

ON DIFFERENTIATING *MYOTIS YUMANENSIS* AND *MYOTIS LUCIFUGUS* IN THE FIELD: A REPLY TO CARRAWAY

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The central concern of Rodhouse et al. (2008) was the identification of *Myotis yumanensis* and *Myotis lucifugus* under field conditions. We demonstrated the potential utility of morphological key characteristics for differentiating the 2 species but also found that the expression of these characteristics could be contradictory within individual bats. We expressed concern over the possibility of high misidentification rates for these 2 species and of spurious conclusions that may result. We suggested that multiple lines of diagnostic evidence should be considered, including those from acoustic and genetic tools. We encouraged future studies of this kind to be undertaken to improve field identification approaches, and we noted several opportunities for improving our study, including the limited use of voucher specimens and involvement of multiple observers.

Carraway (2009) raises several salient and interesting points of criticism applicable to a larger philosophical debate on the role of genetic and echolocation techniques in questions involving taxonomy. Such a debate is beyond the scope of our original manuscript, and we will primarily focus on the points specific to Rodhouse et al. (2008). Carraway (2009) suggests that since type specimens housed in museums are not associated with echolocation calls, acoustic data are of questionable utility. While we recognize that echolocation calls are not available from type specimens housed in museums, we see no reason to discount the compelling evidence that associations of species with call characteristics are very real indeed, especially where species identification involves both morphological and genetic verification (Barratt et al. 1997, Jacobs et al. 2006, Weller et al. 2007). These associations are built on

statistical expectations resulting from many replicate samples, a widely accepted practice in many disciplines. The published keys that we rely on as a morphometric standard in field studies such as ours (e.g., Nagorsen and Brigham 1993, Verts and Carraway 1998), and which are used to associate morphometrics with acoustic and genetic data, are themselves products of assessing voucher specimens.

Carraway (2009) expressed concern over our insufficient methodological description for distinguishing subspecies and the absence of a listed depository for laboratory samples. We concede the point and agree that more could have been said on that subject. This may result from editorial processes limiting content in a published manuscript more than from some egregious failure of scientific method, and we are quite willing to entertain direct requests for information on tissue disposition and mitochondrial DNA sequences. Distinguishing among subspecies of *M. lucifugus* in the field is even more difficult than distinguishing between the 2 *Myotis* species, and we made no attempt to do so in our study. Our sample of different *M. lucifugus* subspecies was too small for any meaningful inferences to be made, and we simply noted that the presence of 3 subspecies in our study may have contributed to the lower identification success rate observed in that species.

More importantly, Carraway raised the interesting question of how 3 subspecies of *M. lucifugus* can overlap in a single locality given the classic definition of subspecies that depends on allopatry. Since the publication of Zinck et al. (2004), the question of how the described intraspecific genetic variation relates to the subspecies of *M. lucifugus* has been investigated using both nuclear and mitochondrial

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DNA analysis (Dewey et al. 2003, unpublished, Dewey 2004, 2006, Lausen et al. 2008). Whereas mitochondrial DNA analysis results in distinct clades that correspond to the subspecies of *M. lucifugus* (Dewey et al. 2003, unpublished, Dewey 2004, 2006), nuclear DNA analysis (microsatellite DNA) suggests that the subspecies are interbreeding (Lausen et al. 2008). Although the phylogenetic status of subspecies for *M. lucifugus* is an ongoing debate that has not been resolved, mitochondrial DNA sequences from Zinck et al. (2004) and sequences obtained from samples used in Rodhouse et al. (2008) match DNA sequences from vouchered samples for the corresponding subspecies of *M. lucifugus* in GenBank. We acknowledge that the inclusion of genetic signatures from vouchered specimens in GenBank is critical to accurate species identification.

Carraway raised a final point of concern regarding our cautious endorsement of limited collection of full-body voucher specimens. We agree that vouchers would be helpful and stated so (Rodhouse et al. 2008:442). Our concern, however, is that the conservation status of many bat species is uncertain and the widespread collection of bats constitutes an unknown and potentially negative impact. New and emerging threats to temperate North American bats, such as the infectious fungal disease known as “white-nosed syndrome” and the rapid increase in mortality associated with wind-power developments, underscores our concern. Bats are long-lived and not as fecund as other small mammals that are often collected during field research, and we do not condone widespread collection of bats for studies like ours. We would welcome a concerted effort by museum curators to secure genetic signatures of correctly identified voucher bat specimens (already housed in museums) that could be made available on GenBank as a standard for our field identifications. Also, a coordinated effort to collect field information on bats by researchers following a common protocol, such as is currently underway by the U.S. Forest Service and Bureau of Land Management’s “Bat Grid” program in the Pacific Northwest, provides an opportunity to cross-reference genetic, acoustic, and morphometric

data to refine species and subspecies identification (Ormsbee et al. 2006).

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