

DAFTAR PUSTAKA

- Achigan-Dako, E. G., H. Degbey, L. Hale, F. R. Blattner. 2021. Georeferenced phylogenetic analysis of a global collection of wild and cultivated *Citrullus* species. *Ecology and Evolution*, Vol. 11(4): 1918-1936. <https://doi.org/10.1002/ece3.7189>
- AGRF, Australian Genome Research Facility. 2014. *Sanger Sequencing: Troubleshooting Guide* (GNGFM00346) v1.1. Link: https://www.ucdenver.edu/docs/librariesprovider48/facility-cores/sanger-sequencing-troubleshooting-guide-1.pdf?sfvrsn=8da250b9_4
- Akashi Y, Fukuda N, Wako T, Masuda M, Kato K. 2002. Genetic variation and phylogenetic relationships in East and South Asian melons, *Cucumis melo* L., based on the analysis of five isozymes. *Euphytica*, 125(3):385-96 <https://doi.org/10.1023/A:1016086206423>
- Álvarez I, Wendel JF. 2003. Ribosomal ITS sequences and plant phylogenetic inference. *Molecular Phylogenetics and Evolution* 29: 417–434.
- Alfiyani, A dan B.S Daryono. 2018. Perakitan dan Karakterisasi Molekular Melon Hibrida (*Cucumis melo* L. 'Melona'). *Skripsi*. Universitas Gadjah Mada. Yogyakarta.
- Androsiuk, P., Jastrzębski, J.P., Paukszto, Ł. et al. 2020. Evolutionary dynamics of the chloroplast genome sequences of six *Colobanthus* species. *Sci Rep* **10**, 11522. <https://doi.org/10.1038/s41598-020-68563-5>
- Anggraini, N. B., A. Sholihah, E. N. Khasna., R. W. Retnaningtyas, Suharti, D. Listyorini. 2020. Genetic relationship between local rice varieties based on MatK and rbcL genes. *AIP Conf. Proc.* 2260, 020020. <https://doi.org/10.1063/5.0015756>
- Aristya, G.R., B.S Daryono, Y. Rachmawati. 2014. Karakter Gen *CmBG1* Melon (*Cucumis melo*) pada Pengaruh Cekaman Tanah Karst. *Sains & Matematika*. Vol 3 No.1.
- Bandelt, H. J., Forster, P., Röhl, A. 1999. Median-joining networks for inferring intraspecific phylogenies. *Mol Biol Evol* 16(1): 37-48.
- Basith, A. 2015. Peluang Gen *rbcL* sebagai DNA Barcode Berbasis DNA Kloroplas untuk Mengungkap Keanekaragaman Genetik Pada Beras Hitam (*Oryza sativa* L.) Lokal Indonesia. *Conference: Seminar Nasional XII Pendidikan Biologi*.
- Batnihi, M. A., H. Bourguiba, N. T. Farah, L. Krichen. 2019. Molecular diversity and phylogeny of Tunisian *Prunus armeniaca* L. by evaluating three candidate barcodes of the chloroplast genome. *Scientia Horticulturae*, Vol. 245, pp. 99-106. <https://doi.org/10.1016/j.scienta.2018.09.071>
- Boehme, P. & J. D. Wells. 2013. Methods for Sequencing the Mitochondrial DNA A+T-Rich Region of *Cochliomyia macellaria* (Diptera: Calliphoridae) from North America. *Canadian Society of Forensic Science Journal*. Vol. 40, pp. 165-172. <https://doi.org/10.1080/00085030.2007.10757157>
- Boster antibody and ELISA experts. PCR Principle. <https://www.bosterbio.com/protocol-and-troubleshooting/pcr-principle> diakses pada 6 Februari 2023.
- Brinkman, F. and D. Leipe. 2001. *Phylogenetic analysis*. In: Bioinformatics: A Practical Guide to The Analysis of Gene and Protein. Baxevanis, A. D. and B.F.F. Queller (Eds.). John Wiley & Sons. Pp. 323-358

- Burger, Y.; Sa'ar, U.; Paris, H.S.; Lewinsohn, E.; Katzir, N.; Tadmor, Y.; Schaffer, A. 2006. Genetic variability for valuable fruit quality traits in *Cucumis melo*. *Isr. J. Plant Sci*, 54: 233–242
- Cao, H., Mingxi Gong, Tingquan Wu, Changyuan Zhang, Ali Anwar, Liangliang Shi, Shiwei Song. 2024. Identification of the G2-like transcriptional factor gene family reveals their critical roles in controlling chlorophyll accumulation of melon fruit. *Scientia Horticulturae*, 328. <https://doi.org/10.1016/j.scienta.2024.112925>
- Cavalli and L.L. Sforza. 1997. Genes, Peoples and Language. *Proc. Natl. Acad. Sci USA*. 94(15): 7719-7724
- Chang, YJ., Cao, YF., Zhang, JM. *et al.* 2017. Study on chloroplast DNA diversity of cultivated and wild pears (*Pyrus* L.) in Northern China. *Tree Genetics & Genomes* **13**, 44. <https://doi.org/10.1007/s11295-017-1126-z>
- Chen, S.L., Yao, H., Han, J.P., Liu, C., Song, J.Y., Shi, L.C., Zhu, Y.G., Ma, X.Y., Gao, T., Pang, X.H., Luo, K., Li, Y., Li, X.W., Jia, X.C., Lin, Y.L., Leon, C., 2010. Validation of the ITS2 region as a novel DNA barcode for identifying medicinal plant species. *PLoS One* 5, e8613.
- Cheng, H., Wei-Ping K., Min-Min Z., Dong H. 2020. The complete chloroplast genome of *Cucumis melo* L. 'Shengkaihua' (*Cucurbitaceae*) and its phylogenetic implication. *Mitochondrial DNA Part B*, 5:2, 1253-1254, DOI: [10.1080/23802359.2020.1731364](https://doi.org/10.1080/23802359.2020.1731364)
- Chesnokov, Yu V., N. V. Pohepnnya, A. Börner, U. Lohwasser, E. A. Goncharova, and V. A. Dragavtse. 2008. Ecological-Genetic Organization of Plant Quatitative Traits and Mapping of the Loci Determining Agronomically Important Traits in Soft Wheat. *Doklady Biochemistry and Biophysics*, Vol. 418, pp. 36-39. DOI: [10.1134/S1607672908010092](https://doi.org/10.1134/S1607672908010092)
- Chiang, T.Y., Schaal, B.A & Peng, C. 1998. Universal primers for amplification and sequencing noncoding spacer between the *atpB* and *rbcL* genes of chloroplast DNA. *Botanical Bulletin of Academia Sinica*, (39), 245-250.
- Chikh-Rouhou H, Gómez-Guillamón ML, González V. Sta-Baba R, Garcés-Claver A. 2021. *Cucumis melo* L. germplasm in Tunisia: Unexploited sources of resistance to FusariumWilt. *Horticulturae*, 7(8):208. DOI: [10.3390/horticulturae7080208](https://doi.org/10.3390/horticulturae7080208)
- Choudhuri, S. 2014. Bioinformatics for Beginners: Genes, Genomes, Molecular Evolution, Databases and Analytical Tools. *Bioinformatics for Beginners: Genes, Genomes, Molecular Evolution, Databases and Analytical Tools*, 1–225.
- Cortese, L.M., Honig, J., Miller, C., and Bonos, S.A. 2010. Genetic Diversity of Twelve Switchgrass Populations Using Molecular and Morphological Markers. *Bioenerg. Res.* Springer Science+Business Media. DOI [10.1007/s12155-010-9078-2](https://doi.org/10.1007/s12155-010-9078-2).
- Cui, H., Ding, Z., Zhu, Q. *et al.* 2021. Population structure, genetic diversity and fruit-related traits of wild and cultivated melons based on chloroplast genome. *Genet Resour Crop Evol* **68**, 1011–1021. <https://doi.org/10.1007/s10722-020-01041-z>
- Cui, H., Ding, Z., Zhu, Z., Liu, S., Wang, X., Luan, F., Gao, P. 2022. Identification of major-effect QTL CmFpl3.1 controlling fruit pedicel length in melon (*Cucumis melo*). *Scientia Horticulturae*, 110717.
- Dai, Xiao-Jun, Ou Li-Jun, Li Wen-Jia, Liang Man-Zhong, and Chen Liang-Bi. 2008. Analysis of rDNA Intergenic Spacer (IGS) Sequences in *Oryza sativa* L. and Their Phylogenetic Implications. *Acta Agronomica Sinica*, 34(9):1569-1573. DOI: [10.3724/SP.J.1006.2008.01569](https://doi.org/10.3724/SP.J.1006.2008.01569).
- Daryono, B.S. 2015. Application of Molecular Biology for Identification of Virus Resistance Gene in Melon. *Indonesian Journal of Biotechnology*. 20(1): 19-33.

- Daryono, B.S. 2016. Produksi dan Pemasaran Buah serta Benih Gama Melon: Dari Inovasi Laboratorium ke Dunia Industri dan Pemberdayaan Masyarakat. Prosiding Seminar Nasional Sains dan Entrepreneurship III Tahun 2016. *Entrepreneurship*: 15-38. Semarang.
- Daryono, B.S., A.R. Ibrohim, S.D. Maryanto. 2015. Aplikasi Teknologi Budidaya Melon (*Cucumis melo* L.) Kultivar Gama Melon Basket di Lahan Karst Pantai Porok Kabupaten Gunungkidul D.I. Yogyakarta. *Biogenesis: Jurnal Ilmiah Biologi*. Vol. 3(1): 39-46.
- Daryono, B.S., A.S. Subiastuti, A. Fatmadanny, D. Sartika. 2019. Phenotypic and genetic stability of new Indonesian melon cultivar (*Cucumis melo* L. 'Melonia') based on ISSR markers. *Biodiversitas*, Vol. 20 (4): 1069-1075. DOI: [10.13057/biodiv/d200419](https://doi.org/10.13057/biodiv/d200419)
- Daryono, B.S., E. Setyani, A. Alfiani and P.R. Rivaldi. 2017. Fruit characters of *Cucumis melo* L: 'Tacapa Green Black', 'Melona' and 'Meloni'. Proceeding of the 2nd International Conference on Tropical Agriculture. *Life Science*, 1: 15-20. [10.29037/digitalpress.21241](https://doi.org/10.29037/digitalpress.21241)
- Daryono, B.S., F. Husnun, D. Sartika. 2020. Genetic variation analysis of melon (*Cucumis melo* L. 'Tacapa Gold') using inter-simple sequence repeat. AIP Conference Proceedings, 2260. <https://doi.org/10.1063/5.0017611>
- Daryono, B.S. dan Maryanto, S.D. 2017. *Keanekaragaman dan Potensi Sumber Daya Genetik Melon*. Yogyakarta: Gadjah Mada University Press.
- de Almaeida, Rafael & Martin Cheek, Marco de Oliveira Pellegrini, I. Lucia de Moraes. 2023. Barking up the wrong tree: the importance of morphology in plant molecular phylogenetic studies. DOI:[10.1101/2023.01.30.526223](https://doi.org/10.1101/2023.01.30.526223)
- DeSalle R. 2006. Species discovery versus species identification in DNA barcoding efforts: response to Rubinoff. *Conservation Biology* .20 (5):1545–1547
- Dharmayanti, N.LP. Indi. 2011. *Filogenetika Molekuler: Metode Taksonomi Organisme Berdasarkan Sejarah Evolusi*. Makalah. Balai Besar Penelitian Veteriner. Bogor.
- Direktorat Jenderal Hortikultura Kementerian Pertanian. 2023. *Si Melon dari Serang*. <https://hortikultura.pertanian.go.id/si-melon-manis-dari-serang/> Diakses: 29 Desember 2023.
- Dong, W., Jing Liu, Jing Yu, Ling Wang, Shiliang Zhou. 2012. Highly Variable Chloroplast Marker for Evaluating Plant Phylogeny at Low Taxonomic Levels and for DNA Barcoding. *PLOS ONE*. <https://doi.org/10.1371/journal.pone.0035071>
- Dong W, Xu C, Wu P, Cheng T, Yu J, Zhou S, Hong D-Y. 2018. Resolving the systematic positions of enigmatic taxa: manipulating the chloroplast genome data of Saxifragales. *Mol Phylogenet Evol*, 126:321–30.
- Duong TT, Dung TP, Tanaka K, Nhi PTP, Shigita G, Imoh ON, Nishida H, Kato K. 2021. Distribution of two groups of melon landraces and inter-group hybridization enhanced genetic diversity in Vietnam. *Breeding Sci*, 574: 564-574. DOI: [10.1270/jsbbs.20090](https://doi.org/10.1270/jsbbs.20090)
- Dwivedi, M. D., S. Barfield, A. K. Pandey, H. Schaefer. 2018. Phylogeny of Zehneria (Cucurbitaceae) with special focus on Asia. *Taxon*, Vol. 67(1): 55-65. <https://doi.org/10.12705/671.4>
- Enzellina, G., D. Suhaedi. 2022. Penggunaan Metode Principal Component Analysis dalam Menentukan Faktor Dominan. *Jurnal Riset Matematika (JRM)*. Unisba Press. Vol. 2 (2): 101-110. DOI : <https://doi.org/10.29313/jrm.v2i2.1192>
- Fatchiyah, Arumingtyas, E.L, Widyarti, S., dan Rahayu, S. (2011). *Biologi Molekular: Prinsip Dasar Analisis*. Jakarta: Penerbit Erlangga.
- Fatmawati, Annis & B.S. Daryono. 2016. Detection of Powdery Mildew (*Podosphaera xanthii* (Castagne) U. Braun & N. Shiskoff) Resistance Gene in Melon (*Cucumis melo* L.) Cultivar

- Tacapa Green Black. *Bioengineering and Bioscience* 4(4): 51-55. DOI: [10.13189/bb.2016.040401](https://doi.org/10.13189/bb.2016.040401)
- Fazekas AJ, Kesanakurti PR, Burgess KS, Percy DM, Graham SW, et al. 2009. Are plant species inherently harder to discriminate than animal species using DNA barcoding markers? *Molecular Ecology Resources* 9: 130–139.
- Feder, A.; Burger, J.; Gao, S.; Lewinsohn, E.; Katzir, N.; Schaffer, A.A.; Meir, A.; Davidovich-Rikanati, R.; Portnoy, V.; Gal-On, A.; et al. 2015. A Kelch domain-containing F-Box coding gene negatively regulates flavonoid accumulation in muskmelon. *Plant Physiol*, 169: 1714–1726.
- Feng, S., Kaili Jiao, Yujia Zhu, Hongfen Wang, Mengying Jiang, and Huizhong Wang. 2018. Molecular identification of species of *Physalis* (Solanaceae) using a candidate DNA barcode: the chloroplast *psbA-trnH* intergenic region. *Genome*. 61(1): 15-20. <https://doi.org/10.1139/gen-2017-0115>
- Ghorbani, A., Y. Saeedi, H. J. de Boer. 2017. Unidentifiable by morphology: DNA barcoding of plant material in local markets in Iran. *PLoS ONE* 12(4): 1-15. DOI: <https://doi.org/10.1371/journal.pone.0175722>
- Gostel MR, Kress WJ. 2022. The Expanding Role of DNA Barcodes: Indispensable Tools for Ecology, Evolution, and Conservation. *Diversity*; 14(3):213. <https://doi.org/10.3390/d14030213>
- Govindaraghavan, S., Hennell, J.R., Sucher, N.J., 2012. From classical taxonomy to genome and metabolome: towards comprehensive quality standards for medicinal herb raw materials and extracts. *Fitoterapia* 83, 979–988.
- Govindaraj, M., M. Vetriventhan, and M. Srinivasan. 2015. Importance of Genetic Diversity Assessment in Crop Plants and Its Recent Advances: An Overview of Its Analytical Perspectives. *Genetic Research International*. Hindawi Publishing Corporation. <http://dx.doi.org/10.1155/2015/431487>.
- Griffiths, A.J.F., Miller J.H, Suzuki D.T. 2000. An Introduction to Genetic Analysis, 7th edition. New York: W.H. Freeman. Source Variation. <https://www.ncbi.nlm.nih.gov/books/NBK22012/>
- Gu, X.; Zhu, M.; Su, Y.; Wang, T. 2022. A Large Intergenic Spacer Leads to the Increase in Genome Size and Sequential Gene Movement around IR/SC Boundaries in the Chloroplast Genome of *Adiantum malesianum* (Pteridaceae). *Int. J. Mol. Sci*, 23, 15616. <https://doi.org/10.3390/ijms232415616>
- Guo, YY., JX. Yang, HK. Li, HS. Zhao. 2021. Chloroplast Genome of two species of *Cypripedium*: Expanded Genome Size and Proliferation of AT-Biased Repeat Sequences. *Front. Plant Sci*, Vol. 12. <https://doi.org/10.3389/fpls.2021.609729>
- Guo, Zhansheng, Leng Han, Zhenlin Liang and Xuguang Hou. 2019. Comparative analysis of the ribosomal DNA repeat unit (rDNA) of *Perna viridis* (Linnaeus, 1758) and *Perna canaliculus* (Gmelin, 1791). *Peer J*. DOI 10.7717/peerj.7644
- Group, C.P.W. 2009. A DNA barcode for land plants. *Proc. Natl Acad. Sci. USA* 106, 12794–12797.
- Gupta, Mohan and Sagar Aryal. 2022. *DNA Sequencing – Definition, Principle, Steps, Types, Uses*. The Biology Notes. <https://thebiologynotes.com/dna-sequencing-principle-steps-types-uses/>
- Hamilton MB. 1999. Four primer pairs for the amplification of chloroplast intergenic regions with intraspecific variations. *Mol Ecol* 8:513-525

- Hasbullah, U. H. A., S. Supriyadi, B. S. Daryono. 2021. Volatile compounds trigger the pleasant strong aroma of new cultivar Gama Melon Parfum during growth and maturation. *Advance in Food Science, Sustainable Agriculture and Agroindustrial Engineering (AFSSAAE)*, Vol. 4. No.1. DOI: <https://doi.org/10.21776/ub.afssaae.2021.004.01.5>
- Hauvermale, Amber L and Marwa N.M.E. Sanad. 2020. *Phenological Plasticity of Wild and Cultivated Plants*. IntechOpen. doi: 10.5772/intechopen.85070
- Hebert, P. D. N., Ratnasingham, S. & De, W. J. R. 2003. Barcoding animal life: Cytochrome c oxidase subunit 1 divergences among closely related species. *Proc. R. Soc. Lond. B Biol. Sci.* **270**, S96–S99.
- Herlina, Lina. 2021. Yield Components and Diversity of Qualitative Characters of Fifty Accessions of Inbred Maize Lines. *E3S Web of Conferences* **316**, 2021, 03009, IConARD. <https://doi.org/10.1051/e3sconf/202131603009>
- Hidzroh, Faridatul & B.S. Daryono. 2021. Keceragaman dan Kestabilan Karakter Tanaman Melon (*Cucumis melo* L. ‘Tacapa Gold’) Berdasarkan Karakter Fenotip dan *Inter-Simple Sequence Repeat*. *J. Biospecies*, Vol. 14 (2): 11-19.
- Hollingsworth PM, Forrest LL, Spouge JL, Hajibabaei M, Ratnasingham S, van der Bank M, et al. 2009. A DNA barcode for land plants. *Proc Natl Acad Sci USA*; 106:12794–7.
- Hollingsworth PM, Graham SW, Little DP. 2011. Choosing and Using a Plant DNA Barcode. *PLoS ONE* 6(5): e19254. <https://doi.org/10.1371/journal.pone.0019254>
- Hoveka, L.N., M. VD. Bank, J.S. Boatwright, B.S. Bezeng, K. Yessoufou. 2016. The noncoding trnH-psbA spacer, as an effective DNA barcode for aquatic freshwater plants, reveals prohibited invasive species in aquarium trade in South Africa. *South African Journal of Botany*, 102: 208-216. <http://dx.doi.org/10.1016/j.sajb.2015.06.014>
- Huda, I. N. 2009. Perakitan dan Pembandingan Karakter Fenotip Buah Melon (*Cucumis melo* L.) Kultivar Gama Melon Basket dengan Kultivar Melon Komersial. *Seminar*. Fakultas Biologi, Universitas Gadjah Mada. Yogyakarta.
- Huda, I. N., B. S. Daryono. 2013. Analisis variasi genetik melon (*Cucumis melo* L.) kultivar Gama Melon Basket dengan metode Random Amplified Polymorphic DNA. *Jurnal Ilmiah Biologi Biogenesis*, Vol. 1 No. 1. <https://doi.org/10.24252/bio/v1i1.446>
- Ilahy R, Tlili I, Rouhou HC, Siddiqui MW, Mishra PM, Kuchi VS, Homa F, Hdider C, Jebari H, Lenucci MS. 2020. Determining the main agronomic traits of snake melon (*Cucumis melo* var. *flexuosus* L.) fruits as affected by genotypic differences. *AdvHortSci* 34(1): 113-119. DOI: 10.13128/ahsc8254.
- Ishak, M.A & B.S. Daryono. 2018. Kestabilan karakter fenotip melon (*Cucumis melo* L. ‘Sun Lady’) hasil budidaya di dusun Jamusan, Prambanan, D.I. Yogyakarta. Paper Presentation. *Prosiding Seminar Nasional Pendidikan Biologi dan Saintek III*, Surakarta
- Ishak, M.A & B.S. Daryono. 2020. Detection of Powdery Mildew Resistance Gene in Melon Cultivar Meloni Based on SCAR Markers. *Journal of Biology & Biology Education. Biosaintifika* 12(1): 76-82. DOI: <http://dx.doi.org/10.15294/biosaintifika.v12i1.22198>
- Isola D, Bartoli F, Langone S, Ceschin S, Zucchini L, Caneva G. 2021. Plant DNA Barcode as a Tool for Root Identification in Hypogaea: The Case of the Etruscan Tombs of Tarquinia (Central Italy). *Plants*. 2021; 10(6):1138. <https://doi.org/10.3390/plants10061138>
- Izhaki, I., Tsahar, E., Paluy I., and Friedman, J. 2002. Within population variation and interrelationships between morphology, nutritional content, and secondary compounds of *Rhamnus alaternus* fruits. *New Phytologist*, 156: 217-223

- Jeffrey, C. 1980. A review of the Cucurbitaceae. *Botanical Journal Linnean Society* 81:233-247.
- Jiang S, Chen F, Qin P, Xie H, Peng G, Li Y, Guo X. 2022. The specific DNA barcodes based on chloroplast genes for species identification of *Theaceae* plants. *Physiol Mol Biol Plants*, 28(4):837-848. doi: 10.1007/s12298-022-01175-7.
- Joshi, Jyoti, R. K. Salar, P. Banerjee, Upasna S., M. S. Tania, R. K. Vijh. 2013. Genetic Variation and Phylogenetic Relationships of Indian Buffaloes of Uttar Pradesh. *Asian Australas. J. Anim. Sci*, Vol. 26(9): 1229-1236. <http://dx.doi.org/10.5713/ajas.2012.12669>
- Judd W.S., Campbell, C.S., Kellogg, E., and Stevens, P. 2008. Plant Systematics: A phylogenetic approach. *Taxon* 56(4), p.1316. DOI: 10.2307/25065934
- Karim, N.A., T. Derajavan, A. Ahmad. 2022. Principal Component Analysis for Phenotypic Characterization of Sweet Potato (*Ipomoea batatas* (L.) Lam.) Genotypes in Malaysia. *Trends In Sciences*; 19 (12): 4612. <https://doi.org/10.48048/tis.2022.4612>
- Kementerian Pertanian. 2017. Lampiran Surat Keputusan Menteri Pertanian Republik Indonesia Nomor: 039/Ktps/SR.120/D.2.7/4/2017, *Deskripsi Melon Varietas Meloni*. Jakarta.
- Kim, J. S., Kim, H. T., and Kim, J.-H. (2015). The largest plastid genome of monocots: a novel genome type containing AT residue repeats in the slipper orchid *Cypripedium japonicum*. *Plant Mol. Biol. Rep.* 33, 1210–1220. doi: 10.1007/s11105-014-0833-y
- Kim, Young-Kyu, Chong-wook Park, Ki-Joong Kim. 2009. Complete Chloroplast DNA Sequence from a Korean Endemic Genus, *Megaleranthus saniculifolia*, and Its Evolutionary Implication. *Molecules and Cells* 27(3): 365-81. DOI:10.1007/s10059-009-0047-6
- 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.
- Kong BL, Park HS, Lau TD, Lin Z, Yang TJ, Shaw PC. 2021. Comparative analysis and phylogenetic investigation of Hong Kong Ilex chloroplast genomes. *Sci Rep.* 4;11(1):5153. doi: 10.1038/s41598-021-84705-9.
- Korir, N.K, Han J, Shangguan L, Wang C, Kayesh E, Zhang Y, Fang J. 2012. Plant variety and cultivar identification: Advances and prospects. *Crit Rev Biotechnol* 33: 111-125.DOI: 10.3109/07388551.2012.675314
- Krastev, V., D. Dimova, D. Svetleva. 2014. Inheritance of Some Quantitative Traits in Common Bean Cross. *Turkish Journal of Agricultural and Natural Sciences*, pp. 761-769.
- Krawczyk, K., M. Nobis, A. Nowak, M. Szczecinska & J. Sawicki. 2017. Phylogenetic implication of nuclear rRNA IGS variation in *Stipa* L. (Poaceae). *Scientific Reports* 7: 11506 | DOI:10.1038/s41598-017-11804-x
- Kress, W.J., Wurdack, J.K., Zimmer A, A.E., Weight, A.L., Janzen H, H.D., 2005. Use of DNA barcodes to identify flowering plants. *Proc. Natl. Acad. Sci. USA* 102 (23), 8369–8374.
- Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. *Molecular Biology and Evolution*, 35(6): 1547-1549. doi: 10.1093/molbev/msy096.
- Kustanto, Heri. 2023. The phenotypic and genetic diversity test of several inbred lines on the 7th generation of melon (*Cucumis melo*). *Biodiversitas* 24(5): 2623-2629. DOI: 10.13057/biodiv/d240514

- Latifah, Y.W dan B.S Daryono. 2016. Kestabilan Karakter Fenotip dan Molekuler Melon (*Cucumis melo* L. 'Melona') Hasil Segregasi dan Seleksi Populasi. *Skripsi*. Universitas Gadjah Mada. Yogyakarta.
- Lemey, P., M. Salemi and A.M. Vandamme. 2009. *The Phylogenetic Handbook A Practical Approach to Phylogenetic Analysis and Hypothesis Testing*. Cambridge University Press.
- Li, Y., S. Shen, Lihong He, Pu Xu, Shan Lu. 2010. Sequence analysis of rDNA intergenic spacer (IGS) of *Porphyra haitanensis*. *J. Appl Phycol*, 22:187-193. DOI 10.1007/s10811-009-9441-x
- Li, H., Xiao, W., Tong, T. *et al.* 2021. The specific DNA barcodes based on chloroplast genes for species identification of *Orchidaceae* plants. *Sci Rep* **11**, 1424. <https://doi.org/10.1038/s41598-021-81087-w>
- Li, HT., Yang, JB., Li, DZ. *et al.* 2010. A molecular phylogenetic study of *Hemsleya* (Cucurbitaceae) based on ITS, *rpl16*, *trnH-psbA*, and *trnL* DNA sequences. *Plant Syst Evol* **285**, 23–32. <https://doi.org/10.1007/s00606-009-0252-y>
- Li J, Xie D-F, Guo X-L, Zheng Z-Y, He X-J, Zhou S-D. 2020. Comparative Analysis of the Complete Plastid Genome of Five *Bupleurum* Species and New Insights into DNA Barcoding and Phylogenetic Relationship. *Plants*, 9(4):543. <https://doi.org/10.3390/plants9040543>
- Li W, Liu Y, Yang Y, Xie X, Lu Y, Yang Z, Jin X, Dong W, Suo Z. 2018. Interspecific chloroplast genome sequence diversity and genomic resources in *Diospyros*. *BMC Plant Biol*, 18(1):210.
- Li, X.W., Yang, Y., Henry, R.J., Rossetto, M., Wang, Y.T., Chen, S.L., 2015. Plant DNA barcoding: from gene to genome. *Biol. Rev.* 90, 157–166.
- Liang X, Li Q, Cao L, Du X, Qiang J, Hou J, Li X, Zhu H, Yang S, Liu D, Zhu L, Yang L, Wang P, Hu J. 2023. Natural allelic variation in the EamA-like transporter, CmSN, is associated with fruit skin netting in melon. *Theor Appl Genet*, 136(9):192. doi: 10.1007/s00122-023-04443-6
- Lija, M, Beevy S. S. 2021. A review on the diversity of melon. *Plant Science Today*, 8(4):995-1003. <https://doi.org/10.14719/pst.1300>
- Lin, Ssu-Yu, Huang J-H, Wang Y-H. 2020. Morphological Diversity and Resistance to Powdery Mildew in Melon (*Cucumis melo* L.) Accessions. *Journal of Taiwan Agricultural Research*. Vol. 69(2): 169-183
- Linh NN, Hang PLB, Hue HTT, Ha NH, Hanh HH, Ton ND, Hien LTT. 2022. Species discrimination of novel chloroplast DNA barcodes and their application for identification of *Panax* (Aralioideae, Araliaceae). *PhytoKeys* 188: 1–18. <https://doi.org/10.3897/phytokeys.188.75937>
- Lipscomb, D. 1998. *Basics of Cladistic Analysis*. Student Guide Paper. Department of Biological Sciences. George Washington University, Washington D.C, USA. <https://www2.gwu.edu/~clade/faculty/lipscomb/Cladistics.pdf>
- Liu JIE, Möller M, Gao L-M, Zhang D-Q, Li D-Z. 2010. DNA barcoding for the discrimination of Eurasian yews (*Taxus* L., Taxaceae) and the discovery of cryptic species. *Molecular Ecology Resources* 11: 89–100.
- Maryanto, S.D. & B.S. Daryono. (2011). Perbandingan Karakter Fenotipe Buah Melon (*Cucumis melo* L.) Kultivar Melodi Gama-1, Gama Melon Basket dan Kultivar Komersial pada Uji Multilokasi dan Multimusim. *Skripsi*. Fakultas Biologi, Universitas Gadjah Mada. Yogyakarta.

- Maryanto, S.D., Ranis R.E., B.S Daryono. 2014. Stability phenotypic characters and the scent of gama melon perfume cultivar. *IPTEK J.Proc Ser* (1):523-5238
- Meyer, C. P. and G. Paulay. 2005. DNA Barcoding: Error Rates Based on Comprehensive Sampling. *PLoS Biol* 3(12): e422. <https://doi.org/10.1371/journal.pbio.0030422>
- Miller, J. S., Kamath, A., & Levin, R. A. 2009. Do Multiple Tortoises Equal a Hare? The Utility of Nine Noncoding Plastid Regions for Species-Level Phylogenetics in Tribe Lycieae (Solanaceae). *Systematic Botany*, 34(4), 796–804. <http://www.jstor.org/stable/40540510>
- Mishra P, Kumar A, Nagireddy A, Shukla AK, Sundaresan V. 2017. Evaluation of single and multilocus DNA barcodes towards species delineation in complex tree genus *Terminalia*. *PLoS ONE* 12(8): e0182836. <https://doi.org/10.1371/journal.pone.0182836>
- Morrissey, E., Mau, R., Schwartz, E. 2017. Bacterial carbon use plasticity, phylogenetic diversity and the priming of soil organic matter. *ISME J* 11: 1890–1899. <https://doi.org/10.1038/ismej.2017.43>
- Moura, M. D. C., L.S. Gonçalves, C.P. Sudré, R. Rodrigues, A. T. D. A. Júnior; T. N. S. Pereira. 2010. The Grower's algorithm on the estimate of genetic diversity in chili pepper germoplasm. *Horticultura Brasileira* 28: 155-161.
- Mu Z, Zhang Y, Zhang B, Cheng Y, Shang F, Wang H. 2023. Intraspecific Chloroplast Genome Variation and Domestication Origins of Major Cultivars of *Styphnolobium japonicum*. *Genes*, 14(6):1156. <https://doi.org/10.3390/genes14061156>
- Muslimah, R.N., Z. Millah, Susiyanti, A. Natawijaya. 2022. Keragaan dan Keragaman Karakter Vegetatif dan Generatif pada Empat Galur Elit Melon (*Cucumis melo* L.) Berumur Genjah. *Prosiding Seminar Nasional Peripi 2022*.
- Nazar, N. and Mahmood, T. 2011. Morphological and molecular characterization of selected *Artemisia* species from Rawalakot, Azad Jammu and Kashmir. *Acta Physiol Plant* 33: 625-633. DOI: 10.1007/s11738-010-0545-3.
- Nei, M. 1987. *Molecular evolutionary genetics*. New York: Colombia University Press. 512 p.
- Nei, M., & Li, W.-H. 1979. Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences*, 76(10), 5269–5273.
- Nei, M. & S. Kumar. 2000. *Molecular Evolution and Phylogenetics*. Oxford University Press, New York. p. 333.
- Newell, P. D., A. D. Fricker, C. A. Roco, P. Chandrangsu, S. M. Merkel. 2013. A Small-Group Activity Introducing the Use and Interpretation of BLAST. *J. Microbiol Biol Educ.*, 14(2): 238-243. doi: [10.1128/jmbe.v14i2.637](https://doi.org/10.1128/jmbe.v14i2.637)
- Nieto-Lugilde, Marta, Sean Robinson, Blanka Agüero, Aaron Duffy, Karn Imwattana, Kristian Hassel, Kjell Ivar Flatberg, Hans K. Stenøien, Anna V. Shkurko, Vladimir E. Fedosov, A. Jonathan Shaw. 2022. Morphological-molecular incongruence in *Sphagnum majus* ssp. *majus* and ssp. *Norvegicum*. *The Bryologist*, 125(2), 294-310
- Nonić, M., Šijačić-Nikolić, M. 2019. Genetic Diversity: Sources, Threats, and Conservation. In: Leal FW, Azul A, Brandli L, Özuyar P, Wall T. (eds). *Life on Land. Encyclopedia of the UN Sustainable Development Goals*. Springer, Cham. DOI: 10.1007/978-3-319-71065-5_53-1.
- Núñez-Palenius HG, Gomez-Lim M, Ochoa-Alejo N, Grumet R, Lester G, Cantliffe DJ. 2008. Melon fruits: genetic diversity, physiology, and biotechnology features. *Crit Rev Biotechnol* 28:13–55. <https://doi.org/10.1080/07388550801891111>

- Olsson S, Giovannelli G, Roig A, Spanu I, Vendramin GG, Fady B. 2022. Chloroplast DNA barcoding genes *matK* and *psbA-trnH* are not suitable for species identification and phylogenetic analyses in closely related pines. *iForest* 15: 141-147. doi:10.3832/for3913-015
- Paradis, E. 2018. Analysis of haplotype networks: The randomized minimum spanning tree method. *British Ecological Society* 9(5): 1308-1317.
- Paran, I., D. Zamir. 2003. Quantitative traits in plants: beyond the QTL. *Trends in Genetics*. DOI: 10.1016/S0168-9525(03)00117-3
- Paul, F., Otte, J., Schmitt, I. *et al.* 2018. Comparing Sanger sequencing and high-throughput metabarcoding for inferring photobiont diversity in lichens. *Sci Rep* 8, 8624. <https://doi.org/10.1038/s41598-018-26947-8>
- Pere K, Mburu K, Muge EK, Wagacha JM, Nyaboga EN. 2023. Molecular Discrimination and Phylogenetic Relationships of *Physalis* Species Based on ITS2 and *rbcL* DNA Barcode Sequence. *Crops*, 3(4):302-319. <https://doi.org/10.3390/crops3040027>
- Permata, D.A. and Susandarini R. 2022. Morphological diversity and phenetic relationship of wild and cultivated *Begonia* on morphology and leaf venation. *Biodiversitas* 23 (2): 928-937. DOI: 10.13057/biodiv/d230235
- Pitrat, Michel. 2016. *Plant Genetics and Genomics: Crops and Models*, Melon Genetic Resources: Phenotypic Diversity and Horticultural Taxonomy. Genetics and Genomics Cucurbitaceae, pp. 25-60.
- Pitrat, Michel. 2008. *Vegetables I; Cucurbitaceae; Chapter: Melon*. pp.283-315. DOI:10.1007/978-0-387-30443-4_9
- Pitrat, Michel. 2013. Phenotypic diversity in wild and cultivated melons (*Cucumis melo*). *Plant Biotechnology* 30(3): 273–278. DOI: 10.5511/plantbiotechnology.13.0813a
- Poczai, P., Hyvonen, J. 2010. Nuclear ribosomal spacer regions in plant phylogenetics: Problems and prospects. *Mol. Biol. Rep*, 37, 1897–1912.
- Pratama, O. A., W. A. S. Tunjung, S. Sutikno, B. S. Daryono. 2019. Bioactive compound profile of melon leaf extract (*Cucumis melo* L. ‘Hikapel’) infected by downy mildew. *Biodiversitas*, Vol. 20(11). DOI <https://doi.org/10.13057/biodiv/d201143>
- Purbasari, I., R. Pancasasti, H. A., Maulana. 2018. Pemanfaatan Golden Melon Sebagai Produk Unggulan yang Bernilai Ekonomis, Ekologi, Sosial dan Budaya Masyarakat di Provinsi Banten. *Jurnal Pengabdian Dinamika*, Vol. 5(1)
- Qin, Y., M. Li, Y. Cao, Y. Gao, W. Zhang. 2017. Molecular thresholds of ITS2 and their implications for molecular evolution and species identification in seed plants. *Nature Scientific Reports*, 7: 17316. DOI:10.1038/s41598-017-17695-2
- Quezada, E. T. 2023. Basic melon (*Cucumis melo* L.) physiology and morphology. VCE Publications and Educational Resources, spes-507. https://www.pubs.ext.vt.edu/content/pubs_ext_vt_edu/en/SPES/spes-507/spes-507.html

- Ramadan, A. M., Z. Millah, S. Hilal, A. Natawijaya. 2022. Evaluasi Keceragaman Genetik Empat Galur Melon (*Cucumis melo* L.) Berumur Genjah. *Prosiding Seminar Nasional Peripi 2022*.
- Rini, M. V., F. Yelli, D. L. Tambunan, I. Damayanti. 2021. Morphological and molecular identifications of three native arbuscular mycorrhizal fungi isolated from the rhizosphere of *Elaeis guineensis* and *Jatropha curcas* in Indonesia. *Biodiversitas*, Vol. 22(11): 4940-4947. DOI: 10.13057/biodiv/d221128
- Ritonga AW, Chozin MA, Syukur M, Maharijaya A, Sobir. 2018. Short Communication: Genetic variability, heritability, correlation, and path analysis in tomato (*Solanum Lycopersicum*) under shading condition. *Biodiversitas* 19(4):1527-1531. DOI: 10.13057/biodiv/d190445
- Robinson, R.W and D. S Decker-Walters. 1997. *Cucurbits*. CAB International. New York, NY, USA.
- Rodríguez-Moreno, L., V. M. González, A. Benjak, M. C. Martí, P. Puigdomènech, M. A. Aranda, J. Garcia-Mas. 2011. Determination of the melon chloroplast and mitochondrial genome sequences reveals that the largest reported mitochondrial genome in plants contain a significant amount of DNA having a nuclear origin. *BMC Genomics*, 12:424
- Ruang-areerate, P., Kongkachana W, Naktang C, Sonthirod C, Narong N, Jomchai N, Maprasop P, Maknual C, Phormsin N, Shearman JR, Pootakham W, Tangphatsornruang S. 2021. Complete chloroplast genome sequences of five *Bruguiera* species (Rhizophoraceae): comparative analysis and phylogenetic relationships. *PeerJ* 9:e12268 DOI 10.7717/peerj.12268
- Saputra, H. E., M. Syukur, W. B. Suwarno, Sobir. 2022. Diversity and similarity of melon (*Cucumis melo* L.) groups and determination of distinguishing morphological characters. *Biodiversitas*, Vol. 23(12): 6245-6261. DOI: 10.13057/biodiv/d231221
- Saputri, A. P., W. A. Wibowo, B. S. Daryono. 2020. Phenotypical characters and biochemical compound of cucurbitacin melon (*Cucumis melo* L. 'Gama Melon Parfum') resulted from breeding. *AIP Conf. Proc.* 2260, 060006. <https://doi.org/10.1063/5.0017615>
- Sayed, H.A., Mostafa, S., Haggag, I.M. *et al.* 2023. DNA Barcoding of *Prunus* Species Collection Conserved in the National Gene Bank of Egypt. *Mol Biotechnol* **65**, 410–418. <https://doi.org/10.1007/s12033-022-00530-z>
- Schaefer, Hanno, S. S. Renner. 2011. Phylogenetic relationships in the order Cucurbitales and a new classification of the gourd family (Cucurbitaceae). *Taxon*, Vol. 60(1): 122-138. <https://doi.org/10.1002/tax.601011>
- Sebastian, P., H. Schaefer, I. R. H. Telford, and S.S. Renner. 2010. Cucumber (*Cucumis sativus*) and melon (*C. melo*) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. *Proceedings of the National Academic of Science* (PNAS), vol. 107(32): 14269-14273. DOI: 10.1073/pnas.1005338107
- Shaik, R.S., Gopurenko, D., Urwin, N.A.R. *et al.* 2015. Population genetics of invasive *Citrullus lanatus*, *Citrullus colocynthis* and *Cucumis myriocarpus* (Cucurbitaceae) in Australia: inferences based on chloroplast and nuclear gene sequencing. *Biol Invasions* **17**, 2475–2490. <https://doi.org/10.1007/s10530-015-0891-6>
- Shaw, J., E. B. Lickey, J. T. Beck, S. B. Farmer, W. Liu, J. Miller, K. C. Siripun, C. T. Winder, E. E. Schilling, R. L. Small. 2005. The tortoise and the hare II: relative utility of 21

- noncoding chloroplast DNA sequence for phylogenetic analysis. *Am. J. Bot.*, 92, pp. 142-166.
- Shaw, Joey, E.B. Lickey, E. E. Schilling, 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. *Journal of Botany* 94(3): 275-288.
- Shaw, Joey, H. L. Shafer, O. R. Leonard, M. J. Kovach, M. Schorr, A. B. Morris. 2014. Chloroplast DNA Sequence Utility for The Lowest Phylogenetic and Phylogeographic Inference in Angiosperms: The Tortoise and The Hare IV. *American Journal of Botany* 101(11): 1987-2004. <https://doi.org/10.3732/ajb.1400398>
- Shen, Chang-Hui. 2023. *Dianostic Molecular Biology*. Second Edition. Chapter 7: Quantification and analysis of nucleic acids. pp. 181-208. Academic Press. Elsevier. <https://doi.org/10.1016/C2020-0-01054-6>
- Shubhanand, N., Agrawal, M., John, K. J., Sutar, S., Yadav, S. R., Rao, S. R., & Bhat, K. V. 2015. Phylogenetic informativeness of plastid regions in inferring the species relationships among *Cucumis* species. *INDIAN JOURNAL OF GENETICS AND PLANT BREEDING*, 75(02), 232–236. <https://doi.org/10.5958/0975-6906.2015.00035.8>
- Silva, A. R. D., P. R. Cecon, C. T. D. S. Dias, M. Puiatti, F. L. Finger, A. P. S. Carneiro. 2014. Morphological phenotypic dispersion of garlic cultivars by cluster analysis and multidimensional scaling. *Scientia Agricola*. Vol. 71, p. 38-43
- Simpson, M. G. 2013. *Plant Systematics*. Boston, Elsevier (Academic Press), Amsterdam. pp. 10-13, 409
- Singh, A. K., S. Kumar, H. Singh, V. P. Rai, B. D. Singh, S. Pandey. 2015. Genetic diversity in Indian snapmelon (*Cucumis melo* var. *momordica*) accessions revealed by ISSR markers. *Plant Omics Journal* 8(1): 9-16
- Singh, D., Leskovar, D.I., Sharma, S.P. *et al.* 2020. Genetic diversity and interrelationship among Indian and exotic melons based on fruit morphology, quality components and microsatellite markers. *Physiology Molecular and Biology of Plants* 26, 985–1002. <https://doi.org/10.1007/s12298-020-00814-1>
- Small, R. L., E. B. Lickey, J. Shaw, W. D. Hauk. 2005. Amplification of noncoding chloroplast DNA for phylogenetic studies in lycophytes and monilophytes with comparative example o relative phylogenetic utility from Ophioglossaceae. *Molecular Phylogenetics and Evolution*, Vol. 26(3): 509-522. <https://doi.org/10.1016/j.ympev.2005.04.018>
- Sokal, R.H. and P. A. Sneath. 1963. *Principal Numerical Taxonomy*. Freeman and Co. San Fransisco. pp 60-163
- Soltani F, Shajari M, Mirbehbahani GS, Bihamta MR. 2022. Assessment of melon genetic diversity based on fruit phenotypic traits and flowering habits. *Intl J Horti Sci Technol* 9 (1): 97-116. DOI: 10.22059/ijhst.2021.313939.415
- Song, Shiqiang, Kenneth. M. Cameron, Y. Wang, S. Wang, Xinjie Jin, Faiza Hina, Zhaoping Yang, Pan Li. 2023. Phylogenomics and phylogeography of *Menispermum* (Menispermaceae). *Front. Plant Sci.*, Vol. 14. <https://doi.org/10.3389/fpls.2023.1116300>
- Steele, P. R., L. M. Friar, L. E. Gilbert, R. K. Jansen. 2010. Molecular systematics of the neotropical genus *Psiguria* (Cucurbitaceae): Implications for phylogeny and species identification. *American Journal of Botany*, Vol. 97(1): 156-173. <https://doi.org/10.3732/ajb.0900192>
- Suhardi, A. Wibowo, W. P. B. Putra, P. Sumppunn. 2023. The Phylogeny of Bornean Swamp Buffalo (*Bubalus bubalis*) Analysis Based on D-loop Mitochondrial DNA Sequence

- Variation. *Tropical Animal Science Journal*, 46(2): 139-145.
<https://doi.org/10.5398/tasj.2023.46.2.139>
- Sumarlina & B.S. Daryono. 2018. Karakterisasi Molekuler Melon (*Cucumis melo* L.) Grup 'Tacapa' Berdasarkan Multiple Multilocus DNA Barcodes. *Thesis*. Fakultas Biologi, Universitas Gadjah Mada. Yogyakarta
- Sun J, Wang Y, Qiao P, Zhang L, Li E, Dong W, Zhao Y, Huang L. 2023. *Pueraria montana* Population Structure and Genetic Diversity Based on Chloroplast Genome Data. *Plants*, 12(12):2231. <https://doi.org/10.3390/plants12122231>
- Sungkawati, M., L. Hidayati, B. S. Daryono, Purnomo. 2019. Phenetic analysis of *Curcuma* spp. in Yogyakarta, Indonesia based on morphological and anatomical characters. *Biodiversitas*, Vol. 20(8): 2340-2347. DOI: 10.13057/biodiv/d200832
- Supriyadi, F. Husnun, B.S. Daryono. 2022. Sifat kimia dan kinetika degradasi termal antioksidan jus melon (*Cucumis melo* L.) kultivar Gama Melon Parfum. *Jurnal Teknologi Pertanian Andalas* 26(1): 71. DOI:10.25077/jtpa.26.1.71-83.2022
- Swetha, V.P. Parvathy, V.A., Sheeja, T.E., and Sasikumar B. 2014. DNA Barcoding for Discriminating the Economically Important *Cinnamomum verum* from Its Adulterans. *Food Biotechnology*. 28:183-194
- Tadmor, Y.; Burger, J.; Yaakov, I.; Feder, A.; Libhaber, S.E.; Portnoy, V.; Meir, A.; Tzuri, G.; Sa'ar, U.; Rogachev, I.; et al. 2010. Genetics of flavonoid, carotenoid, and chlorophyll pigments in melon fruit rinds. *J. Agric. Food Chem*, 58, 10722–10728
- Tajima F. 1989. Statistical method for testing the neutral mutation hypotheses by DNA polymorphism. *Genetics* 123:585–595
- Tam, N. T., M. S. Dwiyantri, Y. Koide, A. J. Nagano, H. Ky, H. Q. Tin, N. L. Hien, L. V. Dung, Y. Kishima. 2019. Profiling SNP and Nucleotide Diversity to Characterize Mekong Delta Rice Landraces in Southeast Asian Populations. *The Plant Genome*, Vol. 12(3). <https://doi.org/10.3835/plantgenome2019.06.0042>
- Tamura K, D. Peterson, N. Peterson, G. Stecher. M. Nei, and S. Kumar. 2011. MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Molecular Biology and Evolution*. 28: 2731-2739
- Tanaka K., Mitsuhiro Sugiyama, Gentaro Shigita, Ryoma Murakami, Thanh-Thuy Duong, Yasheng Aierken, Anna M Artemyeva, Zharas Mamypbelov, Ryuji Ishikawa, Hidetaka Nishida, Kenji Kato. 2023. Melon diversity on the Silk Road by molecular phylogenetic analysis in Kazakhstan melons. *Breeding Science*, Volume 73(2), pp. 219-229
- Tanaka K., Y. Akashi, K. Fukunaga, T. Yamamoto, Y. Aierken, H. Nishida, Chun Lin L, H. Yoshino, Yo-Ichiro Sato, Kenji Kato. 2013. Diversification and genetic differentiation of cultivated melon inferred from sequence polymorphism in the chloroplast genome. *Breeding Science* 63: 183–196. doi:10.1270/jsbbs.63.183
- Tao, X. F., T. Huang, X. F Li, D. P. Peng. 2016. Application of a PCA based water quality classification method in water quality assessment in the Tongjiyan Irrigation Area, China. *International Conference on Energy and Environmental Protection (ICEEP 2016)*. Atlantis Press. pp. 118-125
- Tateno Y, Takezaki N, Nei M. 1994. Relative efficiencies of the maximum-likelihood, neighbor-joining, and maximum-parsimony methods when substitution rate varies with site. *Mol Biol Evol*; 11(2):261-77. doi: 10.1093/oxfordjournals.molbev.a040108.

- Techen, N., Parveen, I., Pan, Z., dan Khan, I.A. 2014. DNA Barcoding of Medicinal Plant Material for Identification. *Current Opinion in Biotechnology*. 25(103): 103-110
- Tian, Y., Liu, X., Xu, Y. *et al.* 2023. Comparative and phylogenetic analysis of *Asparagus meiocladus* Levl. and *Asparagus munitus* Wang et S. C. Chen plastomes and utility of plastomes mutational hotspots. *Sci Rep* **13**, 15622. <https://doi.org/10.1038/s41598-023-42945-x>
- Timme RE, Kuehl JV, Boore JL, Jansen RK. 2007. A comparative analysis of the *Lactuca* and *Helianthus* (Asteraceae) plastid genomes: Identification of divergent regions and categorization of shared repeats. *Am. J. Bot.*; 94:302–312. doi: 10.3732/ajb.94.3.302.
- Tjitrosoepomo, G. 1991. *Taksonomi Tumbuhan Spermatophyta*. Gadjah Mada University Press. Yogyakarta. pp 379-380.
- Tjitrosoepomo, G. 2009. *Taksonomi Tumbuhan*. Gadjah Mada University Press. Yogyakarta.
- Tnah, L.H., Lee, S.L., Tan, A.L., Lee, C.T., Ng, K.K.S., and Ng, C.H. 2016. Intraspecific classification of *Ficus deltoidea* Jack subsp. *Deltoidei* (Moraceae) in Peninsular Malaysia based on morphological and molecular variations. *Biochem Syst Ecol* 67: 119-128. DOI: 10.1016/j.bse.2016.06.001.
- Tonti-Filippini, J.; Nevill, P.G.; Dixon, K.; Small, I. 2017. What Can We Do with 1000 Plastid Genomes? *Plant J.*, 90, 808–818.
- Van Gestel J, Weissing F.J., 2018. Is plasticity caused by single genes? *Nature*, 555: 19-20.
- Verma, M.K., S. Lal, N. Ahmed. 2012. PCA and genetic divergence analysis in Indian pomegranate (*Punica granatum* L.) cultivars. *Progressive Horticulture*, Vol. 44(2): 265-270.
- Wahyuni, D. K., S. R. Mukarromah, P. Rakhmad, M. Ilham, G. A Rakashiwi, D. T. Indriati, B. F. Yoku, H. Purnobasuki, Junairiah, S. Prasongsuk. 2022. Morpho-anatomical characterization and DNA barcoding analysis of *Pluchea indica* (L.) Less. *Biodiversitas*, Vol. 23(8): 4272:4282. DOI: 10.13057/biodiv/d230851
- Wang X, Chen X, Yang P, Wang L, Han J. 2017. Barcoding the *Dendrobium* (Orchidaceae) Species and Analysis of the Intragenomic Variation Based on the Internal Transcribed Spacer 2. *Biomed Res Int*. doi: 10.1155/2017/2734960.
- Warseno, T., A. R. Chasani, B. S. Daryono. 2022. Genetic variability and phylogenetic relationships of *Begonia multangula* based on *atpB-rbcL* non-coding spacer of cpDNA sequences. *Biodiversitas* 23(10): 5491-5501. DOI: 10.13057/biodiv/d231061
- Wehner, T.C., R.P. Naegele, J.R. Myers, N.P.S Dhillon, and K. Crosby. 2020. *Cucurbits* 2nd edition. CABI, Boston, MA, USA.
- Wibowo, W. A., M. F. Al Rasyid, S. E. Maharani, B. S. Daryono. 2022. Genetic Stability Analysis Based on Inter-Simple Sequence Repeat and β -Carotene Content Analysis in Melon (*Cucumis melo* L. Gama Melon Parfum). *International Journal on Advanced Science Engineering and Information Technology* 12(4): 1606. DOI:10.18517/ijaseit.12.4.15641
- WFO Plant List. 2022. *WFO Plant List: Snapshots of the Taxonomy*. <https://wfoplantlist.org/plant-list/taxon/> . Diakses tanggal 1 Februari 2023.
- Xu L, He Y, Tang L, Xu Y, Zhao G. 2022. Genetics, Genomics, and Breeding in Melon. *Agronomy*, 12(11):2891. <https://doi.org/10.3390/agronomy12112891>
- Yan R, Gu L, Qu L, Wang X, Hu G. 2023. New Insights into Phylogenetic Relationship of *Hydrocotyle* (Araliaceae) Based on Plastid Genomes. *International Journal of Molecular Sciences*, 24(23):16629. <https://doi.org/10.3390/ijms242316629>

- Yang, K., A. H. Khan Robin, Go-Eun Yi, Jonghoon Lee, Mi-Young Chung, Tae-Jin Yang, Ill-Sup Nou. 2015. Diversity and Inheritance of Intergenic Spacer Sequences of 45S Ribosomal DNA among Accessions of *Brassica oleracea* L. var. *capitata*. *International Journal of Molecular Sciences*, 16: 28783-28799. doi:10.3390/ijms161226125
- Yilmaz, Nihat, H. P. Kaya, H. Pinar, F. Hanci, A. Uzun. 2021. Detailed Morphological and Molecular Characterizations of Melon (*Cucumis melo* L.) Accessions Collected from Northern Cyprus and Turkey. *Horticultural Science and Technology*, pp. 471-481. <https://doi.org/10.7235/HORT.20210042>
- Yoo, Eunae, Mesfin Haile, Ho-Cheol Ko, Yu-Mi Choi, Gyu-Taek Cho, Hee-Jong Woo, Xiaohan Wang, Pilmo Sung, Jundae Lee, Jungu Lee, Nayoung Ro. 2023. Development of SNP markers for *Cucurbita* species discrimination. *Scientia Horticulturae*, Vol. 318. <https://doi.org/10.1016/j.scienta.2023.112089>
- Yu, Jie, Xi Wu, Chang Liu, S. Newmaster, S. Ragupathy, W. John Kress. 2021. Progress in the use of DNA barcodes in the identification and classification of medicinal plants. *Ecotoxicology and Environmental Safety*, 208 (2021) 111691. <https://doi.org/10.1016/j.ecoenv.2020.111691>
- Yusuf, A. F., B. S. Daryono. 2021. Studies of Genetic and Morphological Characteristics of Indonesia Melon (*Cucumis melo* L. 'Hikapel') Germplasm. *International Journal on Advanced Science Engineering Information Technology*, Vol. 11(5): 2023-2030. DOI:10.18517/ijaseit.11.5.14047
- Yusuf, A. F., W. A. Wibowo, A.S. Subiastuti. 2020. Morphological studies of stability and identity of melon (*Cucumis melo* L.) 'Hikapel' and comparative cultivars. *AIP Conference Proceedings* 2260. <https://doi.org/10.1063/5.0017606>
- Yusuf, A. F., W. A. Wibowo, B. S. Daryono. 2022. Genetic stability of melon (*Cucumis melo* L. cv. Meloni) based on inter-simple sequence repeat and phenotypic characteristics. *Biodiversitas*, Vol. 23(6): 3042-3049. DOI: 10.13057/biodiv/d230631
- Yusuf, A. F., A. Alfiani, T. A. S. Salsabila, P. S. Kusnanda, I. N. Hidayati, B. S. Daryono. 2023. Assessment of maturity stage and stability of new Indonesian melon cultivar 'Melona' based on ISSR markers and morphological characteristics. *Biodiversitas*, Vol. 24(1): 308-316. DOI: 10.13057/biodiv/d240137
- Zhang, C., A. S. Pratap, S. Natarajam, L. Pugalendhi, S. Kikuchi, H. Sassa, N. Senthil, and T. Koba. 2012. Evaluation of Morphological and Molecular Diversity among South Asian Germplasms of *Cucumis sativus* and *Cucumis melo*. *International Scholarly Research Notices*, vol. 2012, Article ID 134134, 11 pages, 2012. <https://doi.org/10.5402/2012/134134>
- Zhang H., Mittal N., Leamy L.J., Barazani O., Song B-H. 2017. Back into the wild; applying untapped genetic diversity of wild relatives for crop improvement. *Evolutionary Application*, 10:5-24.
- Zhang L, Lu X, Lu J, Liang H, Dai Q, Xu G-L, et al. 2012. Thymine DNA glycosylase specifically recognizes 5-carboxylcytosine-modified DNA. *Nature Chemical Biology*, 8:328-330.
- Zhang X, Zhou T, Yang J, Sun J, Ju M, Zhao Y, Zhao G. 2018. Comparative Analyses of Chloroplast Genomes of Cucurbitaceae Species: Lights into Selective Pressures and Phylogenetic Relationships. *Molecules*, 23(9): 2165. <https://doi.org/10.3390/molecules23092165>

- Zhao, G., Lian, Q., Zhang, Z., Fu, Q., He, Y., Ma, S *et al.* 2019. A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. *Nature Genetics*, 51(11), 1607-1615. <https://doi.org/10.1038/s41588-019-0522-8>
- Zhao, YJ., Liu, J., Yin, GS. *et al.* 2023. Characteristics of plastid genomes in the genus *Ceratostigma* inhabiting arid habitats in China and their phylogenomic implications. *BMC Plant Biol* **23**, 303. <https://doi.org/10.1186/s12870-023-04323-7>
- Zhou, C., Wang, P., Zeng, Q. *et al.* 2023. Comparative chloroplast genome analysis of seven extant *Citrullus* species insight into genetic variation, phylogenetic relationships, and selective pressure. *Sci Rep* **13**, 6779. <https://doi.org/10.1038/s41598-023-34046-6>
- Zubaidah, Siti. 2011. *Integrasi Pendekatan Morfologi dan Molekuler DNA (Deoxyribonucleic acid) dalam Taksonomi*. Universitas Negeri Malang.