

TEMA 1. ¿Qué es una filogenia molecular y para qué sirve?

- AVISE, J.C. 1989. A Role for Molecular Genetics in the Recognition and Conservation of Endangered Species. *Trends in Ecology and Evolution* 4: 279-281.
- AVISE, J.C. 2000. *Phylogeography: the history and formation of species*. Harvard University Press, Cambridge, MA.
- AVISE, J.C. 2009. Phylogeography: retrospect and prospect. *Journal of Biogeography* 36: 3-15.
- CRANDALL, K.A., BININDA-EMONDS, O.R.P., MACE, G.M. AND R.K. WAYNE. 2000. Considering evolutionary processes in conservation biology. *Trends in Ecology and Evolution* 15: 290-295.
- HENNIG W. 1966. *Phylogenetic Systematics*. University of Illinois Press, Urbana. Pp. 263.
- KLEPPE, K., OHTSUKA, E., KLEPPE, R., MOLINEUX, I., AND H.G. KHORANA. 1971. Studies on polynucleotides: XCVI. Repair replication of short synthetic DNA's as catalyzed by DNA polymerases. *Journal of Molecular Biology* 56: 341-361.
- MULLIS, K.B. AND F.A. FALOONA. 1987. Specific synthesis of DNA *in vitro* via a polymerase-catalyzed chain reaction. *Methods in Enzymology* 155: 335-350.
- RICKLEFS, R.E. 2007. Estimating diversification rates from phylogenetic information. *Trends Ecology and Evolution* 22: 601-610.
- RONQUIST, F. AND I. SANMARTÍN. 2011. Phylogenetic methods in historical biogeography. *Annual Review of Ecology, Evolution and Systematics* 42: 441-464.
- SANGER, F. AND A.R. COULSON. 1975. A rapid method for determining sequences in DNA by primed synthesis with DNA polymerase. *Journal of Molecular Biology* 94: 441-446.
- SCHAAL, B.A., HAYWORTH, D.A., OLSEN, K.M., RAUSCHER, J.T., AND W.A. SMITH. 1998. Phylogeographic studies in plants: Problems and prospects. *Molecular Ecology* 7: 465-474.
- SHAW J., E. B. LICKEY, J. T. BECK, S. B. FARMER, W. LIU, J. MILLER, K. C. SIRIPUN, C. T. WINDER, E. E. SCHILLING, AND R. L. SMALL. 2005. The tortoise and the hare II: Relative utility of 21 noncoding chloroplast DNA sequences for phylogenetic analysis. *American Journal of Botany* 92: 142-166.
- SHAW J., E. B. LICKEY, E. E. SCHILLING, AND R. L. SMALL. 2007. Comparison of whole chloroplast genome sequences to choose noncoding regions for phylogenetic studies in angiosperms: The Tortoise and the hare III. *American Journal of Botany* 94: 275-288.
- SMALL R. L., J. A. RYBURN, R. C. CRONN, T. SEELANAN, AND J. F. WENDEL. 1998. The tortoise and the hare: Choosing between noncoding plastome and nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant group. *American Journal of Botany* 85: 1301-1315.
- ZIMMERMANN, W. 1930. *Die Phylogenie der Pflanzen*. G. Fischer, Jena, Germany.
- ZIMMERMANN, W. 1934. Research on phylogeny of species and of single characters. *American Naturalist* 68: 381-384.
- ZUCKERKANDL E. and L. PAULING. 1965. Evolutionary divergence and convergence in proteins. *Evolving Genes and Proteins* 97-166.

TEMA 2.1. Breve introducción a las técnicas y métodos de reconstrucción filogenética

- FARRIS J. S., V. A. ALBERT, M. KÄLLERSJÖ, D. LIPSCOMB, AND A. G. KLUGE. 1996. Parsimony jackknifing outperforms neighbor-joining. *Cladistics* 12: 99-124.

- GAUT B. S. and P. O. LEWIS. 1995. Success of maximum likelihood phylogeny inference in the four-taxon case. *Molecular Biology and Evolution* 12: 152-162.
- HENDY M. D. and D. PENNY. 1982. Branch and bound algorithms to determine minimal evolutionary trees. *Mathematical Biosciences* 59: 277-290.
- HILLIS D. M., C. MORITZ, AND B. K. MABLE. 1996. *Molecular Systematics*. Sinauer Associates, Sunderland. Pp. 665.
- HUELSENBECK J. P. 1995. Performance of phylogenetic methods in simulation. *Systematic Biology* 44: 17-48.
- HUELSENBECK J. P. 1998. Systematic Bias in Phylogenetic Analysis: Is the Strepsiptera Problem Solved? *Systematic Biology* 47: 519-537.
- NEI, S. AND, M. KUMAR. 2000. *Molecular evolution and phylogenetics*. Oxford university Press, New York.
- PIONTKIVSKA H. 2004. Efficiencies of maximum likelihood methods of phylogenetic inferences when different substitution models are used. *Molecular Phylogenetics and Evolution* 31: 865-873.
- PLATNICK N. I. 1985. Philosophy and the transformation of cladistics revisited. *Cladistics* 1: 87-94.
- SALTER L. A. and D. K. PEARL. 2001. Stochastic search strategy for estimation of maximum likelihood phylogenetic trees. *Systematic Biology* 50: 7-17.
- STEEL M. A., M. D. HENDY, AND D. PENNY. 1988. Loss of information in genetic distances. *Nature* 336: 118.
- WILLIAMS D. M. 1992. DNA analysis: Theory. In Forey P. L., C. J. Humphries, I. J. Kitching, R. W. Scotland, D. J. Siebert and D. M. Williams [eds.], *Cladistics: A practical course in sistematics*, 89-101. Oxford Univsersity Press, Oxford.

TEMA 2.2. Puntos clave en el diseño y elaboración de una filogenia molecular

- ÁLVAREZ I. and J. F. WENDEL. 2003. Ribosomal ITS sequences and plant phylogenetic inference. *Molecular Phylogenetics and Evolution* 29: 417-434.
- BALDWIN B. G., M. J. SANDERSON, J. M. PORTER, M. F. WOJCIECHOWSKI, C. S. CAMPBELL, AND M. J. DONOGHUE. 1995. The ITS region of nuclear ribosomal DNA: A valuable source of evidence on angiosperm phylogeny. *Annals of the Missouri Botanical Garden* 82: 247-277.
- BREMER K. 1990. Combinable Component Consensus. *Cladistics-the International Journal of the Willi Hennig Society* 6: 369-372.
- BREMER K. 1994. Branch support and tree stability. *Cladistics* 10: 295-304.
- CUMMINGS M. P., S. A. HANDLEY, D. S. MYERS, D. L. REED, A. ROKAS, AND K. WINKA. 2003. Comparing bootstrap and posterior probability values in the four-taxon case. *Systematic Biology* 52: 477-487.
- DOYLE J. J. 1992. Gene trees and species trees: Molecular systematics as one-character taxonomy. *Systematic Botany* 17: 144-163.
- DOYLE J. J. and B. S. GAUT. 2000. Evolution of genes and taxa: A primer. *Plant Molecular Biology* 42: 1-23.
- EDGAR, R.C. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research* 32: 1792-1979.
- FELINER G. N. and J. A. ROSSELLÓ. 2007. Better the devil you know? Guidelines for insightful utilization of nrDNA ITS in species-level evolutionary studies in plants. *Molecular Phylogenetics and Evolution* 44: 911-919.
- FELSENSTEIN J. 1978. Cases in which parsimony or compatibility methods will be positively misleading. *Systematic Zoology* 27: 401-410.
- GLADSTEIN D. and W. WHEELER. 1996. POY. Software for Direct Optimization of DNA and Other Data. Available anonymously via <ftp://ftp.amnh.org/pub/molecular/POY>.

- HILLIS D. M. and J. J. BULL. 1993. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Systematic Biology* 42: 182-192.
- HILLIS D. M., C. MORITZ, AND B. K. MABLE. 1996. *Molecular Systematics*. Sinauer Associates, Sunderland. Pp. 665.
- HILLIS D. M. 1997. Primer: phylogenetic analysis. *Current Biology* 7: R129-R131.
- HUGHES C. E., R. J. EASTWOOD, AND C. D. BAILEY. 2006. From famine to feast? Selecting nuclear DNA sequence loci for plant species-level phylogeny reconstruction. *Philosophical Transactions of the Royal Society B: Biological Sciences* 361: 211-225.
- JUDD W. S., C. S. CAMPBELL, E. A. KELLOGG, P. F. STEVENS, AND M. J. DONOGHUE. 2002. *Plant systematics. A phylogenetic approach*. Sinauer Associates, Inc., Massachusetts.
- LEE M. S. Y. 2001. Unalignable sequences and molecular evolution. *Trends in Ecology and Evolution* 16: 681-685.
- MADDISON W. P. 1997. Gene trees in species trees. *Systematic Biology* 46: 523-536.
- MARGUSH T. and F. R. MCMORRIS. 1981. Consensus trees. *Bull. Math. Biol.* 43: 239-244.
- MORGENSTERN B., K. FRECH, A. DRESS, AND T. WERNER. 1998. DIALIGN: Finding local similarities by multiple sequence alignment. *Bioinformatics* 14: 290-294.
- MURPHY W. J., E. EIZIRIK, S. J. O'BRIEN, O. MADSEN, M. SCALLY, C. J. DOUADY, E. TEELING, O. A. RYDER, M. J. STANHOPE, W. W. DE JONG, AND M. S. SPRINGER. 2001. Resolution of the early placental mammal radiation using bayesian phylogenetics. *Science* 294: 2348-2351.
- NEE S., E. C. HOLMES, R. M. MAY, AND P. H. HARVEY. 1994. Extinction rates can be estimated from molecular phylogenies. *Philosophical Transactions - Royal Society of London, B* 344: 77-82.
- NELSON G. 1979. *Cladistic Analysis and Synthesis - Principles and Definitions, with a Historical Note on Adansons Familles Des Plantes (1763-1764)*. *Systematic zoology* 28: 1-21.
- NIXON K. C. and J. M. CARPENTER. 1993. On outgroups. *Cladistics* 9: 413-426.
- PALMER J. D. 1992. Mitochondrial DNA in plant systematics: Applications and limitations. In Soltis, Soltis and Doyle, *Molecular Systematics of Plants* pp. 36-49. Kluwer Academic Publisher.
- PAMILO P. and M. NEI. 1988. Relationship between gene trees and species trees. *Molecular Biology and Evolution* 5: 568-583.
- PHILIPPE H., ZHOU, Y., BRINKMANN, H., RODRIGUE, N., AND F. DELSUC. 2005. Heterotachy and long-branch attraction in phylogenetics. *BMC Evolutionary Biology* 5: 50.
- POSADA D. 2001. The effect of branch length variation on the selection of models of molecular evolution. *Journal of Molecular Evolution* 52: 434-444.
- POSADA D. AND T.R. BUCKLEY. 2004. Model Selection and Model Averaging in Phylogenetics: Advantages of Akaike Information Criterion and Bayesian Approaches Over Likelihood Ratio Tests. *Systematic Biology* 53: 793-808.
- SHAW J., E. B. LICKEY, J. T. BECK, S. B. FARMER, W. LIU, J. MILLER, K. C. SIRIPUN, C. T. WINDER, E. E. SCHILLING, AND R. L. SMALL. 2005. The tortoise and the hare II: Relative utility of 21 noncoding chloroplast DNA sequences for phylogenetic analysis. *American Journal of Botany* 92: 142-166.
- SHAW J., E. B. LICKEY, E. E. SCHILLING, AND R. L. SMALL. 2007. Comparison of whole chloroplast genome sequences to choose noncoding regions for phylogenetic studies in angiosperms: The Tortoise and the hare III. *American Journal of Botany* 94: 275-288.
- SIMMONS M. P., H. OCHOTERENA, AND T. G. CARR. 2001. Incorporation, relative homoplasy, and effect of gap characters in sequence-based phylogenetic analyses. *Systematic Biology* 50: 454-462.

- SIMMONS M. P. and J. V. FREUDENSTEIN. 2003. The effects of increasing genetic distance on alignment of, and tree construction from, rDNA internal transcribed spacer sequences. *Molecular Phylogenetics and Evolution* 26: 444-451.
- SMALL R. L., J. A. RYBURN, R. C. CRONN, T. SEELANAN, AND J. F. WENDEL. 1998. The tortoise and the hare: Choosing between noncoding plastome and nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant group. *American Journal of Botany* 85: 1301-1315.
- SMITH A. B. 1994. Rooting molecular trees - Problems and strategies. *Biological Journal of the Linnean Society* 51: 279-292.
- SOLTIS D. E. and P. S. SOLTIS. 1998. Choosing an approach and an appropriate gene for phylogenetic analysis. *Molecular Systematics of Plants II: DNA Sequencing* pp.1-42. Kluwer academic Publishers, Boston.
- SOLTIS D. E. and P. S. SOLTIS. 2003. The role of phylogenetics in comparative genetics. *Plant Physiology* 132: 1790-1800.
- SULLIVAN J. and D. L. SWOFFORD. 1997. Are guinea pigs rodents? The importance of adequate models in molecular phylogenies. *Journal of Mammal Evolution* 4: 77-86.
- SUZUKI Y., G. V. GLAZKO, AND M. NEI. 2002. Overcredibility of molecular phylogenies obtained by Bayesian phylogenetics. *Proceedings of the National Academy of Sciences of the United States of America* 99: 16138-16143.
- TABERLET P., L. GIELLY, G. PAUTOU, AND J. BOUVET. 1991. Universal primers for amplification of three non-coding regions of chloroplast DNA. *Plant Molecular Biology* 17: 1105-1109.
- THOMPSON J. D., D. G. HIGGINS, AND T. J. GIBSON. 1994. CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Research* 22: 4673-4680.
- WENZEL J. W. and M. E. SIDDALL. 1999. Noise. *Cladistics* 15: 51-64.
- WHELAN S., P. LIO, AND N. GOLDMAN. 2001. Molecular phylogenetics: state-of-the-art methods for looking into the past. *Trends in Genetics* 17: 262-272.
- WHEELER W. C. 1990. Nucleic acid sequence phylogeny and random outgroups. *Cladistics* 6: 363-367.
- WHEELER W. C. 1992. Extinction, sampling, and molecular phylogenetics. In Novacek M. J. and Q. D. Wheeler [eds.], *Extinction and phylogeny*, 205-215. Columbia University Press, New York.
- WHEELER W. and D. GLADSTEIN. 2000. "MALIGN." Version 2.8.
- YANG Z. 1994. Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: approximate methods. *Journal of Molecular Evolution* 39: 306-314.

TEMA 3.2. Obtención de matrices: búsqueda de homologías, alineamiento

- DOYLE J.J. y GAUT, B.S. 2000. Evolution of genes and taxa: A primer. *Plant Molecular Biology* 42: 1-23.
- EDGAR, R.C. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* 32(5):1792-1797. doi:10.1093/nar/gkh340
- KELCHNER, S.A. 2000. The Evolution of Non-Coding Chloroplast DNA and Its Application in Plant Systematics. *Annals of the Missouri Botanical Garden* 87, 4: 482-498.
- LARKIN, M.A., BLACKSHIELDS, G., BROWN, N.P., CHENNA, R., MCGETTIGAN, P.A., MCWILLIAM, H., VALENTIN, F., WALLACE, I.M., WILM, A., LOPEZ, R., THOMPSON, J.D., GIBSON, T.J. AND D.G. HIGGINS. 2007. Clustal W and Clustal X version 2.0 *bioinformatics applications note* 23, 21: 2947-2948.

- SIMMONS, M.P. y FREUDENSTEIN, J.V. 2003. The effects of increasing genetic distance on alignment of, and tree construction from, rDNA internal transcribed spacer sequences. *Molecular Phylogenetics and Evolution* 26: 444-451.
- SIMMONS, M.P. y OCHOTERENA, H. 2000. Gaps as characters in sequence-based phylogenetic analyses. *Systematic Biology* 49: 369-381.
- SIMMONS M. P., H. OCHOTERENA, AND T. G. CARR. 2001. Incorporation, relative homoplasy, and effect of gap characters in sequence-based phylogenetic analyses. *Systematic Biology* 50: 454-462.
- THOMPSON J. D., D. G. HIGGINS, AND T. J. GIBSON. 1994. CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Research* 22: 4673-4680.

TEMA 3.4. Selección del modelo evolutivo que mejor se ajuste a nuestros datos

- JUKES, T.H., AND C.R. CANTOR. 1969. Evolution of protein molecule, pp:21-132. En H.N. Munro (ed.), *Mammalian Preprotein Metabolism*. Academic Press, New York.
- KIMURA, M. 1980. A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16: 111-120.
- LEMMON A.R., AND E.C. MORIARTY. 2004. The importance of proper model assumption in Bayesian phylogenetics. *Systematic Biology* 53: 265-277.
- NYLANDER, J.A.A. 2004a. MrModeltest v2. Program distributed by the author. Available from: <http://www.abc.se/~nylander/>. Evolutionary Biology Centre, Uppsala University.
- NYLANDER, J.A.A. 2004b. MRAIC.PL. Program distributed by the author. Available from: <http://www.abc.se/~nylander>. Evolutionary Biology Centre, Uppsala University.
- POSADA D., AND K.A. CRANDALL. 1998. Modeltest: testing the model of DNA substitution. *Bioinformatics*. 14:817-818.
- POSADA D. 2004. Model selection and model averaging in phylogenetics: advantages of Akaike Information Criterion and Bayesian Information Criterion over Likelihood Ratio Tests. *Systematic Biology* 53: 793-808.
- POSADA D. 2008. JModeltest: Phylogenetic Model Averaging. *Molecular Biology and Evolution* 25: 1253-1256.
- SWOFFORD, D.L. 2002. PAUP*: Phylogenetic analysis using parsimony (*and other methods), version 4.0b10. Sunderland, Massachusetts: Sinauer.

TEMA 3.5. Obtención de árboles mediante el método de inferencia bayesiana

- HUELSENBECK, J.P., F. RONQUIST. 2001. MrBayes: Bayesian inference of phylogeny. *Bioinformatics* 17: 754-755.
- SIMMONS, M.P., AND H. OCHOTERENA. 2000. Gaps as characters in sequence-based phylogenetic analyses. *Systematic Biology* 49: 369-381.