrínsecos a esos grupos locales.

When a new parasite or predator is introduced into a host population, the resulting population fluctuations can range from unstable oscillations that may lead to extinction of one of the pair to a monotonic equilibrium without oscillations. In host–disease systems, the rate of transmission of disease between hosts and the severity of the disease's effects are two of the key parameters that determine the pattern of change in host abundance. Thus, a clear understanding of host–disease dynamics can only be obtained following identification of the factors that affect rates of disease transmission and the subsequent probability of mortality. However, direct identification of these factors can be extremely difficult, especially for disease transmission rates in wild populations of animals. For a social species, one indirect method of inferring variation may be available, because transmission rate is likely to be affected by the sizes of groups in which animals interact (e.g. May and Anderson 1984). The disease will, in turn, affect the sizes of groups in which animals occur. Thus, any factor, such as group size or climatic severity, that is correlated with the size of a disease-induced population decline can be inferred to potentially mediate the rate of disease transmission or mortality following infection. Such inferences can be used

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