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Avian Raptor Evolution

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ABSTRACT

Despite decades of research using a variety of data sources (such as morphological, paleontological, immunological, DNA hybridization and short DNA sequences) both the relationships between modern avian orders of raptors and their times of origin remain uncertain. This prior work is discussed in the opening introductory chapter. In order to address these issues, the second chapter reports a study that I undertook to develop a database that would have all sequence data from avian raptors (although it could easily be modified for other groups as well). Complete mitochondrial (mt) genomes have been used extensively to help study evolution, and I sequenced seven new bird mt genomes: from owls, secretary bird, falcons, and eagles in order to provide improved taxon sampling for the avian raptors. Adding three of these taxa to the avian mt genome dataset aids in resolving deep bird phylogeny and strongly supports the independent origin of the raptor life-style – so there is now agreement between nuclear and mitochondrial sequences. The final four newer genomes were then added in for a more detailed analysis of raptor relationships, and good progress is made on this. We had issues with one of the final four newer genomes where the sample was mis-identified. Therefore, it is emphasized that it is always important to keep good reference samples to check identifications. For the fifth chapter I undertook a population level study of spotted owl (*Athene brama*) a nocturnal raptor from Pakistan, and so my study includes the use of sequence data to study both micro- and macro-evolution. The final chapter is a current overview of where we are at now in relation to avian raptor evolution.

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