

manhos corporais e hábitos, similares, mesmo em uma área de clima claramente sazonal, sugere que as espécies, também, utilizam outros recursos distintos daqueles analisados no presente estudo (e.g. fungos, folhas, insetos voadores, frutos disponíveis na árvore-mãe). Alternativamente, as espécies podem usar subgrupos distintos dentro das categorias alimentares avaliadas (e.g. determinadas ordens de invertebrados) que variam de forma distinta ao longo do ano.

### **ECTOPARASITIC ASSEMBLAGES OF PARAGUAYAN BATS: ECOLOGICAL AND EVOLUTIONARY PERSPECTIVES**

Tesis doctoral, defendida por **STEVEN J. PRESLEY**. Ecology Program, Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409-3131, USA, 326 pp.: 02 de Noviembre de 2004; Miembros del tribunal: Michael Willig, Robert Owen, Don Gettinger, Mark McGinley, Richard Strauss, Daryl Moorhead.

Community ecology fundamentally addresses two interrelated questions: what determines the number of species in a community, and what processes are responsible for the identity of those species (Strong et al., 1984). Ecological and evolutionary determinants (e.g., competition, natural selection) and the availability of species (i.e., species pool) combine to determine the number, identity, and relative abundances of species that occur in a community or assemblage. In addition, patterns at one scale may be a result of mechanisms operating at different scales of space and time (Pickett et al., 1994).

The equilibrium theory of island biogeography (ETIB) is a mechanistic theory (MacArthur and Wilson, 1963) that provides a quantitative framework for understanding variation in biodiversity. ETIB predicts that larger islands maintain greater species richness than do smaller islands, and that islands more distant from a source area support fewer species than do islands closer to a source area. Distance primarily affects richness by molding immigration rates, whereas area primarily affects richness by molding extinction rates. The ETIB has been applied to island systems including habitat patches, lakes, caves, and mountaintops. Application of ETIB to host-ectoparasite systems may be reasonable because two of the primary factors that determine ectoparasite diversity are host body size and distance to a source of infestation, analogs to island size and distance to a source population, respectively (Kuris et al., 1980).

I investigated assemblages at multiple taxonomic levels from the perspective of hosts and ectoparasite species. I quantitatively described the arthropod assemblages on bats of Paraguay, presented patterns of host specificity, and investigated resource partitioning and species abundance distributions (SADs) of ectoparasite assemblages inhabiting common species of bats. In addition, I assessed the importance of host body size and abundance on ectoparasite biodiversity (e.g., abundance, richness, and diversity) within the context of ETIB, and provided a synthetic discussion concerning the effect of host traits on ectoparasite assemblages.

Mammals and their associated ectoparasites were collected from July 1995 to June 1997, and again from July to August in 1998, as part of an investigation entitled "Paraguayan Mammals and Their Ectoparasites: an Intensive Survey in a Temperate-Subtropical Interface." Bats were surveyed at 28 sites, representing all major biomes, including many protected areas, and spanning gradients of moisture and temperature in Paraguay (Willig et al., 2000). Ectoparasites were collected from 2909 of the 4143 bats captured during the study, representing 44 species and five families of hosts. Over 17 500 ectoparasites were collected, representing 104 species and 11 families. In abundance, five families (Insecta: Streblidae; Arachnida: Spinturnicidae, Macronyssidae, Chirodiscidae, and Argasidae) accounted for 94.5% of all ectoparasites.

The protocol for collecting ectoparasites (Sheeler-Gordon and Owen, 1999) resulted in less cross-host contamination (< 1/3 the contamination rate) than in previous studies (e.g., Herrin and Tipton, 1975). In general, host-parasite associations in Paraguay corroborate previously reported associations. Attributes of SADs of ectoparasite assemblages (restricted to primary host-parasite associations) suggest that limiting resources (i.e., space on the host) are relatively evenly divided among ectoparasite taxa. Ectoparasite SADs most closely conformed to expectations of the broken stick model and were not consistent with a model (i.e., geometric series) based on niche preemption. Competition may be reduced by specializations for locomotion on particular parts of the host (i.e., microhabitats). For example, co-existence of fly species on individual hosts often is attained by microhabitat specialization; flies are adapted to live in fur, on fur, or on patagia.

For all bat species as a group, ectoparasite abundance did not respond significantly to host size. However, in analyses restricted to phyllostomids or to molossids, larger species harbored more ectoparasites than did smaller species of bat. After accounting for sex-related differences in size, host

sex affected ectoparasite abundance on nine of 22 common host species. In all cases of significance, females harbored significantly more ectoparasites than did males. For all bat species as a group, average ectoparasite richness was the only metric of ectoparasite biodiversity that responded to host size; larger bats exhibited higher mean richness than did smaller bats.

If larger host individuals within a host species harbor greater ectoparasite loads (i.e., greater ectoparasite abundance) by providing more habitat, all significant responses of ectoparasite abundance to host body size should be positive. However, more than half of significant responses were negative (i.e., smaller hosts had significantly greater ectoparasite abundances than did larger hosts). Therefore, within the context of ETIB, increases in host size (i.e., island size) do not lead to increases in ectoparasite abundance that would reduce extinction rates, and may not be the most important host character in determining ectoparasite abundance within a host species. Females were larger in host species for which larger hosts had greater ectoparasite abundances, and were smaller for host species in which smaller hosts had greater ectoparasite abundances. This suggests that size captures sex-specific differences in host quality or behavior that affect ectoparasite abundance and diversity, and that female bats are preferred hosts regardless of host body size. Any aspect of host ecology that enhances host availability to ectoparasites will result in increased ectoparasite diversity and abundance. Because female bats roost in colonies (e.g., harems, maternity colonies) more often than do males, females provide more opportunities of host transfer than do males, which may result in ectoparasites preferentially selecting female hosts.

Regional (i.e., country-wide) host abundance did not affect biodiversity of ectoparasite assemblages on host species. Although many measures of biodiversity responded to regional host abundance, all significant results were associated with increased opportunities to observe contamination, transients, or rare ectoparasite species as a consequence of larger sample sizes (i.e., passive sampling; Coleman, 1981). Analyses of the effect of local host abundance on ectoparasite assemblage biodiversity within 13 common, wide-spread host species yielded similar conclusions to those at the regional scale. Significant, positive responses were associated with the number of rare species or transients, or with contamination associated with larger ectoparasite sample sizes.

Biodiversity of ectoparasite assemblages may increase with host abundance as an artifact of collection or passive sampling. Nonetheless, parallels

exist between the effect of host abundance on ectoparasite species richness and species-area relationships. Larger habitats harbor more rare species than do smaller habitats by reducing the risk of stochastic extinction of rare species. The ectoparasite assemblages from bats of Paraguay are consistent with this prediction.

Because bats are small and space for ectoparasites is limited, opportunities for host transfer are important for avoiding stochastic extinction. Consequently, location of new resources (i.e., additional host individuals) is paramount. Bats that roost in colonies, maintain harems, or form maternity colonies should support more diverse ectoparasite assemblages than do solitary bat species. In addition, common bat species should provide more transfer opportunities than do rare species. Group size was not measured during the study; however, evidence suggests that ectoparasite assemblages of gregarious bats (e.g., harem members such as female *Sturnira lilium* and *Noctilio albiventris*) are more species-rich than are those of more solitary bats (e.g., sub-adult male *S. lilium* and *N. albiventris* that are solitary). Moreover, ectoparasite assemblages on common bat species (e.g., *Artibeus lituratus*, *S. lilium*, *Eumops patagonicus*, *Molossus molossus*) are more species-rich than are those on rare bat species (e.g., *Chiroderma doriae*, *Pygoderma bilabiatum*, *Eumops auripendulus*, *Molossus planirostris*).

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**DETERMINACIÓN ESPECÍFICA  
Y NIVELES DE POLIMORFISMO  
ALOZÍMICO DE *Graomys* (RODENTIA,  
MURIDAE) DE LOS ALREDEDORES  
DE COMODORO RIVADAVIA**

Tesis de Licenciatura en Ciencias Biológicas, defendida por **VALERIA ANDREA RODRÍGUEZ**. Universidad Nacional de la Patagonia San Juan Bosco, sede Comodoro Rivadavia, Chubut, Argentina; 48 pp., 25 de agosto de 2003; Director: Gerardo Raúl Theiler; Miembros del tribunal: Elena González, Rubén Martínez y Ana María Berastegui.

El orden Rodentia constituye el grupo de mamíferos más diverso en América del Sur. En nuestro territorio dicho orden está constituido por varias familias, entre éstas ña familia Muridae. Entre los filotinos, *Graomys griseoflavus* (Waterhouse, 1837) se caracteriza por su amplia distribución geográfica. Se halla en América del Sur, desde Paraguay, Brasil, Bolivia hasta Santa Cruz en Argentina, desde el nivel del mar hasta los 2000 metros de altitud (Rosi, 1983). En poblaciones de *Graomys* de distintas regiones del país se han hallado polimorfismos cromosómicos que determinan diferentes números diploides. En el sudoeste de la provincia de Catamarca, noroeste de La Rioja, norte y centro de Mendoza, sur de Buenos Aires y centro de La Pampa se han hallado ejemplares con complementos diploides 36, 37 ó 38, mientras que en el norte y centro de Córdoba y sudeste de la provincia de La Rioja se capturaron individuos con  $2n = 42$  (Pearson y Patton, 1976; Rosi, 1983; Zambelli et al., 1994; Theiler y Blanco, 1996; Theiler, 1997; Tiranti, 1998). El área de distribución de los citotipos  $2n = 36$ , 37 y 38 corresponde preferentemente a la región fitogeográfica llamada “Monte” mientras los del citotipo  $2n = 42$  se hallan en la región del “Espinal” y “Chaco Occidental” (Theiler y Blanco, 1996). En base a la evidencia experimental, Theiler y Blanco (1996) propusieron que el complejo  $2n = 36$ , 37 y 38 y el citotipo  $2n = 42$  constituyen dos especies completamente separadas. Theiler (1997) ha propuesto conservar el nombre específico *Graomys griseoflavus* para el complejo  $2n = 36-38$  y denominar *Graomys centralis* (Thomas, 1902) a la especie  $2n = 42$ . Como las dos especies son

morfológicamente indistinguibles, la única manera de determinar la pertenencia de un individuo a una de ellas es determinando su número diploide. Estudios relacionados con los niveles de variabilidad genética detectables por electroforesis de enzimas y otras proteínas han demostrado que tanto *Graomys griseoflavus* como *G. centralis*, tienen altos niveles de polimorfismo (Theiler y Gardenal, 1994; Theiler et al., 1999). El alto grado de variabilidad génica observada en las poblaciones podría explicarse apelando a la hipótesis que propone que los valores de polimorfismo genético están directamente relacionados a la diversidad ambiental a la que se ven enfrentados (Markert, 1975; Nevo, 1978; Nevo et al., 1984). Otra posibilidad es que la gran variabilidad genética sea reflejo de factores demográficos (como elevado tamaño efectivo, ausencia de endogamia, altos niveles de flujo génico, etc.). Dado que la composición de las comunidades de micromamíferos que habitan las cercanías de Comodoro Rivadavia es poco conocida, se propuso determinar taxonómicamente algunas especies de roedores componentes de la fauna de micromamíferos que habitan la zona; precisar cuál de las especies de *Graomys* se halla en la región y conocer los niveles de variabilidad genética presentes en las poblaciones de esta especie. Se realizaron muestreos en un sitio distante a 14 km del centro de la ciudad de Comodoro Rivadavia (departamento Escalante, provincia del Chubut). Las trampas se colocaron debajo de grandes arbustos, en los cuales se observaron cuevas o señales de actividad de roedores. Las capturas se realizaron durante los meses de mayo, junio, julio, octubre, noviembre y diciembre del año 2002 y enero del año 2003. El total de animales capturados fue de 35 roedores: 19 *Graomys*; 11 *Akodon*; 4 *Reithrodon*; 1 *Phyllotis* y 1 marsupial *Lestodelphys halli* (Thomas, 1921). También se capturaron unos 80 cuises, *Microcavia australis* (Geoffroy y d’Orbigny, 1833), los cuales fueron liberados. La asignación de los animales capturados a estos géneros fue realizada por análisis morfológico y de caracteres externos de los ejemplares vivos en base a los trabajos de Olrog y Lucero (1981), Rosi (1983) y Redford y Eisenberg (1984). Los resultados de los estudios cariotípicos y morfométricos permiten afirmar que la especie de *Graomys* que habita en la zona de Comodoro Rivadavia es *Graomys griseoflavus* (Waterhouse, 1937), ya que se determinó el número diploide de 36, 37 y 38 cromosomas, similar a los descriptos para la especie en otras regiones. Los cariotipos de ejemplares de *Akodon* presentan un número diploide de 44 cromosomas. La única especie de *Akodon* citada para la Patagonia que posee  $2n = 44$  es *Akodon molinae* (Contreras, 1968). El cariotipo de los ejemplares estudiados no