**Default settings Phylip**

Nucleic acid sequence Distance Matrix program, version 3.695

Settings for this run:

D Distance (F84, Kimura, Jukes-Cantor, LogDet)? F84

G Gamma distributed rates across sites? No

T Transition/transversion ratio? 2.0

C One category of substitution rates? Yes

W Use weights for sites? No

F Use empirical base frequencies? Yes

L Form of distance matrix? Square

M Analyze multiple data sets? No

I Input sequences interleaved? Yes

0 Terminal type (IBM PC, ANSI, none)? ANSI

1 Print out the data at start of run No

2 Print indications of progress of run Yes

Protein distance algorithm, version 3.695

Settings for this run:

P Use JTT, PMB, PAM, Kimura, categories model? Jones-Taylor-Thornton matrix

G Gamma distribution of rates among positions? No

C One category of substitution rates? Yes

W Use weights for positions? No

M Analyze multiple data sets? No

I Input sequences interleaved? Yes

0 Terminal type (IBM PC, ANSI)? ANSI

1 Print out the data at start of run No

2 Print indications of progress of run Yes

Neighbor-Joining/UPGMA method version 3.695

Settings for this run:

N Neighbor-joining or UPGMA tree? Neighbor-joining

O Outgroup root? No, use as outgroup species 1

L Lower-triangular data matrix? No

R Upper-triangular data matrix? No

S Subreplicates? No

J Randomize input order of species? No. Use input order

M Analyze multiple data sets? No

0 Terminal type (IBM PC, ANSI, none)? ANSI

1 Print out the data at start of run No

2 Print indications of progress of run Yes

3 Print out tree Yes

4 Write out trees onto tree file? Yes

DRAWGRAM from PHYLIP version 3.695

Reading tree ...

Tree has been read.

Loading the font ....

Font loaded.

Rooted tree plotting program version 3.695

Here are the settings:

0 Screen type (IBM PC, ANSI): ANSI

P Final plotting device: Postscript printer (Preview no longer available)

H Tree grows: Horizontally

S Tree style: Phenogram

B Use branch lengths: Yes

L Angle of labels: 90.0

R Scale of branch length: Automatically rescaled

D Depth/Breadth of tree: 0.53

T Stem-length/tree-depth: 0.05

C Character ht / tip space: 0.3333

A Ancestral nodes: Weighted

F Font: Times-Roman

M Horizontal margins: 1.65 cm

M Vertical margins: 2.16 cm

# Pages per tree: one page per tree