Ancient Wings

Evolution of *Bicyclus* Wing Patterns

By Samuel Arbesman

Overview

Phylogenetic trees of taxa are often created and used for the calculation of ancestral traits of the internal nodes of these trees. However, seldom are these ancestral traits visualized in an intuitive manner.

Ancient Wings allows users to see how the ventral hindwing of 54 butterflies in the genus *Bicyclus* have putatively changed over time. By clicking on each of the nodes within the evolutionary tree, the user can see how eyespots' sizes and positions relative the wing margin have evolved. The ancestral wing pattern traits were calculated using COMPARE 4.4 (http://compare.bio.indiana.edu/), a program by Amelia Martins of Indiana University.

These calculations were done using a Brownian Motion model of evolution in which changes accumulate in a random fashion at constant rates. Evolutionary mechanisms that fit a Brownian Motion model include random genetic drift (with or without mutation), strong stabilizing selection with randomly changing optima, and directional selection that has random fluctuation. This model explicitly assumes that weaker stabilizing selection has not occurred. The phylogenetic tree and its historical calibration were calculated in Monteiro and Pierce (2001).

About the Program

There are two panels in this program, *The Wing* and *The Evolutionary Tree*.

The Wing

This panel shows a schematic view of the butterfly hindwing pattern (ancient or extant) currently being viewed. One of the longitudinal wing veins (the one posterior to the fourth eyespot) was used to align the eyespot patterns to the same relative x-y coordinates.

The "bull's-eye" shapes represent eyespots of this species and the black line represents an outline of the wing margin. The actual eyespot measurements were diameter measurements of the black center parallel to the wing veins and the gold ring proportions were extrapolated using a constant ratio (these proportions can also evolve across the genus *Bicyclus* but were not modeled here).

The plus inside a circle marks the intersection of the vein mentioned above and the vein posterior to the fourth eyespot. This may be dragged around if the wing begins to be drawn outside its panel.

The Evolutionary Tree

This panel shows the evolutionary tree of 54 species of *Bicyclus*, based on sequence divergence of one nuclear and two mitochondrial genes (Monteiro and Pierce 2001). The tree was time calibrated with one of the mitochondrial genes (Cytochrome Oxidase I) assuming that 2% sequence divergence corresponds to one million years of evolution (Monteiro and Pierce 2001). Each node represents either an extant or an ancestral *Bicyclus* species. Upon moving the mouse over the extant species, the name of the species will be displayed. The reddish-pink circle shows what position in the

evolutionary tree the Wing panel is displaying. The bar that crosses through the circle and the entire tree is simply an easy reference to watch if you are mainly concentrating on the wing pattern animation. To the right of this panel, a historical timeline may be used as a guide to see the approximate ages of points in the evolutionary tree.

By clicking on a node, *Ancient Wings* moves from the currently displayed node to the clicked-on node by way of the most direct route in the tree. The program looks for the most-recent common ancestor of the original node and the clicked-on node. The program then goes back to that common node (animating the wing pattern along the way) and then up the tree to the clicked-on node. Clicking on another node has no effect until the position circle has reached its original destination.

Scale: The scale bar allows for scaling of the size of the wing and may be done at any time. This is useful for making sure the wing stays inside the Wing panel.

Speed: The speed bar allows for changes in the speed of the movement from node to node. The changes take effect at the beginning of the next movement (after the change) from one node to the next.

The radio buttons that alter the display are as follows:

Size: the eyespots do not change position and only change in their diameter. They maintain the position of the last selected taxon.

Position: the eyespots disappear and are replaced with small x-marks that allows one to concentrate on position changes alone.

Size & Position: the eyespots change in size and position simultaneously.

Selected Bibliography

Martins, E. P. 2001. COMPARE, version 4.4. Computer programs for the statistical analysis of comparative data. Distributed by the author via the WWW at http://compare.bio.indiana.edu/. Department of Biology, Indiana University, Bloomington IN.

Monteiro A and N Pierce. 2001. *Molecular phylogeny of Bicyclus butterflies (Satyridae) using COI, COII and EF1a.* **Molecular Phylogenetics and Evolution** 18: 264-281.

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Samuel Arbesman is a junior at Brandeis University and made *Ancient Wings* in Antónia Monteiro's lab during the summer of 2002. Sam is majoring in computer science and biology.

Antónia Monteiro is an assistant professor of evolutionary developmental biology at SUNY at Buffalo. Her lab focuses on the evolution and development of butterfly wing patterns.

Ancient Wings was made in Macromedia Flash MX on a Power Mac G4 desktop running Mac OS X. The program made heavy use of Flash's built-in programming language Actionscript (many, many lines of code). Object-Image 2.08, COMPARE 4.4, and Perl were used in the gathering, analysis and manipulation of the data.