

DAFTAR PUSTAKA

- Alvarez, I., & Wendel, J. F. (2003). Ribosomal ITS Sequences and Plant Phylogenetic Inference. *Molecular Phylogenetics and Evolution*, 29(3), 417–434. [https://doi.org/10.1016/S1055-7903\(03\)00208-2](https://doi.org/10.1016/S1055-7903(03)00208-2)
- Amos, A. (2010). Kandungan Katekin Gambir Sentra Produksi di Indonesia. *Jurnal Standardisasi*, 12(3), 149. <https://doi.org/10.31153/js.v12i3.152>
- Armenia, A., Badriyya, E., Rahmita, S., Rachmaini, F., & Abdillah, R. (2024). Malondialdehyde and TNF- α Lowering Effects of Purified Gambier (Uncaria gambir Roxb.) in Diabetic Rats. *J. Ayurveda Integr. Med*, 15(1), 100855. <https://doi.org/10.1016/j.jaim.2023.100855>
- Baldwin, B. G., Sanderson, M. J., Porter, J. M., Campbell, C. S., & Donoghue, M. J. (1995). The ITS Region of Nuclear Ribosomal DNA: A Valuable Source of Evidence on Angiosperm Phylogeny. *Ann. Mo. Bot. Gard*, 82(2), 245–277.
- Baraket, G., Olfa, S., Khaled, C., Messaoud, M., Mohamed, M., Mokhtar, T., & Amel, S.-H. (2008). Chloroplast DNA Analysis in Tunisian Fig Cultivars (*Ficus Carica* L.): Sequence Variations of The trnL-trnF Intergenic Spacer. *Biochemical Systematics and Ecology*, 36(11), 828–835. <https://doi.org/10.1016/j.bse.2008.09.005>
- Borsch, T., & Quandt, D. (2009). Mutational Dynamics and Phylogenetic Utility of Noncoding Chloroplast DNA. *Journal Plant Systematics and Evolution*, 282(3), 169–199.
- Chen, M.-M., Zhang, M., Liang, Z.-S., & He, Q.-L. (2022). Characterization and Comparative Analysis of Chloroplast Genomes in Five Uncaria Species Endemic to China. *International Journal of Molecular Sciences*, 23(19), 11617. <https://doi.org/10.3390/ijms231911617>
- Choudhuri, S. (2014). Phylogenetic Analysis. In *Bioinformatics for Beginners* (pp. 209–218). Elsevier. <https://doi.org/10.1016/B978-0-12-410471-6.00009-8>
- Dai, J., Liu, Q., Xu, X., Tan, Z., Lin, Y., Gao, X., & Zhu, S. (2023). Comparative and Phylogenetic Analysis of The Complete Chloroplast Genomes of Uncaria (Rubiaceae) Species. *Front. Plant Sci*, 14, 1271689. <https://doi.org/10.3389/fpls.2023.1271689>
- Dharmayanti, I. (2011). Filogentika Molekuler: Metode Taksonomi Organisme Berdasarkan Sejarah Evolusi. *Wartazoa*, 21(1), 1–10.
- Ding, G., Zhang, D., Yu, Y., Zhao, L., & Zhang, B. (2012). Phylogenetic Relationship Among Related Genera of Plumbaginaceae and Preliminary Genetic Diversity of Limonium Sinense in China. *Gene*, 506(2), 400–403. <https://doi.org/10.1016/j.gene.2012.06.062>
- Doyle, J., & Doyle, J. (1987). A Rapid DNA Isolation Procedure for Small Quantities of Fresh Leaf Tissue. *Phytochem. Bull*, 19, 11–15.

- Ellestad, P., Farrera, M. A. P., Forest, F., & Buerki, S. (2022). Uncovering Haplotype Diversity in Cultivated Mexican Vanilla Species. *American Journal of Botany*, 109(7), 1120–1138. <https://doi.org/10.1002/ajb2.16024>
- Fitmawati, & Hartana, A. (2010). Phylogenetic Study of *Mangifera laurina* and its Related Species Using cpDNA trnL-F Spacer Markers. *HAYATI Journal of Biosciences*, 17(1), 9–14. <https://doi.org/10.4308/hjb.17.1.9>
- Ghada, B., Olfa, S., Khaled, C., Messaoud, M., Mohamed, M., Mokhtar, T., & Amel, S.-H. (2009). Sequence Analysis of The Internal Transcribed Spacers (ITSs) Region of The Nuclear Ribosomal DNA (NrDNA) in Fig Cultivars (*Ficus Carica* L.). *Scientia Horticulturae*, 120(1), 34–40. <https://doi.org/10.1016/j.scienta.2008.09.013>
- Hidayat, T., Abdullah, F. I., Kuppusamy, C., Samad, A. A., & Wagiran, A. (2012). Molecular Identification of Malaysian Pineapple Cultivar based on Internal Transcribed Spacer Region. *APCBEE Procedia*, 4, 146–151. <https://doi.org/10.1016/j.apcbee.2012.11.025>
- Hidayat, T., Kusumawaty, D., & Kusdianti, K. (2008). Analisis Filogenetik Molekuler pada *Phyllanthus niruri* L. (Euphorbiaceae) Menggunakan Urutan Basa DNA Daerah Internal Transcribed Spacer (ITS). *Jurnal Matematika dan Sains*, 13(1), 16–21.
- Hidayat, T., & Pancoro, A. (2008). Kajian Filogenetika Molekuler dan Peranannya dalam Menyediakan Informasi Dasar untuk Meningkatkan Kualitas Sumber Genetik Anggrek. *Journal Agro Biogen*, 4(1), 35–40.
- Hillis, D., Moritz, C., & Mable, B. (1996). *Molecular Systematic*. 2nd Ed. (2nd ed.). Sinauer Associates.
- Holt, S. D., Horova, L., Bures, P., Janecek, J., & Cernoch, V. (2005). The trnL-F Plastid DNA Characters of Three *Poa Pratensis* (Kentucky bluegrass) Varieties. *Plant, Soil and Environment*, 51(2), 94–99. <https://doi.org/10.17221/3561-PSE>
- Hu, G., Wu, Y., Guo, C., Lu, D., Dong, N., Chen, B., Qiao, Y., Zhang, Y., & Pan, Q. (2022). Haplotype Analysis of Chloroplast Genomes for Jujube Breeding. *Frontiers in Plant Science*, 13, 841767. <https://doi.org/10.3389/fpls.2022.841767>
- Huda, M., Syamsuwardi, Nurainas, Murni, P., & Maulidah, R. (2019). Genetic divergence landrace of langsung (*Lansium parasiticum*) from Siberut Island based on ITS and MatK markers. *Indian Journal of Agricultural Research*, 53(3), 338–342. <https://doi.org/10.18805/A-398>
- Ingkiriwang, M., Repi, R., & Nanlohy, F. (2017). Analisis Filogeni Molekuler Tanaman Pala (*Myristica* sp.) Dari Tahuna Menggunakan Gen rbcL DNA Kloroplas. *Jurnal Sains, Matematika Dan Edukasi*, 5, 137–144.
- Kress, W. J., Erickson, D. L., Jones, F. A., Swenson, N. G., Perez, R., Sanjur, O., & Bermingham, E. (2009). Plant DNA Barcodes and A Community

Phylogeny of a Tropical Forest Dynamics Plot in Panama. *Proceedings of the National Academy of Sciences*, 106(44), 18621–18626. <https://doi.org/10.1073/pnas.0909820106>

- Kristina, N., Lestari, J., & Fauza, H. (2016, September 1). *Keragaman Morfologi dan Kadar Katekin Tanaman Gambir Berdaun Merah yang Tersebar pada Berbagai Ketinggian Tempat di Sumatera Barat*. Seminar Nasional Masyarakat Biodiversitas Indonesia. <https://doi.org/10.13057/psnmbi/m020109>
- Lee, S.-C., Wang, C.-H., Yen, C.-E., & Chang, C. (2017). DNA Barcode and Identification of The Varieties and Provenances of Taiwan's Domestic and Imported Made Teas Using Ribosomal Internal Transcribed Spacer 2 Sequences. *Journal of Food and Drug Analysis*, 25(2), 260–274. <https://doi.org/10.1016/j.jfda.2016.06.008>
- Lestari, D. A., Azrianingsih, R., & Hendrian, H. (2018). Filogenetik Jenis-jenis Annonaceae dari Jawa Timur Koleksi Kebun Raya Purwodadi Berdasarkan Coding dan Non-coding sekuen DNA. *Journal of Tropical Biodiversity and Biotechnology*, 3(1), 1–7. <https://doi.org/10.22146/jtbb.28308>
- Letsiou, S., Madesis, P., Vasdekis, E., Montemurro, C., Grigoriou, M. E., Skavdis, G., Moussis, V., Koutelidakis, A. E., & Tzakos, A. G. (2024). DNA Barcoding as a Plant Identification Method. *Applied Sciences*, 14(4), 1415. <https://doi.org/10.3390/app14041415>
- Li, W. (1997). *Molecular Evolution*. Sinauer, Sunderland.
- Liu, G.-Q., Lian, L., & Wang, W. (2022). The Molecular Phylogeny of Land Plants: Progress and Future Prospects. *Diversity*, 14(10), 782. <https://doi.org/10.3390/d14100782>
- Lopez, A., & Bonasora, M. G. (2017). Phylogeography, Genetic Diversity and Population Structure in a Patagonian Endemic Plant. *AoB Plants*, 9(3). <https://doi.org/10.1093/aobpla/plx017>
- Mildawati, Sobir, Sulistijorini, & Chikmawati, T. (2023). Phylogeny of Davallia (Davalliaceae) from Sumatra and Mentawai Islands, Indonesia: Evidence from trnL-F Intergenic Spacer. *Biodiversitas Journal of Biological Diversity*, 24(8), 4589–4596. <https://doi.org/10.13057/biodiv/d240841>
- Minter, M., Nielsen, E. S., Blyth, C., Bertola, L. D., Kantar, M. B., Morales, H. E., Orland, C., Segelbacher, G., & Leigh, D. M. (2021). What Is Genetic Diversity and Why Does it Matter? *Frontiers for Young Minds*, 9, 656168. <https://doi.org/10.3389/frym.2021.656168>
- Mulyatni, A. S., Priyatmojo, A., & Purwantara, A. (2011). Sekuen Internal Transcribed Spacer (ITS) DNA Ribosomal *Oncobasidium theobromae* dan Jamur Sekerabat Pembanding. *Menara Perkebunan*, 79(1), 1–5. <https://doi.org/10.22302/iribb.jur.mp.v79i1.75>

- Munggari, I. P., Kurnia, D., Deawati, Y., & Julaeha, E. (2022). Current Research of Phytochemical, Medicinal and Non-Medicinal Uses of *Uncaria gambir* Roxb.: A Review. *Molecules*, 27(19), 6551. <https://doi.org/10.3390/molecules27196551>
- Mursyidin, D. H., Ahyar, G. M. Z., Saputra, A. W., & Hidayat, A. (2021). Genetic Diversity and Relationships of *Phalaenopsis* Based on the *rbcL* and *trnL-F* Markers: In Silico Approach. *Biosaintifika: Journal of Biology & Biology Education*, 13(2), 212–221. <https://doi.org/10.15294/biosaintifika.v13i2.29904>
- Musdja, M. Y., Rahman, H. A., & Hasan, D. (2018). Antioxidant Activity of Catechins Isolate of *Uncaria gambier* Roxb in Male Rats. *LIFE: International Journal of Health and Life-Sciences*, 4(2), 34–46. <https://doi.org/10.20319/ijhls.2018.42.3446>
- Nasrul, W., Purnawati, Y., Reza, M., Suwita, L., & Santo, A. (2023). Analisis Kelayakan Usaha Tani Gambir di Nagari Lubuak Alai Kecamatan Kapur IX Kabupaten Lima Puluh Kota. *Menara Ilmu*, 17(1), 121–132.
- Nei, M. (1987). *Molecular Evolutionary Genetics*. Columbia University Press.
- Ng, A. E., Sandoval, E., & Murphy, T. M. (2016). Identification and Individualization of *Lophophora* using DNA Analysis of the *trnL/trnF* Region and *rbcL* Gene. *Journal of Forensic Sciences*, 61, 226–229. <https://doi.org/10.1111/1556-4029.12936>
- Nuratika, E., Aseny, N., Syamsuardi, Nurainas, Fitmawati, & Friardi. (2020). Clarification of Sumatran Mulberry (*Morus macroura* var. *Macroura*, Moraceae) from West Sumatra, Indonesia using Nucleus Ribosomal ITS (Internal Transcribed Spacer) Gene. *Indian J. Agric. Res*, 54(5), 635–640. <https://doi.org/10.18805/IJARE.A-508>
- Ohied, B. M., & Al-Badran, A. I. (2020). Mitochondrial DNA (hypervariable region I) diversity in Basrah population – Iraq. *Genomics*, 112(5), 3560–3564. <https://doi.org/10.1016/j.ygeno.2020.04.004>
- Pangestika, Y., Budiharjo, A., & Pancasakti, H. (2015). Analisis Filogenetik *Curcuma zedoaria* (Temu Putih) Berdasarkan Gen Internal Transcribed Spacer (ITS). *Jurnal Biologi*, 4(4), 8–13.
- Rauf, A., Rahmawaty, & Siregar, A. Z. (2015). The Condition of *Uncaria gambir* Roxb. As One of Important Medicinal Plants in North Sumatra Indonesia. *Procedia Chem*, 14, 3–10. <https://doi.org/10.1016/j.proche.2015.03.002>
- Resida, E., Chikmawati, T., Ariyanti, N., & Fitmawati. (2023). *Mangifera kemanga* Blume (Anacardiaceae) Taxonomic Assessment for Genetic Diversity Based on Molecular Substantiation. *SABRAO Journal of Breeding and Genetics*, 55(1), 175–186. <https://doi.org/10.54910/sabrado2023.55.1.17>
- Romdhane, M., Riahi, L., Selmi, A., Jardak, R., Bouajila, A., Ghorbel, A., & Zoghalmi, N. (2017). Low Genetic Differentiation and Evidence of Gene

- Flow among Barley Landrace Populations in Tunisia. *Crop Science*, 57, 1585–1593. <https://doi.org/10.2135/cropsci2016.05.0298>
- Rosidiani, E., Arumingtyas, E., & Azrianingsih, R. (2013). Analisis Variasi Genetik *Amorphophallus muelleri* Blume Dari Berbagai Populasi Di Jawa Timur Berdasarkan Sekuen Intron trnL. *Floribunda*, 4(6), 129–137.
- Roslim, D. I., & Herman, H. (2017). Application of rps16 Intron and trnL-trnF Intergenic Spacer Sequences to Identify Rengas clone Riau. *Biosaintifika: Journal of Biology & Biology Education*, 9(2), 209–216. <https://doi.org/10.15294/biosaintifika.v9i2.9108>
- Rova, J. H. E., Delprete, P. G., Andersson, L., & Albert, V. A. (2002). A trnL-F cpDNA Sequence Study of The Condamineae-Rondeletieae-Sipaneeae Complex With Implications on The Phylogeny of The Rubiaceae. *American Journal of Botany*, 89(1), 145–159. <https://doi.org/10.3732/ajb.89.1.145>
- Saitou, N., & Nei, M. (1987). The Neighbor-Joining Method: A New Method for Reconstructing Phylogenetic Trees. *Molecular Biology and Evolution*, 4, 406–425. <https://doi.org/10.1093/oxfordjournals.molbev.a040454>
- Sakka, H., Baraket, G., Dakhlaoui Dkhil, S., Zehdi Azzouzi, S., & Salhi-Hannachi, A. (2013). Chloroplast DNA Analysis in Tunisian Date-Palm Cultivars (*Phoenix Dactylifera* L.): Sequence Variations and Molecular Evolution of trnL (UAA) Intron and trnL (UAA) trnF (GAA) Intergenic Spacer. *Scientia Horticulturae*, 164, 256–269. <https://doi.org/10.1016/j.scienta.2013.09.038>
- Small, R. L., Lickey, E. B., Shaw, J., & Hauk, W. D. (2005). Amplification of Noncoding Chloroplast DNA for Phylogenetic Studies in Lycophytes and Monilophytes with A Comparative Example of Relative Phylogenetic Utility from Ophioglossaceae. *Molecular Phylogenetics and Evolution*, 36(3), 509–522. <https://doi.org/10.1016/j.ympev.2005.04.018>
- Smarda, P., Bures, P., Horova, L., Leitch, I. J., Mucina, L., Pacini, E., Tichy, L., Grulich, V., & Rotreklova, O. (2014). Ecological and Evolutionary Significance of Genomic GC Content Diversity in Monocots. *Proceedings of the National Academy of Sciences*, 111(39). <https://doi.org/10.1073/pnas.1321152111>
- Stuessy, T. F., Bloch, C., Villasenor, J. L., Rebernig, C. A., & Weiss-Schneeweiss, H. (2011). Phylogenetic Analyses of DNA Sequences with Chromosomal and Morphological Data Confirm and Refine Sectional and Series classification within *Melampodium* (Asteraceae, Millerieae). *Taxon*, 60(2), 436–449. <https://doi.org/10.1002/tax.602013>
- Syamsuardi, S., Chairul, C., & Murni, P. (2018). Analysis of Genetic Impurity of An Original Cultivar Duku (*Lansium parasiticum* (Osbeck.) K.C. Sahni & Bennet.), from Jambi, Indonesia Using ITS and MatK Gene. *IJEAB*, 3(2), 441–446. <https://doi.org/10.22161/ijeab/3.2.16>

- Tabatabaee, Y., Zhang, C., Warnow, T., & Mirarab, S. (2023). Phylogenomic branch length estimation using quartets. *Bioinformatics*, 39, i185–i193. <https://doi.org/10.1093/bioinformatics/btad221>
- Taberlet, P., Gielly, L., Pautou, G., & Bouvet, J. (1991). Universal Primers for Amplification of Three Non-Coding Regions of Chloroplast DNA. *Plant Molecular Biology*, 17(5), 1105–1109. <https://doi.org/10.1007/BF00037152>
- Tang, Y., Wu, Y., Huang, R., Chao, N., Liu, Y., Xu, P., Li, K., Cai, D., & Luo, Y. (2016). Molecular identification of *Uncaria* (Gouteng) through DNA barcoding. *Chinese Medicine*, 11(3). <https://doi.org/10.1186/s13020-015-0072-7>
- Techen, N., Parveen, I., Pan, Z., & Khan, I. A. (2014). DNA Barcoding of Medicinal Plant Material for Identification. *Current Opinion in Biotechnology*, 25, 103–110. <https://doi.org/10.1016/j.copbio.2013.09.010>
- Tripathi, A. M., Tyagi, A., Kumar, A., Singh, A., Singh, S., Chaudhary, L. B., & Roy, S. (2013). The Internal Transcribed Spacer (ITS) Region and trnH-psbA Are Suitable Candidate Loci for DNA Barcoding of Tropical Tree Species of India. *PLoS ONE*, 8(2). <https://doi.org/10.1371/journal.pone.0057934>
- Ulukapi, K., & Nasircilar, G. A. (2019). Induced Mutation: Creating Genetic Diversity in Plants. In *Genetic Diversity in Plant Species* (pp. 41–55). <https://doi.org/10.5772/intechopen.81296>
- Wardi, E. S., Jamsari, J., Sartika, D., & Ningsih, A. R. (2020). Barkod DNA Pada Tanaman Gambir (*Uncaria gambir* (Hunter) Roxb.) Berdasarkan Gen MatK dan rbcL. *As-Syifaa Jurnal Farmasi*, 12(1), 22–28.
- Wardi, E. S., Syukur, S., Chaidir, Z., Jamsari, J., & Nova, B. (2022). DNA Barcoding for the Discrimination of *Uncaria gambir* and Its Closely Related Species Using Internal Transcribed Spacer Genes. *F1000Res*, 11, 106. <https://doi.org/10.12688/f1000research.74254.1>
- Wardi, E. S., Syukur, S., Chaidir, Z., Jamsari, J., Verawati, & Mukti, S. K. (2021). Molecular Identification of *Uncaria gambir* [Hunter] Roxb. Through DNA Barcoding. *IOP Conference Series: Earth and Environmental Science*, 741(1), 012056. <https://doi.org/10.1088/1755-1315/741/1/012056>
- White, T. J., Bruns, T., Lee, S., & Taylor, J. (1990). Amplification and Direct Sequencing of Fungal Ribosomal RNA Genes for Phylogenetics. In *PCR Protocols* (pp. 315–322). CA: Academic Press. <https://doi.org/10.1016/B978-0-12-372180-8.50042-1>
- Yonemori, K., Honsho, C., Kanzaki, S., Eiadthong, W., & Sugiura, A. (2002). Phylogenetic Relationships of Mangifera Species Revealed by ITS Sequences of Nuclear Ribosomal DNA and A Possibility of Their Hybrid Origin. *Plant Systematics and Evolution*, 231, 59–75. <https://doi.org/10.1007/s006060200011>

- Yurtseva, O., Kuznetsova, O., & Mavrodiev, E. (2016). A Broadly Sampled 3-Loci Plastid Phylogeny of *Atraphaxis* (Polygoneae, Polygonoideae, Polygonaceae) Reveals New Taxa: I. *Atraphaxis kamelinii* Spec. Nov. From Mongolia. *Journal Phytotaxa*, 268(1), 1–24.
- Zhu, S., Li, Q., Chen, S., Wang, Y., Zhou, L., Zeng, C., & Dong, J. (2018). Phylogenetic Analysis of *Uncaria* Species Based on Internal Transcribed Spacer (ITS) Region and ITS2 Secondary Structure. *Pharmaceutical Biology*, 56(1), 548–558. <https://doi.org/10.1080/13880209.2018.1499780>
- Zohary, D., Hopf, M., & Weiss, E. (2012). *Domestication of plants in the Old World: The origin and spread of domesticated plants in Southwest Asia, Europe, and the Mediterranean Basin* (Vol. 50). Oxford University Press. <http://choicereviews.org/review/10.5860/CHOICE.50-4995>
- Zulaspita, W., Syafira, F., Nurainas, & Syamsuardi. (2023). Phylogenetic Analysis of Sumatran *Gecharis* (Zingiberaceae) Based on ITS Sequences Data. *IOP Conference Series: Earth and Environmental Science*, 1160(1), 012076. <https://doi.org/10.1088/1755-1315/1160/1/012076>

