

other groups as suggested allies. It was first assigned to the "Ralliformes" by Fürbringer (1888), an arrangement not accepted by Gadow (1892: 244), but adopted by Wetmore and Miller (1926) and Wetmore (1930), who placed the Turnicidae with the rails in the Gruiformes. Also, it is only captive *Turnix* that begin to breed at "three to five months"—does any one know the age at first breeding for wild buttonquail?

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Response to E. Mayr

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Although Mayr is sharply critical of some aspects of the classification, I was generally pleased with his comments on the merits of the system. With respect to the DNA-DNA hybridization technique, he and I have been in much the same boat: our training and experience in the field of systematics were without much of the necessary background and knowledge in this field or in the techniques, at least initially, to appreciate fully the value of such studies to systematics. It is only recently that I have become involved in this classification project, and then only in the

aspect of providing a measure of expertise in classification and nomenclature techniques. I was not involved directly in any of the laboratory studies and certainly am not cognizant of all the techniques involved in achieving this classification. I am, however, totally convinced that the biochemical/genetic approach (and specifically DNA-DNA hybridization) is the most effective to understand the real relationships of birds, and avoids most of the pitfalls of other approaches (especially those that are morphological in nature). I sense from Mayr's comments that he feels much the same way as I did initially with the results of this technique. Many of the items not only made beautiful sense (e.g. the Corvida-Passerida evolutionary picture), but also have been supported subse-

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quently as correct either by independent molecular studies or by the discovery of *a posteriori* morphological characters that support the classification. Yet, there are enough "radical" changes (e.g. "Ciconiiformes") that lead one to wonder if the technique really works all the time! Sibley's response addresses the DNA findings, but let me address a few specific issues that spill over more into my realm.

Mayr mentioned a reluctance to accept the whole classification because of doubts about some parts. Also, he expressed a concern that such acceptance will further disrupt basic classification schemes, especially those used to place birds sequentially in collections, although such "disruption" still prevails today, because some museums use the Wetmore sequence (nine-primaried oscines-last) whereas others use the Basel sequence (crows-last). I believe that a further disruptive situation will prevail in the near future anyway, even if only the most reasonable of the DNA findings are accepted (e.g. the Passerida-Corvida split totally disrupts the passerine sequence of today, regardless of whether you now follow the Wetmore or Basel sequences). The main point is that the new classification is the first one ever to be based on an *objective* criterion, not on subjective interpretation of sometimes misleading sets of characters. If the new classification is accepted as largely correct, it would be easier to change the whole thing at once, rather than deviate slightly if a few of the earlier sequences prove to be somewhat out of line. It would be better if a few doubtful items from the new classification were later changed (e.g. the pelecaniiform arrangement) than to modify continually the present classification as more of the new classification becomes widely accepted. Otherwise, we will be forever accepting in a piecemeal way parts of the classification that prove to be right. Despite the furor over the DNA-DNA hybridization data in the past few years and all the attacks on Sibley and Ahlquist or the technique, no one yet has proved *any* part of this classification unequivocally wrong via any biochemical or genetic data; only some classifications based on morphological characters have deviated from these results. All along I have had the gut feeling that the DNA-DNA data give us the true picture, and I have seen nothing to disprove that as of yet.

One thing about Mayr's comments disturbs me considerably. For the past few years, both in my capacity as Chairman of the A.O.U. Check-list Committee and basic compiler of the forthcoming Sibley-Monroe "Classification of Birds of the World," I have corresponded with more than a dozen groups worldwide

who are working on major regional or world works on birds to attempt to get as much consistency as possible with English names of birds as well as to get views on different classification philosophies. The push again for the "Basel sequence" ("crows-last," or in the new classification "Corvida-last") is most distressing. Currently the world is nearly equally split in usage, and virtually all Americans and American-originated ornithological publications (including the A.O.U.) follow the "nine-primaried oscines-last" concept. It is interesting to note that if one follows a "primitive-derived" concept to sequence the current classification, the reduction in the primary number would clearly dictate that the "crows-last" concept violates this principle. In the Sibley et al. classification, one of my jobs was to insure sequencing in the best possible way. Because "primitive-derived" really has no meaning so far as the birds themselves are concerned (all living birds are equally "derived" genetically, only individual characters or sets thereof may be regarded as in the "primitive" or "derived" states) and genetic distance is the primary criterion, the sequence between two sister branches really has little meaning (e.g. with the Passerida-Corvida branch, either line can be treated first depending upon one's preference or upon some other artificial criterion). We generally operated on two principles. First, if there were more than two branches at a categorical level within a higher category, then the single line that emerged from the oldest branch (= greatest delta value) was treated first. Second, if there were but two such branches (e.g. only two Parvorders, the Corvida and Passerida, within the Suborder Passeri), then the sequence used was the least disruptive one with respect to the current "traditional" taxonomy, thus we generally followed a "primitive-derived" philosophy simply because that is the way it is "traditionally" done. However, I note that the Corvida are the more "primitive" of the two parvorders in the expression of the only morphological character found to be useful in defining the two groups, namely one humeral fossa (Corvida) versus two fossae (Passerida). Clearly the latter has the derived state (two fossae compared to a single fossa present on all Tyranni examined), so no matter what criteria are used in determining sequence, there is no way one can justify the Basel sequence. I would urge that the world shift to the Corvida-first sequence, and I intend to promote this idea, both in the I.O.C. and the A.O.U.

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