

Comparative Biology Educational Module

Written by Bryan McLean and Libby Beckman (UNM Department of Biology and Museum of Southwestern Biology)

Spring 2013

Part I - Data Acquisition

Navigate to '**dryad**' data repository (<http://datadryad.org/handle/10255/dryad.34414>). Data repositories like dryad are an important source of information from published studies, which allow scientists to further test and build upon experimental results of others.

Available on this page are data from a study by Mayrose and colleagues (2011) on the frequency of polyploidy in vascular plants. Polyploidy is defined as a change in the number of chromosomes an organism has. It is actually somewhat widespread in plants and has been an important force in plant evolution. Read the summary of this study under **Abstract**.

Next, scroll to the bottom of the page and download '**polyploidy_database.zip**'. Your machine may automatically unzip and rename this file. If not, do so manually. When downloaded, move the file to a folder on your hard drive where it is easily located.

Open the folder containing the unzipped contents of '**polyploidy_database.zip**'. You will notice a number of folders. Each one represents a different plant genus analyzed by Mayrose and colleagues. Open '**readMe.txt**'. This file tells us that each plant folder contains five files. The contents of '**readMe.txt**' probably will not make much sense, but don't worry. What we are most interested in are File 1 (aligned DNA sequences from multiple species in each plant genus) and File 5 (the corresponding numbers of chromosomes these species have). File 1 and File 5 have the extensions **.fa** and **.fac**, respectively.

Find the folder '**Betula**'. *Betula* (birches) is a genus of broadleaved deciduous trees. There are between 30 and 60 recognized species of birches which range across temperate and boreal habitats of the Northern Hemisphere. We will use the *Betula* data of Mayrose and colleagues to investigate the evolution of polyploidy in this particular plant group.

Part II - Phylogenetic Analysis

Navigate to **Phylogeny.fr** (<http://www.phylogeny.fr/>).

Under **Phylogeny Analysis**, select **One-Click**. Choose and enter a name for your

analysis. Then, select **Choose File** and locate and import **Betula** -> '**Betula.fa**'. Make sure the 'Use the Gblocks program to eliminate poorly aligned positions and divergent regions' option is selected. Now click **Submit**. The results of your Maximum-Likelihood phylogenetic analysis will soon appear.

Notice three things about your birch phylogeny, which were covered in the previous lab:

Red numbers on nodes represent branch support values. Your phylogenetic analysis was run using many different trees; branch support values are the fraction of those trees in which a particular phylogenetic relationship(s) was found. For example, a branch support value of 1 would indicate that a particular relationship was found in all runs, and is thus strongly supported as the true relationship. For *Betula*, you should also notice several very low (or even 0) branch support values. These represent evolutionary relationships that were found in few runs, and are thus poorly supported (i.e., more data will be necessary to fully resolve them).

The scale bar gives a standard amount of evolutionary change (here, genetic change) that can be used to compare relative differences among birch species.

The species ***Corylus avellana*** (Common Hazel) is very divergent from all *Betula* - it has been included in this phylogenetic analysis as an **outgroup**. Outgroups are often used to 'root' phylogenetic trees.

Leave the phylogeny window open for Part III.

Part III - Phylogenetic Comparisons of Polyploidy

Locate and open **Betula** -> '**Betula.fac**' using TextEditor, WordPad, or an equivalent program. This file contains the diploid chromosome numbers of each of the 14 birch species in your phylogeny. You will now map these numbers as traits onto the phylogeny.

Scroll down and select the **Add leaf annotations** tool. The tool will allow you to annotate species names on the birch phylogeny simply by clicking on those names. One by one, enter the chromosome numbers in '**Betula.fac**' onto their corresponding species on the phylogeny. Lastly, to aid in visualization of differences in chromosome number, recolor those species with chromosome numbers different from 14. This is done using the **Colorize** tool with leaf and branch selected.

****Now answer the following questions**:**

In how many species does polyploidy appear to have evolved?

Are these species closely related, or does polyploidy appear to have evolved multiple

times (i.e., on different parts of the tree)?

Mayrose and colleagues presented data on many other plant groups, and the occurrence of polyploidy in those groups. Form a hypothesis as to why polyploidy may promote the creation of new plant species (speciation).