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Introduction

John C. Avise

The last two decades have witnessed an explosion of interest in applying DNA profiling approaches to questions of parentage, genetic mating systems, and reproductive ecology in natural populations of many avian and mammalian species. Other vertebrate groups, by contrast, have been unduly neglected in such appraisals until recently, despite the fact that polymerase chain reaction (PCR)-based microsatellite assays and related molecular profiling techniques have become widely available. This is an ironic state of affairs, because fishes, amphibians, and reptiles exhibit a great variety of reproductive systems and mating tactics that should lend themselves well to critical appraisal by molecular markers.

There are additional reasons for interest in such genetic assessments. For example, individual nests or broods of poikilothermic vertebrates often contain scores to thousands of eggs, so several issues in statistical analysis and optimal sampling design arise that simply were less germane in earlier parentage analyses of birds and mammals. Large clutches also afford novel opportunities to address molecular-level issues, such as mutation rates at microsatellite loci and the incidence of clustered mutations (which arise premeiotically in maternal or paternal germ lines).

Following an introduction by Michael Taborsky to diverse reproductive tactics in fishes, the articles appearing in this symposium represent a mix of original research reports and mini-reviews by leading researchers who are using molecular markers to explore vertebrate reproductive behaviors in nature. Beyond the empirical findings and relevant theory presented herein, I hope that these proceedings will alert readers to the growing body of molecular evidence on reproductive tactics in cold-blooded vertebrates, stimulate further research on these reproductively fascinating creatures, and highlight the relevance of such findings to broader evolutionary concepts, including sexual selection theory.

I would like to take this opportunity to thank the contributors to this effort—the symposium speakers and their coauthors (who with good humor and conscientiousness complied with sequential editorial deadlines), and the external reviewers of each article who provided many constructive comments. I am also grateful to the American Genetic Association for sponsoring this event, and to the Pew Foundation and the University of Georgia for freeing enough of my time to have made this symposium and its proceedings possible.