

LICE OF THE POLYANDROUS GALAPAGOS HAWK: POPULATION GENETIC, COEVOLUTION AND ECOLOGY.

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The objectives of this study are: (1) to unravel the evolutionary relationships among populations of lice occurring on Galapagos (*Buteo galapagoensis*) and Swainson's (*Buteo swainsoni*) hawks using molecular markers, and (2) to examine patterns of parasite prevalence, intensity and diversity in relation to host system of mating (polyandry vs. monogamy) and other ecological parameters. From May-August 2001, lice were collected from hosts via dust-ruffling from four island-populations of *Buteo galapagoensis*. Seventy-one hawks were sampled for ectoparasites. Two louse species were recovered from all populations, an ischnoceran, *Degeeriella regalis* (Giebel), and an amblyceran, *Colpocephalum turbinatum* Denny (both species of lice also occur on Swainson's Hawk, the putative sister taxon of *B. galapagoensis*). Seventy of these birds had one or both species of louse (prevalence = 98.6%). Louse prevalence, intensities and diversity measures were calculated for each island population. For example, on the island of Marchena, a total of 3,186 lice were collected from 25 hawks. Of this total, 2,872 were individuals of *C. turbinatum*, (prevalence = 96.15%) and 314 individuals of *D. r. regalis* (prevalence = 88.46%). Mean intensities of *C. turbinatum* (117.68 ± 162.57) and *D. r. regalis* (13.65 ± 13.35) were significantly different within this host population, although prevalences were not. On Marchena, adult hawks that had obtained year-round territories (N= 16) had lower intensities for both louse species (34.56 ± 33.142) than did 9 non-territorial floating birds (292.56 ± 173.49), whether non-territorial adults are considered separately from juveniles or combined ($t = -4.416$; $p = 0.0040$). The same pattern was observed when each species of louse was analysed separately. Santiago Island was the focus of a comparative study in May-July 2001 which examined the effects of host group size on parasite prevalence, intensity and diversity. We predict that groups with more individuals will have higher parasite prevalence and intensity than groups with fewer individuals, and that birds within groups will have more even parasite intensity than expected by chance. Molecular data (mtDNA) from *D. r. regalis*, although very preliminary, indicate the presence of at least two different haplotypes between the northern-most and southern-most islands in the archipelago. Similar data from more individuals and islands will be presented.