November 2004

Early Bird: A Collaborative Project to Resolve the Deep Nodes of Avian Phylogeny

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· Variation in rates of gene evolution exists, even among

Large datasets confirm that short internodes separate major lineages of birds.

• Preliminary trees show several novel and interesting relationships. We confirm previous hypotheses of a sister

relationship between flamingos and grebes and have strong support for a sister relationship between kagu and sunbittern. We also find that tinamous are nested within the flightless ratites.

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Paleognaths and Galloanserae

Neoaves

20

5

3

0

1.3977

1.6155

NGF

egrl utr 1.2832

noncoding regions.

What we knew, late 1990's



State of Knowledge

Despite the volumes of information that have been gathered for brd at the species and distributional level, our understanding of the relationships among the major lineages remains uncertain. Published phylogenetic studies illustrate the problem-lack of resolution, short internodes and conflicting patterns. Our simulation studies (using a mixed model to capture among-locus heterogeneity) showed that 20 kb of sequence data would be required to resolve a series of divergence events that took place over a short period of time roughly 80 million years ago.

Project Goals

To collect 20,000 base pairs from 300-500 different taxa from a diverse array of nuclear markers (exons, introns, and untranslated regions), which map to different chromosomes.

Data Management

We have developed a web-based relational database to manage data and a web bulletin board to facilitate interaction among consortium members.



Progress to Date

In 2003-2004, we gathered a preliminary dataset of 40,000+ characters of aligned DNA sequence data (23,000 unaligned base pairs) from 19 different gene regions (21 different gene fragments) on 14 different chromosomes for 75 taxa of birds and their closest living relatives. In late 2004, we began to add 150 species to this sample.

Gene Regions Studied

Eukaryotic Elongation Factor Dimerization Co-factor of Hepatocyte Nuclear Factor X Rhodopsin B Clathrin Heavy Chain Alpha A Crystallin

C-myc

Somatotropin

Neurotrophin 3

Myoglobin

Aldolase B

Tropomyosin EGR-1 exon

EGR-I 3' UTR High Mobility Group

Interferon Regulatory Factor 1 and 2 Nerve Growth Factor

Brain-derived Neurotrophic Factor

Beta-Fibrinogen Transforming Growth Factor B-2

Muscle-specific Receptor Tyrosine Kinase

Intr Exo Unt

ons 60% 1s 35% ranslated Regions 5%	
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Rates of Gene Evolution (compared to the C-myc UTR) Introns Exons & UTRs HMG BDNF EEF 1 3887 0.6076 2 0061 myo2 C-myc DCOH CHC AldB tgf fib musk HMG soma Rhod ACA 2.053 07154 DCOH ACA CHC AldB 0 7266 2 3645 0 7965 2 4561 0.8315 2 6509 0.8432 AldB C-myc NT3 Rhod egr1 soma fib 0.8432 0.888 0.9982 1.0281 1.1063 1.1159 2.03 2.8708

3.2248

3.5964

3.9703

3 9997

trop irf2



Scope of Early Bird

Early Bird is a large-scale, cooperative effort among six institutions in the U.S., one in Scotland, and two in Australia to determine the evolutionary relationships among all major groups of birds. The goals of this project are to provide a detailed, comprehensive, and robust estimate of the "Family Tree" of avian relationships, and to facilitate the use of that tree to organize and interpret other information about birds. The impact of this project on science and society will be far reaching. Birds are among the most prominent and engaging creatures in most ecosystems worldwide. They have been the subject of an extraordinary number and diversity of scientific studies that figure largely in our understanding of the natural world and humanity's place in it. Their position high in many food chains and their great mobility make them sensitive indicators of environmental quality, and monitoring of bird populations is widely used to set conservation and management priorities. Their powers of flight, physical beauty and captivating behaviors amaze and inspire us, and birds provide tremendous amounts of recreation for serious hunters and birdwatchers, as well as the millions of backyard birdwatchers each year. All of these human interactions with birds will be enriched by a better understanding of avian evolutionary history and genetic diversity.



Fossils and Collaborations

Our DNA data will be integrated with existing and new DNA, morphological, and fossil data to bring all relevant evidence to bear on the pattern and timing of avian radiations. This is an important area of collaboration between the Early Bird and Archosaur AToL projects.

Needs

• improved data management tools to track data from specimens to publication

 improved analytical tools to take advantage of powerful computing resources

Outreach

Our data will be made accessible to other researchers through an online database with tools for analysis and export. This is another area of collaboration with the Archosaur AToL project. We communicate our project to the public in a variety of ways (websites, educational tools for K-12 teachers, museum exhibitions).

