Research Article

Creating and analyzing systematic data sets using Winclada/Nona programs for the students of plant taxonomy

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Abstract

The main approach of the current study is to use software dealing with cladistics to develop cladogram for hypothetical taxa as a case study. The objective is to elucidate the evolutionary interrelationships between the taxa under investigation using Winclada/Nona softwares from phylogenetics point of view. The program Winclada contains many data editing and tree analysis features as well as a shell for running Nona software to create cladogram in phylogenetic alanlysis. Using such computational software technology, complex understanding of taxonomical interrelationships becomes more clear. In the current paper author has discussed sequence of steps to create dataset using Winclada and run the modules of Nona software to generate a phenogram illustrating the evolutionary interrelationships among the taxa under study from cladistics point of view.

Keywords: Winclada, Nona, phylogenetics, cladistics, digital learning environment

Introduction

Many traditional classifications in plant systematics are phenetic, based on noted similarities between and among taxa, while phylogenetic classification is that which is based on evolutionary history, Ever since Darwin laid down the fundamental principles of evolutionary theory, one of the major goals of the biological sciences has been the determination of life history of descent. This phylogeny of organisms, visualized as a branching pattern called cladogram, that can be determined by an analysis of characters from living or fossil organisms, utilizing phylogenetic principles and methodology (Simpson, 2006).

A very important concept in phylogenetic systematics is that of monophyly, a monophyletic group is one that consists of a common ancestor plus all descendants of that ancestor. The converse of monophyly is paraphyly, a paraphyletic group is one that includes a common ancestor and some, but not all, known descendants of that ancestor. Similarly, a polyphyletic group is one containing two or more common ancestors (Simpson, 2006).

The software Winclada acts as a shell for using other programs such as Nona to submit data matrices and construct a cladogram that clarify the evolutionary relationships among the taxa under investigation (Nixon, 1999 and Goloboff, 1999). Using such computational software technology, complex interrelationships becomes more users friendly and more understandable. In the current paper author has discussed sequence of steps to generate dataset using Winclada/Nona programs ending with constructing a cladogram used to clarify the evolutionary history of the targeted taxa.

The main objective of the present study is to acquire students skills needed for the current century and the digital learning environment where the request of new information and communication technology (ICT) in the educational systems are increased and becomes an urgent need (Anjaria, 2017).

Materials and Methods

Downloading Winclada and Nona programs:

Winclada and Nona programs (Nixon, 1999 and Goloboff, 1999) can be downloaded through http://www.cladistics.com.

Creating a dataset:

The first step in basic cladistic analysis is to determine which character states are plesiomorphic and which are apomorphic using outgroup comparison Hennig (1966) where the outgroup character state that is the same as some of the organisms in the group can be considered as plesiomorphic and coded as (0) other states can be considered as apomorphic and coded as (1). The building of a taxon/characters states matrix is in the form of binary state (0/1) for each character state or in the form of DNA sequences (Table 1 and 2).

Table 1. Data matrix of studied taxa and characters states.

Characters Taxa	1	2	3	4	5	6	7	8	9	10
Outgroup	a	a	a	a	b	a	a	a	a	a
Alpha	a	a	a	b	a	b	a	a	a	a
Beta	a	a	a	b	b	b	a	a	a	a
Gamma	a	a	a	a	b	a	b	a	b	a
Delta	b	b	b	a	b	a	b	b	b	a
Epsilon	b	b	b	a	b	a	b	a	b	b
Zeta	b	b	a	a	b	a	b	a	b	b
Theta	b	a	a	a	b	a	b	a	b	b

Table 2. Coding of the characters states of the studied taxa.

Characters Taxa	1	2	3	4	5	6	7	8	9	10
Outgroup	0	0	0	0	0	0	0	0	0	0
Alpha	0	0	0	1	1	1	0	0	0	0
Beta	0	0	0	1	0	1	0	0	0	0
Gamma	0	0	0	0	0	0	1	0	1	0
Delta	1	1	1	0	0	0	1	1	1	0
Epsilon	1	1	1	0	0	0	1	0	1	1
Zeta	1	1	0	0	0	0	1	0	1	1
Theta	1	0	0	0	0	0	1	0	1	1

Entering taxa and characters:

To start a new matrix, click the winclada.exe, WinClada editor window is displayed (Fig. 1, a), to start a new matrix, select Matrix > New matrix (creat), then set the values of new number of taxa and new number of characters in New Matrix/Resize matrix window (Fig. 1,b). Empty data matrix will be prompted and can be filled with taxa names through Taxon name edit window; Terms > Terminal dialog then apply. Entering characters can be achieved as 0/1 binary state or as DNA bases (Fig. 1,c).
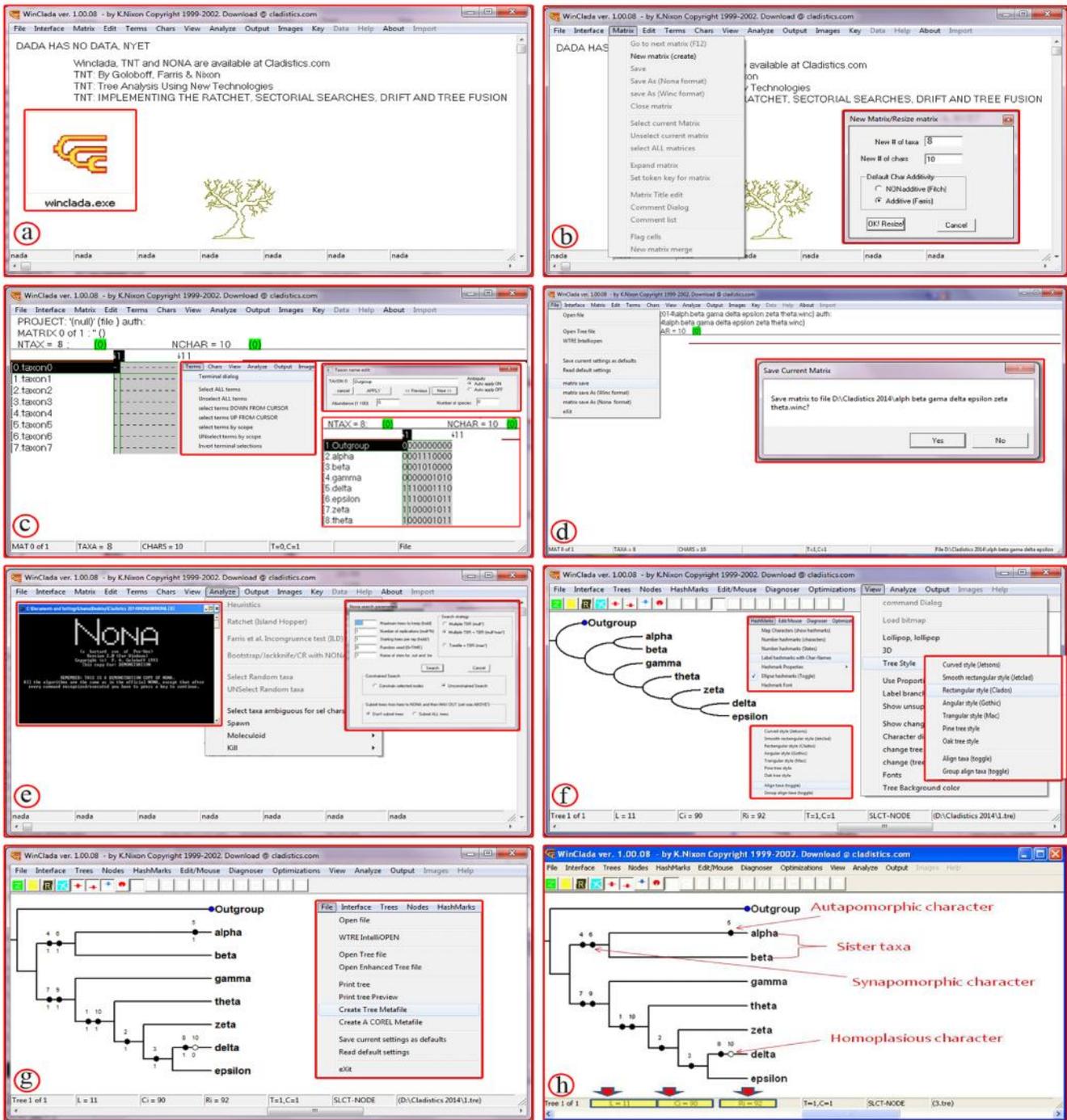
Figure 1. Screem shots of the Winclada software; a. Running winclada.exe. b. Input file format for winclada editor. c. Taxon name edit window. d. Saving the matrix file. e. Running Nona.exe. f. Editing the resulted cladogram. g. Creating tree metafile. h. The cladogram in the final form with descriptive terminology.

Saving the dataset:

Select File > matrix save, then press yes from the displayed Save Current Matrix window, that can be used for the proceeding computations (Fig. 1, d).

Analyzing the dataset:

Winclada acts as a shell for using other programs such as Nona sofware, by clicking on Analyze a submenu will appear containing some modules such as Heuristics by choosing one of them Nona search program window will be displayed that allow Nona program to be launched by pressing on Search icon (Fig. 1, e).

Editing the cladogram:

The previous step ends with the appearance of a cladogram that can be edited through View > Tree Style (Fig. 1, f). The character changes can be tracked on the cladogram through HashMarks > Map Characters. Tree metafilecan be created to save the resulted cladogram; File > Create Tree Metafile (Fig. 1 g). The character map help in the discussion of the relationships among the taxa under investigation such as sister group relationship in addition to the categorization of these characters as apomomorphic, synapomorphic and homoplasious characters (Fig. 1, h).

Results and Discussion

Several cladistic analysis on families of flowering plants were conducted using winclada/Nona programs (Nixon, 1999 and Goloboff, 1999) indicating that the used characters were likely to be useful and valuable taxonomic traits (Abdel-Hameed 2014 and Abdel-Hameed et al., 2014).

The clade comprising all the taxa receives expressing strong support for the monophyly of the family. Among the obtained two lineages of the family, there is support for monophyly of lineages I and II separately through the synapomorphic characters *viz*.(4,6) and (7,9) respectively. In addition, there is a support for a sister group relationship between *Alpha* and *Beta*, *Alpha* is marked with autapomorphic character (5) and this character is considered as a unique character marker for the current taxa.

In lineage II, the basal position of *Gamma* is supported followed by Theta then Zeta, The two latter studied species Viz. *Delta* and *Epsilon* are closely related showing a sister relationship owing to the synapomorphic character (3).

In conclusion, the present paper discussed about skillful utilization of Winclada/Nona programs, for creating learning resources which is useful for graduate and postgraduate students. Teachers may incorporate more taxa and more characters and build cladograms for the interrelationships among the studied taxa.

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