CONSTRUCTING CHECK-LISTS AND AVIFAUNA-WIDE REVIEWS:
MEXICAN BIRD TAXONOMY REVISITED

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Summarizing taxonomic and distributional information of regional avifaunas has been an important task of the American Ornithologists’ Union (AOU) from early in its history up to the present day (AOU 1998). The North American Check-list is updated by yearly supplements (e.g., Banks et al. 2008), and taxonomic changes are incorporated on the basis of a self-described “conservative and cautious” system of consensus among committee members regarding recently published proposals of changes (AOU 1998). The newer South American Check-list follows similar procedures (Renss et al. 2008). Because many communities depend on these regional taxonomies as baseline summaries for diverse applications (e.g., in conservation, biodiversity studies, and systematic studies), consideration of the system employed and its implications is paramount, particularly given the statement that the decisions are made following a “time-honored tradition,” which—as we will argue—may not constitute the optimal strategy for 21st-century taxonomy. An alternative approach is that of regional “sweeps” and broad taxonomic reviews (e.g., Christidis and Boles 2008). This approach may, in the end, base decisions on less-complete information for establishing species limits, but it has the advantage of producing an internally consistent list.

In our ongoing efforts to understand and summarize the Mexican avifauna (Escalante-Pliego et al. 1993, Peterson and Navarro-Sigüenza 2000b), we have become aware of numerous species taxa that merit full recognition as species, under both the biological species concept and the evolutionary species concept (Navarro-Sigüenza et al. 1992, Peterson and Navarro-Sigüenza 2000a, Puebla-Olivares et al. 2008). This realization led to the development of a new, country-wide taxonomic treatment under the evolutionary species concept (Navarro-Sigüenza and Peterson 2004), which was subsequently criticized as cursory and unscientific by Renssen (2005). Instead of miring the discourse in more opinion, the purpose of this commentary is to briefly review new evidence, published after our original analysis, to establish how well that first-pass analysis fares in light of much more detailed evidence. We then reflect on how the process of assembling regional “avifaunas” might be optimized.

REVIEW OF RECENT EVIDENCE REGARDING SPECIES LIMITS IN MEXICAN BIRDS

Our original taxonomic revision covered all Mexican birds and recommended emendations to species limits in 135 biological species (sensu AOU 1998), recognizing an additional 198 species taxa in the country. Here, we have reviewed literature published after 2003 (when we concluded our original studies) for treatment of any of the 135 complexes that we addressed (see appendix in Navarro-Sigüenza and Peterson 2004) using molecular systematic approaches (note that we include one earlier publication [Kirchman et al. 2000] of which we had been unaware). We included only studies that sampled multiple populations of the taxon in question that span multiple evolutionary species from our recommendations; we excluded all species for which molecular evidence was published at the time of our previous analyses (Navarro-Sigüenza and Peterson 2004). We evaluated phylogenetic trees or haplotype networks presented in each study to establish (1) whether our overall portrayal of species limits within the complex had been correct, (2) whether we had missed any distinct forms, and (3) whether each evolutionary species was indeed distinct from other such forms. The latter question was answered in terms of strong differentiation and reciprocal monophyly versus genetic differentiation, which could be incomplete and might not, as yet, include establishment of reciprocal monophyly.

We found recent studies treating 28 of the 135 biological species and 72 of the 323 evolutionary species treated in our previous summary (see Appendix). Our portrayal of species limits in 22 of these 28 complexes was completely correct. For the other six complexes, relationships were not as we had hypothesized—for