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DAFTAR PUSTAKA

Abramson, J., Adler, J., Dunger, J., Evans, R., Green, T., Pritzel, A., Ronneberger, O., Willmore, L., Ballard, A. J., Bambrick, J., Bodenstein, S. W., Evans, D. A., Hung, C., O'Neill, M., Reiman, D., Tunyasuvunakool, K., Wu, Z., Žemgulytė, A., Arvaniti, E., Beattie, C., Bertolli, O., Bridgland, A., Cherepanov, A., Congreve, M., Cowen-Rivers, A. I., Cowie, A., Figurnov, M., Fuchs, F. B., Gladman, H., Jain, R., Khan, Y. A., Low, C. M. R., Perlin, K., Potapenko, A., Savy, P., Singh, S., Stecula, A., Thillaisundaram, A., Tong, C., Yakneen, S., Zhong, E. D., Zielinski, M., Žídek, A., Bapst, V., Kohli, P., Jaderberg, M., Hassabis, D., & Jumper, J. M. (2024). Accurate structure prediction of biomolecular interactions with AlphaFold 3. *Nature*, *630*, 493–500. https://doi.org/10.1038/s41586-024-07487-w

'Aisy, N. R., Agustin, Y., & Supriatna, A. (2024). Perbandingan morfologi stroberi (*Fragaria* SPP) di La Fressa dan Bukit Strawberry Lembang untuk klasifikasi varietas. *Polygon Jurnal Ilmu Komputer Dan Ilmu Pengetahuan Alam*, *2*(4), 123–131. https://doi.org/10.62383/polygon.v2i4.171

Alberts, B., Johnson, A., Lewis, J., Raff, M., Roberts, K., & Walter, P. (2002). *Molecular biology of the cell* (4th ed.). Garland Science.

Almutairi, M. M. (2021). Analysis of chromosomes and nucleotides in rice to predict gene expression through codon usage pattern. *Saudi Journal of Biological Sciences*, *28*(8), 4569–4574. https://doi.org/10.1016/j.sjbs.2021.04.059

Amar, M. H. (2020). *ycf1-ndhF* genes, the most promising plastid genomic barcode, sheds light on phylogeny at low taxonomic levels in *Prunus persica*. *Journal of Genetic Engineering and Biotechnology*, *18*(1), 1–10. https://doi.org/10.1186/s43141-020-00057-3

Anonim. (2024a). *Luas Panen Tanaman Sayuran dan Buah-Buahan Menurut Provinsi dan Jenis Tanaman, 2023*. Badan Pusat Statistik. Retrieved March 16, 2025, from https://www.bps.go.id/id/statistics-table/3/YlhOVmIxcG1abmRxVURoS1dFbFVTamhaUml0aWR6MDkjMw==/luas-panen-tanaman-sayuran-menurut-provinsi-dan-jenis-tanaman--2022.html?year=2023

Anonim. (2024b). *Produksi Tanaman Buah-buahan, 2021-2023*. Badan Pusat Statistik. Retrieved March 13, 2025, from https://www.bps.go.id/id/statistics-table/2/NjIjMg==/produksi-tanaman-buah-buahan.html

Anonim. (2026a). *FAOSTAT*. Food and Agriculture Organization of the United States. Retrieved February 17, 2026, from https://www.fao.org/faostat/en/#data

Anonim. (2026b). *Fragaria × ananassa (Weston) Rozier*. Global Biodiversity Information Facility. Retrieved February 13, 2026, from https://www.gbif.org/species/3029912

Arif, M. F., Aristya, G. R., & Kasiamdari, R. S. (2019). Genetic diversity of strawberry cultivars in Banyuroto, Magelang, Indonesia based on Cleaved Amplified Polymorphic Sequence. *Biodiversitas Journal of Biological*

UNIVERSITAS
GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã—ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Diversity, *20*(6), 1721–1728. https://doi.org/10.13057/biodiv/d200631

Aristya, G. R., Budiman, M. S., Kasiamdari, R. S., Widiastuti, A., & Arif, M. F. (2025). Genetic Variation and Phylogenetic Analysis of Strawberry (*Fragaria* spp.) on Yogyakarta and Central Java, Indonesia, Based on *rbcL* DNA Barcoding. *Pakistan Journal of Biological Sciences*, *28*(3), 121–130. https://doi.org/10.3923/pjbs.2025.121.130

Asaf, S., Khan, A. L., Khan, M. A., Waqas, M., Kang, S., Yun, B., & Lee, I. (2017). Chloroplast genomes of *Arabidopsis halleri* ssp. *gemmifera* and *Arabidopsis lyrata* ssp. *petraea*: Structures and comparative analysis. *Scientific Reports*, *7*(1), 1–15. https://doi.org/10.1038/s41598-017-07891-5

Ashton, P. M., Nair, S., Dallman, T., Rubino, S., Rabsch, W., Mwaigwisya, S., Wain, J., & O'Grady, J. (2015). MinION nanopore sequencing identifies the position and structure of a bacterial antibiotic resistance island. *Nature Biotechnology*, *33*(3), 296–300. https://doi.org/10.1038/nbt.3103

Bailey, T. L., Boden, M., Buske, F. A., Frith, M., Grant, C. E., Clementi, L., Ren, J., Li, W. W., & Noble, W. S. (2009). MEME SUITE: tools for motif discovery and searching. *Nucleic Acids Research*, *37*, W202–W208. https://doi.org/10.1093/nar/gkp335

Bailey, T. L., & Gribskov, M. (1998). Combining evidence using p-values: application to sequence homology searches. *Bioinformatics*, *14*(1), 48–54. https://doi.org/10.1093/bioinformatics/14.1.48

Bailey, T. L., Johnson, J., Grant, C. E., & Noble, W. S. (2015). The MEME suite. *Nucleic Acids Research*, *43*, W39–W49. https://doi.org/10.1093/nar/gkv416

Basantani, M. K., Gupta, D., Mehrotra, R., Mehrotra, S., Vaish, S., & Singh, A. (2017). An update on bioinformatics resources for plant genomics research. *Current Plant Biology*, *11–12*, 33–40. https://doi.org/10.1016/j.cpb.2017.12.002

Bruijns, B., Hoekema, T., Oomens, L., Tiggelaar, R., & Gardeniers, H. (2022). Performance of spectrophotometric and fluorometric DNA quantification methods. *Analytica—A Journal of Analytical Chemistry and Chemical Analysis*, *3*(3), 371–384. https://doi.org/10.3390/analytica3030025

Butler, J. M. (2012). Single nucleotide polymorphisms and Applications. In *Advanced Topics in Forensic DNA Typing* (pp. 347–369). https://doi.org/10.1016/b978-0-12-374513-2.00012-9

Capra, J. A., Laskowski, R. A., Thornton, J. M., Singh, M., & Funkhouser, T. A. (2009). Predicting protein ligand binding sites by combining evolutionary sequence conservation and 3D structure. *PLoS Computational Biology*, *5*(12), 1–18. https://doi.org/10.1371/journal.pcbi.1000585

Carlson, H. A. (2002). Protein flexibility and drug design: how to hit a moving target. *Current Opinion in Chemical Biology*, *6*(4), 447–452. https://doi.org/10.1016/s1367-5931(02)00341-1

Carugo, O. (2023). PLDDT values in AlphaFold2 protein models are unrelated to globular protein local flexibility. *Crystals*, *13*(11), 1–9. https://doi.org/10.3390/cryst13111560

Carugo, O., & Pongor, S. (2001). A normalized root‐mean‐square distance for comparing protein three‐dimensional structures. *Protein Science*, *10*(7), 1470–1473. https://doi.org/10.1110/ps.690101

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Chen, C., Wu, Y., Li, J., Wang, X., Zeng, Z., Xu, J., Liu, Y., Feng, J., Chen, H., He, Y., & Xia, R. (2023). TBtools-II: A "one for all, all for one" bioinformatics platform for biological big-data mining. *Molecular Plant*, *16*(11), 1733–1742. https://doi.org/10.1016/j.molp.2023.09.010

Chen, D., Chang, A. Y., Liao, B., & Yeang, C. (2013). Functional characterization of motif sequences under purifying selection. *Nucleic Acids Research*, *41*(4), 2105–2120. https://doi.org/10.1093/nar/gks1456

Chen, Z., Ong, C. T., Nguyen, L. T., Lamb, H. J., González-Recio, O., Gutiérrez-Rivas, M., Meale, S. J., & Ross, E. M. (2025). Biases from Oxford Nanopore library preparation kits and their effects on microbiome and genome analysis. *BMfC Genomics*, *26*(1), 1–9. https://doi.org/10.1186/s12864-025-11649-z

Cheng, H., Li, J., Zhang, H., Cai, B., Gao, Z., Qiao, Y., & Mi, L. (2017). The complete chloroplast genome sequence of strawberry (*Fragaria* × *ananassa* Duch.) and comparison with related species of Rosaceae. *PeerJ*, *5*, 1–27. https://doi.org/10.7717/peerj.3919

Chevigny, N., Schatz-Daas, D., Lotfi, F., & Gualberto, J. M. (2020). DNA repair and the stability of the plant mitochondrial genome. *International Journal of Molecular Sciences*, *21*(1), 1–24. https://doi.org/10.3390/ijms21010328

Cho, K., Yun, B., Yoon, Y., Hong, S., Mekapogu, M., Kim, K., & Yang, T. (2015). Complete Chloroplast Genome Sequence of Tartary Buckwheat (*Fagopyrum tataricum*) and Comparative Analysis with Common Buckwheat (*F. esculentum*). *PLoS ONE*, *10*(5), 1–14. https://doi.org/10.1371/journal.pone.0125332

Choi, H. G., Moon, B. Y., & Kang, N. J. (2016). Correlation between Strawberry (*Fragaria ananassa* Duch.) Productivity and Photosynthesis-Related Parameters under Various Growth Conditions. *Frontiers in Plant Science*, *7*, 1–13. https://doi.org/10.3389/fpls.2016.01607

Choudhuri, S. (2014). Sequence alignment and similarity searching in genomic databases. In *Elsevier eBooks* (pp. 133–155). https://doi.org/10.1016/b978-0-12-410471-6.00006-2

Cooper, G. M. (2000). *The Cell: A Molecular Approach* (2nd ed.). Sinauer Associates.

Crecca, C. R., & Roitberg, A. E. (2008). Using distances between α‐carbons to predict protein structure. *International Journal of Quantum Chemistry*, *108*(15), 2782–2792. https://doi.org/10.1002/qua.21769

Cui, L., Leebens-Mack, J., Wang, L., Tang, J., Rymarquis, L., Stern, D. B., & dePamphilis, C. W. (2006). Adaptive evolution of chloroplast genome structure inferred using a parametric bootstrap approach. *BMC Evolutionary Biology*, *6*(1), 1–12. https://doi.org/10.1186/1471-2148-6-13

DeLano, W. L. (2002). The PYMOL Molecular Graphics System. *Medical Entomology and Zoology*. https://ci.nii.ac.jp/naid/10020095229/

Dizman, Y. A. (2025). Codon Usage Bias of the Polyphenol Oxidase Genes in *Camellia sinensis*: A Comprehensive Analysis. *Plants*, *14*(19), 1–22. https://doi.org/10.3390/plants14193074

Dobrogojski, J., Adamiec, M., & Luciński, R. (2020). The chloroplast genome: a review. *Acta Physiologiae Plantarum*, *42*(6), 1–13. https://doi.org/10.1007/s11738-020-03089-x

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Donkor, E. S., Dayie, N. T. K. D., & Adiku, T. K. (2014). Bioinformatics with basic local alignment search tool (BLAST) and fast alignment (FASTA). *Journal of Bioinformatics and Sequence Analysis*, *6*(1), 1–6. https://doi.org/10.5897/ijbc2013.0086

Downie, S. R., Katz‐Downie, D. S., & Watson, M. F. (2000). A phylogeny of the flowering plant family Apiaceae based on chloroplast DNA *rpl16* and *rpoC1* intron sequences: towards a suprageneric classification of subfamily Apioideae. *American Journal of Botany*, *87*(2), 273–292. https://doi.org/10.2307/2656915

Doyle, J. J., & Doyle, J. L. (1987). A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin*, *19*(1), 11–15.

Edger, P. P., Poorten, T. J., VanBuren, R., Hardigan, M. A., Colle, M., McKain, M. R., Smith, R. D., Teresi, S. J., Nelson, A. D. L., Wai, C. M., Alger, E. I., Bird, K. A., Yocca, A. E., Pumplin, N., Ou, S., Ben-Zvi, G., Brodt, A., Baruch, K., Swale, T., Shiue, L., Acharya, C. B., Cole, G. S., Mower, J. P., Childs, K. L., Jiang, N., Lyons, E., Freeling, M., Puzey, J. R., &. Knapp, S. J. (2019). Origin and evolution of the octoploid strawberry genome. *Nature Genetics*, *51*(3), 541–547. https://doi.org/10.1038/s41588-019-0356-4

Efrilla, A. V., Sulistyo, S. B., Wijaya, K., Kuncoro, P. H., & Sudarmaji, A. (2020). Klasifikasi Penyakit Pada Daun Stroberi Menggunakan K-Means Clustering dan Jaringan Syaraf Tiruan. *Jurnal Keteknikan Pertanian Tropis Dan Biosistem*, *8*(2), 161–170. https://doi.org/10.21776/ub.jkptb.2020.008.02.06

Eren, K., Taktakoğlu, N., & Pirim, I. (2023). DNA sequencing methods: From past to present. *Eurasian Journal of Medicine*, *54*, S47–S56. https://doi.org/10.5152/eurasianjmed.2022.22280

Espinosa, E., Bautista, R., Larrosa, R., & Plata, O. (2024). Advancements in long-read genome sequencing technologies and algorithms. *Genomics*, *116*(3), 1–12. https://doi.org/10.1016/j.ygeno.2024.110842

Fahira, C. N., Harnelly, E., & Zumaidar. (2024). Complete chloroplast genome, distribution, and pharmacological activities *Pogostemon*: a mini review. *Jurnal Penelitian Pendidikan IPA*, *10*(SpecialIssue), 7–18. https://doi.org/10.29303/jppipa.v10ispecialissue.7048

Fleming, J., Magana, P., Nair, S., Tsenkov, M., Bertoni, D., Pidruchna, I., Afonso, M. Q. L., Midlik, A., Paramval, U., Žídek, A., Laydon, A., Kovalevskiy, O., Pan, J., Cheng, J., Avsec, Ž., Bycroft, C., Wong, L. H., Last, M., Mirdita, M., Steinegger, M., Kohli, P., Váradi, M., & Velankar, S. (2025). AlphaFold Protein Structure Database and 3D-Beacons: New data and capabilities. *Journal of Molecular Biology*, *437*(15), 1–11. https://doi.org/10.1016/j.jmb.2025.168967

Folta, K. M., & Barbey, C. R. (2019). The strawberry genome: a complicated past and promising future. *Horticulture Research*, *6*(1). 1–3. https://doi.org/10.1038/s41438-019-0181-z

Garcia, A. L., Chung, K., Hou, K., Hylton, S., Mosquera, J., & Zhang, C. (2025). Structure of a gene and its control elements. *Genetics and Clinical Genomics,* *3*(2), 52–57. https://doi.org/10.37980/im.journal.ggcl.en.20252684

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Gaston, A., Osorio, S., Denoyes, B., & Rothan, C. (2019). Applying the Solanaceae strategies to strawberry crop improvement. *Trends in Plant Science*, *25*(2), 130–140. https://doi.org/10.1016/j.tplants.2019.10.003

Geng, X., Xue, Y., Wang, H., Tu, H., Jing, R., Li, Z., & Gai, Y. (2026). Comprehensive analysis of chloroplast genome evolution in Poaceae: codon usage patterns, selection pressures, and phylogenomic relationships. *BMC Genomics*, *27*(1), 1–24. https://doi.org/10.1186/s12864-025-12498-6

Gerstein, A. S. (2001). *Molecular Biology Problem Solver*. Wiley‐Liss, Inc. https://doi.org/10.1002/0471223905

Giani, A. M., Gallo, G. R., Gianfranceschi, L., & Formenti, G. (2020). Long walk to genomics: History and current approaches to genome sequencing and assembly. *Computational and Structural Biotechnology Journal*, *18*, 9–19. https://doi.org/10.1016/j.csbj.2019.11.002

Godbey, W. T. (2021). Agarose gels. In *Elsevier eBooks* (pp. 203–218). https://doi.org/10.1016/b978-0-12-817726-6.00009-5

Goodwin, S., McPherson, J. D., & McCombie, W. R. (2016). Coming of age: ten years of next-generation sequencing technologies. *Nature Reviews Genetics*, *17*(6), 333–351. https://doi.org/10.1038/nrg.2016.49

Greiner, S., Lehwark, P., & Bock, R. (2019). OrganellarGenomeDRAW (OGDRAW) version 1.3.1: expanded toolkit for the graphical visualization of organellar genomes. *Nucleic Acids Research*, *47*(W1), W59–W64. https://doi.org/10.1093/nar/gkz238

Gullapalli, R. R., Desai, K. V., Santana-Santos, L., Kant, J. A., & Becich, M. J. (2012). Next generation sequencing in clinical medicine: Challenges and lessons for pathology and biomedical informatics. *Journal of Pathology Informatics*, *3*(1), 40. https://doi.org/10.4103/2153-3539.103013

Guo, Z., Wang, H., Tao, J., Ren, Y., Xu, C., Wu, K., Zou, C., Zhang, J., & Xu, Y. (2019). Development of multiple SNP marker panels affordable to breeders through genotyping by target sequencing (GBTS) in maize. *Molecular Breeding*, *39*(3), 1–12. https://doi.org/10.1007/s11032-019-0940-4

Han, H., Jang, Y. J., Han, K., Park, H., Kim, D., Lee, S., & Oh, Y. (2025). Chromosome-level genome assembly of cultivated strawberry ‘Seolhyang’ (*Fragaria* × *ananassa*). *Scientific Data*, *12*(1), 1–12. https://doi.org/10.1038/s41597-025-05191-6

Hancock, J. F. (2020). *Strawberries, 2nd Edition*. CABI.

Hanif, Z., & Ashari, H. (2012). Sebaran Stroberi (*Fragaria* x *ananassa*) di Indonesia. In *Prosiding Seminar Nasional Pekan Inovasi Teknologi Hortikultura Nasional: Penerapan Inovasi Teknologi Hortikultura dalam Mendukung Pembangunan yang Berdaya Saing dan Berbasis Sumberdaya Genetik Lokal*. https://doi.org/10.13140/rg.2.1.2110.6089

Hannum, S. M. (2004). Potential Impact of strawberries on human Health: A Review of the Science. *Critical Reviews in Food Science and Nutrition*, *44*(1), 1–17. https://doi.org/10.1080/10408690490263756

Haryati, S., Yuliastuti, E. R., Sudiaz, R., Simbolon, H., Eriza, N., Apriyadi, T. E., Dewi, E. K., Baroroh, R. A., Tama, Y. C. P., & Wijaya, R. (2023). *Pedoman Budi Daya Stroberi*. Pertanian Press.

Healey, A., Furtado, A., Cooper, T., & Henry, R. J. (2014). Protocol: a simple

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. *Plant Methods*, *10*(1), 1–8. https://doi.org/10.1186/1746-4811-10-21

Hendre, P. S., Kamalakannan, R., & Varghese, M. (2012). High‐throughput and parallel SNP discovery in selected candidate genes in Eucalyptus camaldulensis using Illumina NGS platform. *Plant Biotechnology Journal*, *10*(6), 646–656. https://doi.org/10.1111/j.1467-7652.2012.00699.x

Hess, J., Kohl, T., Kotrová, M., Rönsch, K., Paprotka, T., Mohr, V., Hutzenlaub, T., Brüggemann, M., Zengerle, R., Niemann, S., & Paust, N. (2020). Library preparation for next generation sequencing: A review of automation strategies. *Biotechnology Advances*, *41*, 1–14. https://doi.org/10.1016/j.biotechadv.2020.107537

Hidaka, K., Dan, K., Imamura, H., Miyoshi, Y., Takayama, T., Sameshima, K., Kitano, M., & Okimura, M. (2013). Effect of Supplemental Lighting from Different Light Sources on Growth and Yield of Strawberry. *Environment Control in Biology*, *51*(1), 41–47. https://doi.org/10.2525/ecb.51.41

Hikmatyar, M. F., Royani, J. I., & Dasumiati. (2015). ISOLASI DAN AMPLIFIKASI DNA KELADI TIKUS (*Thyponium flagelliform*) UNTUK IDENTIFIKASI KERAGAMAN GENETIK. *Jurnal Bioteknologi & Biosains Indonesia (JBBI)*, *2*(2), 42–48. https://doi.org/10.29122/jbbi.v2i2.507

Hiramatsu, K., Matsuda, C., Masago, K., Toriyama, K., Sasaki, E., Fujita, Y., Haneda, M., Ebi, H., Shibata, N., & Hosoda, W. (2023). Diagnostic utility of DNA integrity number as an indicator of sufficient DNA quality in next-generation sequencing–based genomic profiling. *American Journal of Clinical Pathology*, *160*(3), 261–267. https://doi.org/10.1093/ajcp/aqad046

Hu, B., Jin, J., Guo, A., Zhang, H., Luo, J., & Gao, G. (2015). GSDS 2.0: an upgraded gene feature visualization server. *Bioinformatics*, *31*(8), 1296–1297. https://doi.org/10.1093/bioinformatics/btu817

Hu, T., & Banzhaf, W. (2008). Nonsynonymous to Synonymous Substitution Ratio Ka/Ks: Measurement for Rate of Evolution in Evolutionary Computation. In *PPSN X*. https://doi.org/10.1007/978-3-540-87700-4_45

Huang, H., Shi, C., Liu, Y., Mao, S., & Gao, L. (2014). Thirteen *Camellia* chloroplast genome sequences determined by high-throughput sequencing: genome structure and phylogenetic relationships. *BMC Evolutionary Biology*, *14*(1), 1–17. https://doi.org/10.1186/1471-2148-14-151

Huang, X., Coulibaly, D., Tan, W., Ni, Z., Shi, T., Li, H., Hayat, F., & Gao, Z. (2022). The analysis of genetic structure and characteristics of the chloroplast genome in different Japanese apricot germplasm populations. *BMC Plant Biology*, *22*(1), 1–13. https://doi.org/10.1186/s12870-022-03731-5

Hummer, K. E., Bassil, N. V., Zurn, J. D., & Amyotte, B. (2022). Phenotypic characterization of a strawberry (*Fragaria* ×*ananassa* Duchesne ex Rosier) diversity collection. *Plants People Planet*, *5*(2), 209–224. https://doi.org/10.1002/ppp3.10316

Hunter, B., Cromwell, T., & Shim, H. (2025). Nanopore sequencing of protozoa: Decoding biological information on a string of biochemical molecules into human-readable signals. *Computational and Structural Biotechnology*

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
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Journal, *27*, 440–450. https://doi.org/10.1016/j.csbj.2025.01.002

Inouye, M., Takino, R., Ishida, Y., & Inouye, K. (2020). Evolution of the genetic code; Evidence from serine codon use disparity in *Escherichia coli*. *Proceedings of the National Academy of Sciences*, *117*(46), 28572–28575. https://doi.org/10.1073/pnas.2014567117

Isobe, S., Shirasawa, K., & Hirakawa, H. (2020). Advances of Whole Genome Sequencing in Strawberry with NGS Technologies. *The Horticulture Journal*, *89*(2), 108–114. https://doi.org/10.2503/hortj.utd-r012

Jeon, D., Lee, S., Choi, S., Kang, Y., & Kim, C. (2022). Identification of SNPs and Candidate Genes Associated with Salt Stress in Two Korean Sorghum Cultivars and Understanding Selection Pressures in the Breeding Process. *Agronomy*, *12*(10), 1–24. https://doi.org/10.3390/agronomy12102511

Jia, X., Liu, S., Zheng, H., Li, B., Qi, Q., Wei, L., Zhao, T., He, J., & Sun, J. (2015). Non-uniqueness of factors constraint on the codon usage in Bombyx mori. *BMC Genomics*, *16*(1), 1–12. https://doi.org/10.1186/s12864-015-1596-z

Jiajun, L., Yuhua, L., Guodong, D., Hanping, D., & Mingqin, D. (2005). A Natural Pentaploid Strawberry Genotype from the Changbai Mountains in Northeast China. *HortScience*, *40*(5), 1194–1195. https://doi.org/10.21273/hortsci.40.5.1194

Joët, T., Cournac, L., Horvath, E. M., Medgyesy, P., & Peltier, G. (2001). Increased Sensitivity of Photosynthesis to Antimycin A Induced by Inactivation of the Chloroplast *ndhB* Gene. Evidence for a Participation of the NADH-Dehydrogenase Complex to Cyclic Electron Flow around Photosystem I. *PLANT PHYSIOLOGY*, *125*(4), 1919–1929. https://doi.org/10.1104/pp.125.4.1919

Kalendar, R., Ivanov, K. I., Samuilova, O., Kairov, U., & Zamyatnin, A. A. (2023). Isolation of High-Molecular-Weight DNA for Long-Read sequencing using a High-Salt gel electroelution trap. *Analytical Chemistry*, *95*(48), 17818–17825. https://doi.org/10.1021/acs.analchem.3c03894

Kasiamdari, R. S., Aristya, G. R., & Inayati, E. (2017). Phylogenetic Relationships of Nine Cultivars of Strawberries (*Fragaria* spp.) Based on Anatomical and Morphological Characters. *Planta Tropika*, *5*(2), 116–126. https://doi.org/10.18196/pt.2017.072.116-126

Kchouk, M., Gibrat, J. F., & Elloumi, M. (2017). Generations of Sequencing Technologies: From first to Next generation. *Biology and Medicine*, *9*(3), 1–8. https://doi.org/10.4172/0974-8369.1000395

Khetan, D., Gupta, N., Chaudhary, R., & Shukla, J. (2019). Comparison of UV spectrometry and fluorometry-based methods for quantification of cell-free DNA in red cell components. *Asian Journal of Transfusion Science*, *13*(2), 95–99. https://doi.org/10.4103/ajts.ajts_90_19

Kim, J. E., Lee, Y. M., Lee, J., Noh, J. K., Kim, H. C., Park, C., Park, J., & Kim, K. (2014). Development and Validation of Single Nucleotide Polymorphism (SNP) Markers from an Expressed Sequence Tag (EST) Database in Olive Flounder (*Paralichthys olivaceus*). *Development & Reproduction*, *18*(4), 275–286. https://doi.org/10.12717/dr.2014.18.4.275

Krauthammer, M., Rzhetsky, A., Morozov, P., & Friedman, C. (2000). Using BLAST for identifying gene and protein names in journal articles. *Gene*,

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

259(1–2), 245–252. https://doi.org/10.1016/s0378-1119(00)00431-5

Krokidis, M. G., Koumadorakis, D. E., Lazaros, K., Ivantsik, O., Exarchos, T. P., Vrahatis, A. G., Kotsiantis, S., & Vlamos, P. (2025). AlphaFold3: An overview of applications and performance insights. *International Journal of Molecular Sciences*, *26*(8), 1–19. https://doi.org/10.3390/ijms26083671

Laughlin, T. G., Savage, D. F., & Davies, K. M. (2020). Recent advances on the structure and function of NDH-1: The complex I of oxygenic photosynthesis. *Biochimica Et Biophysica Acta (BBA) - Bioenergetics*, *1861*(11), 1–12. https://doi.org/10.1016/j.bbabio.2020.148254

Lee, P. Y., Costumbrado, J., Hsu, C., & Kim, Y. H. (2012). Agarose gel electrophoresis for the separation of DNA fragments. *Journal of Visualized Experiments*, *62*, 1–5. https://doi.org/10.3791/3923

Lehninger, A. L., Nelson, D. L., & Cox, M. M. (2005). *Lehninger Principles of Biochemistry* (4th ed.). Macmillan.

Lei, J., Xue, L., Dai, H., & Deng, M. (2014). The Taxonomy of Chinese Fragaria species. *Acta Horticulturae*, *1049*, 289–294. https://doi.org/10.17660/actahortic.2014.1049.37

Li, C., Cai, C., Tao, Y., Sun, Z., Jiang, M., Chen, L., & Li, J. (2021). Variation and Evolution of the Whole Chloroplast Genomes of *Fragaria* spp. (Rosaceae). *Frontiers in Plant Science*, *12*, 1–14. https://doi.org/10.3389/fpls.2021.754209

Li, W., Wang, L., Zuo, Y., Zhang, H., Zhang, X., Yang, L., Zhang, J., Zheng, F., & Deng, H. (2025). Organelle genomes reveal adaptive evolution and phylogenetic position of the endangered *Primula mallophylla*. *Frontiers in Plant Science*, *16*, 1–16. https://doi.org/10.3389/fpls.2025.1653128

Li, X., Müller-Moulé, P., Gilmore, A. M., & Niyogi, K. K. (2002). *PsbS*-dependent enhancement of feedback de-excitation protects photosystem II from photoinhibition. *Proceedings of the National Academy of Sciences*, *99*(23), 15222–15227. https://doi.org/10.1073/pnas.232447699

Li, X., Yang, J., Wang, H., Song, Y., Corlett, R., Yao, X., Li, D., & Yu, W. (2021). Plastid NDH pseudogenization and gene loss in a recently derived lineage from the largest hemiparasitic plant genus *Pedicularis* (Orobanchaceae) [Dataset]. In *Figshare*. https://doi.org/10.6084/m9.figshare.14633430

Li, Y., Hu, X., Xiao, M., Huang, J., Lou, Y., Hu, F., Fu, X., Li, Y., He, H., & Cheng, J. (2023). An analysis of codon utilization patterns in the chloroplast genomes of three species of *Coffea*. *BMC Genomic Data*, *24*(1), 1–10. https://doi.org/10.1186/s12863-023-01143-4

Lim, T. K. (2012). Fragaria × ananassa. In *Edible Medicinal and Non-Medicinal Plants* (Vol. 4, pp. 395–409). https://doi.org/10.1007/978-94-007-4053-2_47

Liston, A., Cronn, R., & Ashman, T. (2014). *Fragaria*: A genus with deep historical roots and ripe for evolutionary and ecological insights. *American Journal of Botany*, *101*(10), 1686–1699. https://doi.org/10.3732/ajb.1400140

Liu, H., Lyu, W., Tian, S., Zou, X., Zhang, L., Gao, Q., Ni, D., & Duan, K. (2019). The SWEET family genes in strawberry: Identification and expression profiling during fruit development. *South African Journal of Botany*, *125*,

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

176–187. https://doi.org/10.1016/j.sajb.2019.07.002

Liu, L., Li, Y., Li, S., Hu, N., He, Y., Pong, R., Lin, D., Lu, L., & Law, M. (2012). Comparison of Next-Generation sequencing systems. *Journal of Biomedicine and Biotechnology*, *2012*, 1–11. https://doi.org/10.1155/2012/251364

Liu, Q., Li, S., He, D., Liu, J., He, X., Lin, C., Li, J., Huang, Z., Huang, L., Nie, G., Zhang, X., & Feng, G. (2025). Comparative Analysis of Codon Usage Patterns in the Chloroplast Genomes of *Fagopyrum* Species. *Agronomy*, *15*(5), 1–22. https://doi.org/10.3390/agronomy15051190

Liu, X. I., Korde, N., Jakob, U., & Leichert, L. I. (2006). CoSMoS: Conserved Sequence Motif Search in the proteome. *BMC Bioinformatics*, *7*(1), 1–6. https://doi.org/10.1186/1471-2105-7-37

Lu, Y., Li, M., Gao, Z., Ma, H., Chong, Y., Hong, J., Wu, J., Wu, D., Xi, D., & Deng, W. (2025). Advances in whole Genome sequencing: Methods, tools, and applications in population genomics. *International Journal of Molecular Sciences*, *26*(1), 1–18. https://doi.org/10.3390/ijms26010372

Lucena-Aguilar, G., Sánchez-López, A. M., Barberán-Aceituno, C., Carrillo-Ávila, J. A., López-Guerrero, J. A., & Aguilar-Quesada, R. (2016). DNA source selection for downstream applications based on DNA Quality Indicators analysis. *Biopreservation and Biobanking*, *14*(4), 264–270. https://doi.org/10.1089/bio.2015.0064

Luksiyah, Susilowati, D., & Maula, L. R. (2024). ANALISIS PREFERENSI KONSUMEN STROBERI DI AGROWISATA LUMBUNG STROBERI DESA PANDANREJO KECAMATAN BUMIAJI KOTA BATU. *Jurnal Sosial Ekonomi Pertanian Dan Agribisnis*, *12*(7), 1–17.

Ma, M., Liu, Y., Bai, C., & Yong, J. W. H. (2021). The significance of chloroplast NAD(P)H dehydrogenase complex and its dependent cyclic electron transport in photosynthesis. *Frontiers in Plant Science*, *12*, 1–8. https://doi.org/10.3389/fpls.2021.661863

Ma, M., Zhong, M., Zhang, Q., Zhao, W., Wang, M., Luo, C., & Xu, B. (2021). A genome-wide analysis of the chloroplast NADH dehydrogenase-like genes in *Zostera marina*. *Journal of Oceanology and Limnology*, *40*(2), 656–677. https://doi.org/10.1007/s00343-021-0027-z

Maghini, D. G., Moss, E. L., Vance, S. E., & Bhatt, A. S. (2020). Improved high-molecular-weight DNA extraction, nanopore sequencing and metagenomic assembly from the human gut microbiome. *Nature Protocols*, *16*(1), 458–471. https://doi.org/10.1038/s41596-020-00424-x

Mahardika, I. K., Bektiarso, S., Santoso, R. A., Novit, A., Saiylendra, R. B., & Dewi, R. K. (2023). Analisis Peran Suhu pada Pertumbuhan dan Perkembangan Tanaman Stroberi. *PHYDAGOGIC Jurnal Fisika Dan Pembelajarannya*, *5*(2), 86–91. https://doi.org/10.31605/phy.v5i2.2197

Mandlik, J. S., Patil, A. S., & Singh, S. (2024). Next-Generation Sequencing (NGS): Platforms and applications. *Journal of Pharmacy and Bioallied Sciences*, *16*(Suppl 1), S41–S45. https://doi.org/10.4103/jpbs.jpbs_838_23

Mantere, T., Kersten, S., & Hoischen, A. (2019). Long-Read sequencing emerging in medical genetics. *Frontiers in Genetics*, *10*, 1–14. https://doi.org/10.3389/fgene.2019.00426

Mao, J., Wang, Y., Wang, B., Li, J., Zhang, C., Zhang, W., Li, X., Li, J., Zhang, J.,

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã—ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Li, H., & Zhang, Z. (2023). High-quality haplotype-resolved genome assembly of cultivated octoploid strawberry. *Horticulture Research*, *10*(1), 1–12. https://doi.org/10.1093/hr/uhad002

Martiansyah, I., Salim, M. A., Sudrajat, D. J., Primananda, E., Sitepu, B. S., Agustiani, E. L., Yuskianti, V., & Rustam, E. (2025). Characterization of the complete chloroplast genome of *Hopea rudiformis* P.S. Ashton, a critically endangered and endemic tree from Borneo Island. *Forest Science and Technology*, 1–13. https://doi.org/10.1080/21580103.2025.2558649

Martín, M., Funk, H. T., Serrot, P. H., Poltnigg, P., & Sabater, B. (2009). Functional characterization of the thylakoid Ndh complex phosphorylation by site-directed mutations in the *ndhF* gene. *Biochimica Et Biophysica Acta (BBA) - Bioenergetics*, *1787*(7), 920–928. https://doi.org/10.1016/j.bbabio.2009.03.001

Maździarz, M., Zając, S., Paukszto, Ł., & Sawicki, J. (2025). RSCUcaller: an R package for analyzing differences in relative synonymous codon usage (RSCU). *BMC Bioinformatics*, *26*(1), 1–12. https://doi.org/10.1186/s12859-025-06166-5

Mazumdar, P., Othman, R. B., Mebus, K., Ramakrishnan, N., & Harikrishna, J. A. (2017). Codon usage and codon pair patterns in non-grass monocot genomes. *Annals of Botany*, *120*(6), 893–909. https://doi.org/10.1093/aob/mcx112

Mi, H., Endo, T., Ogawa, T., & Asada, K. (1995). Thylakoid Membrane-Bound, NADPH-Specific Pyridine Nucleotide Dehydrogenase Complex Mediates Cyclic Electron Transport in the Cyanobacterium *Synechocystis* sp. PCC 6803. *Plant and Cell Physiology,* *36*(4), 661–668 https://doi.org/10.1093/oxfordjournals.pcp.a078807

Mi, X., Wang, X., Wu, H., Gan, L., Ding, J., & Li, Y. (2017). Characterization and expression analysis of cytokinin biosynthesis genes in *Fragaria vesca*. *Plant Growth Regulation*, *82*(1), 139–149. https://doi.org/10.1007/s10725-016-0246-z

Mollah, A., Ashan, M. A., & Khatimah, A. H. (2022). Uji Kualitas dan Kuantitas DNA Porang (*Amorphophallus muelleri* Blume) pada Beberapa Kawasan di Sulawesi Selatan. *Jurnal Agritechno*, 1–7. https://doi.org/10.20956/at.v15i1.688

Moreira, P., & Oliveira, D. (2011). Leaf age affects the quality of DNA extracted from cons*Dimorphandra mollis* (Fabaceae), a tropical tree species from the Cerrado region of Brazil. *Genetics and Molecular Research*, *10*(1), 353–358. https://doi.org/10.4238/vol10-1gmr1030

Morra, M., Marradi, D., Gandini, L., Ivagnes, V., Ottolini, G., Bovio, A., Jabali, G., Maraschi, L., Dada, I. A., Chawanda, T. V., Gorla, M., Tarasiuk, O., Mocchetti, C., Soluri, M. F., Boccafoschi, F., Sblattero, D., & Cotella, D. (2025). A non-hypothesis-driven practical laboratory activity on functional metagenomics: “fishing” protein-coding DNA sequences from microbiomes. *Frontiers in Bioengineering and Biotechnology*, *13*, 1–9. https://doi.org/10.3389/fbioe.2025.1602982

Moss, E. H. (1983). *Flora of Alberta: A Manual of Flowering Plants, Conifers, Ferns, and Fern Allies Found Growing Without Cultivation in the Province of Alberta, Canada*. University of Toronto Press.

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Munekage, Y., Hashimoto, M., Miyake, C., Tomizawa, K., Endo, T., Tasaka, M., & Shikanai, T. (2004). Cyclic electron flow around photosystem I is essential for photosynthesis. *Nature*, *429*(6991), 579–582. https://doi.org/10.1038/nature02598

Naidoo, A. L. K., Martin, D. P., & Heathfield, L. J. (2025). Establishment of performance parameters for the Qubit™ 1X dsDNA HS Assay for use in forensic genetics casework. *Forensic Science International Reports*, *11*, 1–7. https://doi.org/10.1016/j.fsir.2025.100405

Nakayama, Y., Yamaguchi, H., Einaga, N., & Esumi, M. (2016). Pitfalls of DNA quantification using DNA-Binding fluorescent dyes and suggested solutions. *PLoS ONE*, *11*(3), 1–12. https://doi.org/10.1371/journal.pone.0150528

Napieralski, A., & Nowak, R. (2022). Basecalling using joint raw and event nanopore data Sequence-to-Sequence processing. *Sensors*, *22*(6), 1–14. https://doi.org/10.3390/s22062275

Needleman, S. B., & Wunsch, C. D. (1970). A general method applicable to the search for similarities in the amino acid sequence of two proteins. *Journal of Molecular Biology*, *48*(3), 443–453. https://doi.org/10.1016/0022-2836(70)90057-4

Negi, S., Stenton, S. L., Berger, S. I., Canigiula, P., McNulty, B., Violich, I., Gardner, J., Hillaker, T., O'Rourke, S. M., O'Leary, M. C., Carbonell, E., Austin-Tse, C., Lemire, G., Serrano, J., Mangilog, B., VanNoy, G., Kolmogorov, M., Vilain, E., O'Donnell-Luria, A., Délot, E., Miga, K. H., Monlong, J., & Paten, B. (2025). Advancing long-read nanopore genome assembly and accurate variant calling for rare disease detection. *The American Journal of Human Genetics*, *112*(2), 428–449. https://doi.org/10.1016/j.ajhg.2025.01.002

Nei, M., & Gojobori, T. (1986). Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. *Molecular Biology and Evolution*, *3*(5), 418–426. https://doi.org/10.1093/oxfordjournals.molbev.a040410

Newell, P. D., Fricker, A. D., Roco, C. A., Chandrangsu, P., & Merkel, S. M. (2013). A Small-Group activity introducing the use and interpretation of BLAST. *Journal of Microbiology and Biology Education*, *14*(2), 238–243. https://doi.org/10.1128/jmbe.v14i2.637

Njuguna, W., & Bassil, N. (2011). DNA BARCODING: UNSUCCESSFUL FOR SPECIES IDENTIFICATION IN FRAGARIA L. *Acta Horticulturae*, *918*, 349–356. https://doi.org/10.17660/actahortic.2011.918.45

Nofiyanti, S. H., Setiyo, Y., Muna, M. S., Wirawan, I. P. S., & Yosika, N. I. W. (2025). Analisis Produktivitas dan Kualitas Buah Stoberi var Sujarli (Rosalinda) Berdasarkan Model Budidaya dan Pengolahan Citra Digital. *Jurnal Ilmiah Rekayasa Pertanian Dan Biosistem*, *13*(2), 165–180. https://doi.org/10.29303/jrpb.v13i2.1187

Noviyanti, R., Yuliani, Ratnasari, E., & Ashari, H. (2014). Pengaruh Pemberian Naungan terhadap Pertumbuhan Vegetatif Tanaman Stroberi Varietas Dorit dan Varietas Lokal Berastagi. *LenteraBio Berkala Ilmiah Biologi*, *3*(3), 242–247. https://ejournal.unesa.ac.id/index.php/lenterabio/article/view/9622

Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa
(Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Nugroho, A. S., Dewi, E. R. S., & Ulfah, M. (2023). Adaptation of Four Strawberry Varieties at a Land Altitude of 900 Meters ASL with Different Shade. *BIOMA Jurnal Ilmiah Biologi*, *12*(2), 1–9. https://doi.org/10.26877/bioma.v12i2.16525

Nunes, C. F., Ferreira, J. L., Fernandes, M. C. N., De Souza Breves, S., Generoso, A. L., Soares, B. D. F., Dias, M. S. C., Pasqual, M., Borem, A., & De Almeida Cançado, G. M. (2011). An improved method for genomic DNA extraction from strawberry leaves. *Ciência Rural*, *41*(8), 1383–1389. https://doi.org/10.1590/s0103-84782011000800014

Ohyama, K., Fukuzawa, H., Kohchi, T., Shirai, H., Sano, T., Sano, S., Umesono, K., Shiki, Y., Takeuchi, M., Chang, Z., Aota, S., Inokuchi, H., & Ozeki, H. (1986). Chloroplast gene organization deduced from complete sequence of liverwort Marchantia polymorpha chloroplast DNA. *Nature*, *322*(6079), 572–574. https://doi.org/10.1038/322572a0

Orde, K., & Sideman, B. (2023). *Strawberry Production Guide for the Northeast, Midwest, and Eastern Canada.* (2nd ed.). University of New Hampshire Cooperative Extension.

Pan, W., Yan, W., Li, Z., Wu, Z., Tian, Q., De, Y., Wu, C., & Yan, W. (2026). Analysis of chloroplast genomes and SSR classification and identification of *Agropyron* species and closely related species. *Scientific Reports*, *16*(1), 1–16. https://doi.org/10.1038/s41598-025-33570-x

Paradis, N. J., & Wu, C. (2024). Enhanced detection and molecular modeling of adaptive mutations in SARS-CoV-2 coding and non-coding regions using the c/μ test. *Virus Evolution*, *10*(1), 1–16. https://doi.org/10.1093/ve/veae089

Parvathy, S. T., Udayasuriyan, V., & Bhadana, V. (2022). Codon usage bias. *Molecular Biology Reports*, *49*(1), 539–565. https://doi.org/10.1007/s11033-021-06749-4

Payne, A., Holmes, N., Rakyan, V., & Loose, M. (2019). BulkVis: a graphical viewer for Oxford nanopore bulk FAST5 files. *Bioinformatics*, *35*(13), 2193–2198. https://doi.org/10.1093/bioinformatics/bty841

Peltier, G., & Cournac, L. (2002). CHLORORESPIRATION. *Annual Review of Plant Biology*, *53*(1), 523–550. https://doi.org/10.1146/annurev.arplant.53.100301.135242

Peng, L., & Shikanai, T. (2011). Supercomplex Formation with Photosystem I Is Required for the Stabilization of the Chloroplast NADH Dehydrogenase-Like Complex in *Arabidopsis*. *PLANT PHYSIOLOGY*, *155*(4), 1629–1639. https://doi.org/10.1104/pp.110.171264

Peredo, E. L., King, U. M., & Les, D. H. (2013). The Plastid Genome of *Najas flexilis*: Adaptation to Submersed Environments Is Accompanied by the Complete Loss of the NDH Complex in an Aquatic Angiosperm. *PLoS ONE*, *8*(7), e68591. https://doi.org/10.1371/journal.pone.0068591

Pillai, S., Gopalan, V., & Lam, A. K. (2017). Review of sequencing platforms and their applications in phaeochromocytoma and paragangliomas. *Critical Reviews in Oncology/Hematology*, *116*, 58–67. https://doi.org/10.1016/j.critrevonc.2017.05.005

Potter, D., Luby, J. J., & Harrison, R. E. (2000). Phylogenetic Relationships among Species of *Fragaria* (Rosaceae) Inferred from Non-Coding Nuclear

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

and Chloroplast DNA Sequences. *Systematic Botany*, *25*(2), 337–348. https://doi.org/10.2307/2666646

Pribil, M., Labs, M., & Leister, D. (2014). Structure and dynamics of thylakoids in land plants. *Journal of Experimental Botany*, *65*(8), 1955–1972. https://doi.org/10.1093/jxb/eru090

Psifidi, A., Dovas, C. I., Bramis, G., Lazou, T., Russel, C. L., Arsenos, G., & Banos, G. (2015). Comparison of eleven methods for genomic DNA extraction suitable for Large-Scale Whole-Genome genotyping and Long-Term DNA banking using blood samples. *PLoS ONE*, *10*(1), 1–18. https://doi.org/10.1371/journal.pone.0115960

Qi, J., Liu, X., Shen, D., Miao, H., Xie, B., Li, X., Zeng, P., Wang, S., Shang, Y., Gu, X., Du, Y., Li, Y., Lin, T., Yuan, J., Yang, X., Chen, J., Chen, H., Xiong, X., Huang, K., Fei, Z., Mao, L., Tian, L., Städler, T., Renner, S. S., Kamoun, S., Lucas, W. J., Zhang, Z., & Huang, S. (2013). A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. *Nature Genetics*, *45*(12), 1510–1515. https://doi.org/10.1038/ng.2801

Quiles, M. J. (2006). Stimulation of chlororespiration by heat and high light intensity in oat plants. *Plant Cell & Environment*, *29*(8), 1463–1470. https://doi.org/10.1111/j.1365-3040.2006.01510.x

Ramdhanawati, V. U., Octaviani, W. T., & Supriyatna, A. (2023). Inventarisasi dan Identifikasi Famili Rosaceae di Sekitar Kawasan Farm House Lembang. *International Journal of Engineering, Economic, Social Politic and Government*, *1*(3), 29–35

Rantala, S., Lempiäinen, T., Gerotto, C., Tiwari, A., Aro, E., & Tikkanen, M. (2020). PGR5 and NDH-1 systems do not function as protective electron acceptors but mitigate the consequences of PSI inhibition. *Biochimica Et Biophysica Acta (BBA) - Bioenergetics*, *1861*(3), 1–14. https://doi.org/10.1016/j.bbabio.2020.148154

Ratiu, A. C., Ionascu, A., & Constantin, N. D. (2024). The Impact of Oxford Nanopore Technologies Based Methodologies on the Genome Sequencing and Assembly of Romanian Strains of *Drosophila suzukii*. *Insects*, *16*(1), 1–24. https://doi.org/10.3390/insects16010002

Roberts, R. J., Carneiro, M. O., & Schatz, M. C. (2013). The advantages of SMRT sequencing. *Genome Biology*, *14*(6), 1–4. https://doi.org/10.1186/gb-2013-14-6-405

Romiyadi, & Putri, N. I. (2024). Uji Pertumbuhan dan Hasil Berbagai Varietas Tanaman Stroberi (*Fragaria* sp.) di Dataran Rendah. *Journal Greenation Pertanian Dan Perkebunan*, *2*(2), 51–59. https://doi.org/10.38035/jgpp.v2i2.180

Rozas, J. (2009). DNA Sequence Polymorphism Analysis using DNASP. *Methods in Molecular Biology*, *537*, 337–350. https://doi.org/10.1007/978-1-59745-251-9_17

Rozas, J., & Rozas, R. (1995). DnaSP, DNA sequence polymorphism: an interactive program for estimating population genetics parameters from DNA sequence data. *Computer Applications in the Biosciences*, *11*(6), 621–625. https://doi.org/10.1093/bioinformatics/11.6.621

Russo, A., Mayjonade, B., Frei, D., Potente, G., Kellenberger, R. T., Frachon, L.,

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Copetti, D., Studer, B., Frey, J. E., Grossniklaus, U., & Schlüter, P. M. (2022). Low-Input High-Molecular-Weight DNA extraction for Long-Read sequencing from plants of diverse families. *Frontiers in Plant Science*, *13*, 1–12. https://doi.org/10.3389/fpls.2022.883897

Sabater, B. (2021). On the Edge of Dispensability, the Chloroplast *ndh* Genes. *International Journal of Molecular Sciences*, *22*(22), 1–13. https://doi.org/10.3390/ijms222212505

Saepurohman, A., & Afriyadi, R. (2023). Strategi Pemasaran Stroberi pada Agrowisata Rizky Strawberry Cinumpang Kabupaten Sukabumi. In *Prosiding SEMNASTERA (Seminar Nasional Teknologi dan Riset Terapan)*.

Salamone, I., Govindarajulu, R., Falk, S., Parks, M., Liston, A., & Ashman, T. (2013). Bioclimatic, ecological, and phenotypic intermediacy and high genetic admixture in a natural hybrid of octoploid strawberries. *American Journal of Botany*, *100*(5), 939–950. https://doi.org/10.3732/ajb.1200624

Salisbury, F. B., & Ross, C. W. (1992). *Plant physiology*. Cengage Learning.

Satam, H., Joshi, K., Mangrolia, U., Waghoo, S., Zaidi, G., Rawool, S., Thakare, R. P., Banday, S., Mishra, A. K., Das, G., & Malonia, S. K. (2023). Next-Generation Sequencing Technology: Current trends and advancements. *Biology*, *12*(7), 1–25. https://doi.org/10.3390/biology12070997

Sato, S. (1999). Complete Structure of the Chloroplast Genome of Arabidopsis thaliana. *DNA Research*, *6*(5), 283–290. https://doi.org/10.1093/dnares/6.5.283

Seeram, N. P., Adams, L. S., Zhang, Y., Lee, R., Sand, D., Scheuller, H. S., & Heber, D. (2006). Blackberry, black raspberry, blueberry, cranberry, red raspberry, and strawberry extracts inhibit growth and stimulate apoptosis of human cancer cells in vitro. *Journal of Agricultural and Food Chemistry*, *54*(25), 9329–9339. https://doi.org/10.1021/jf061750g

Seki, M., Katsumata, E., Suzuki, A., Sereewattanawoot, S., Sakamoto, Y., Mizushima-Sugano, J., Sugano, S., Kohno, T., Frith, M. C., Tsuchihara, K., & Suzuki, Y. (2019). Evaluation and application of RNA-Seq by MinION. *DNA Research*, *26*(1), 55–65. https://doi.org/10.1093/dnares/dsy038

Sembada, A. A., Faizal, A., & Sulistyawati, E. (2024). Photosynthesis efficiency as key factor in decision-making for forest design and redesign: A systematic literature review. *Ecological Frontiers*, *44*(6), 1128–1139. https://doi.org/10.1016/j.ecofro.2024.07.008

Senewe, R. W., Loho, A. E., & Sondakh, M. L. (2016). FAKTOR PENUNJANG DAN PENGHAMBAT AGRIBISNIS BUAH STROBERI DI KELURAHAN RURUKAN DAN RURUKAN SATU, KECAMATAN TOMOHON TIMUR, KOTA TOMOHON. *AGRI-SOSIOEKONOMI*, *12*(3A), 95–104. https://doi.org/10.35791/agrsosek.12.3a.2016.14339

Sharma, R. M., Yamdagni, R., Dubey, A. K., & Pandey, V. (2019). *Strawberries: Production, Postharvest Management and Protection*. CRC Press.

Sherman, W., & Beckman, T. (2003). Climatic Adaptation in Fruit Crops. *Acta Horticulturae*, *622*, 411–428. https://doi.org/10.17660/actahortic.2003.622.43

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã—ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Shikanai, T. (2016). Chloroplast NDH: A different enzyme with a structure similar to that of respiratory NADH dehydrogenase. *Biochimica Et Biophysica Acta (BBA) - Bioenergetics*, *1857*(7), 1015–1022. https://doi.org/10.1016/j.bbabio.2015.10.013

Shikanai, T. (2022). The supercomplex formation between the chloroplast NADH dehydrogenase-like complex and photosystem I. *Molecular Plant*, *15*(4), 589–590. https://doi.org/10.1016/j.molp.2022.03.007

Shinozaki, K., Ohme, M., Tanaka, M., Wakasugi, T., Hayashida, N., Matsubayashi, T., Zaita, N., Chunwongse, J., Obokata, J., Yamaguchi-Shinozaki, K., Ohto, C., Torazawa, K., Meng, B., Sugita, M., Deno, H., Kamogashira, T., Yamada, K., Kusuda, J., Takaiwa, F., Kato, A., Tohdoh, N., Shimada, H., & Sugiura, M. (1986). The complete nucleotide sequence of the tobacco chloroplast genome: its gene organization and expression. *The EMBO Journal*, *5*(9), 2043–2049. https://doi.org/10.1002/j.1460-2075.1986.tb04464.x

Shulaev, V., Sargent, D. J., Crowhurst, R. N., Mockler, T. C., Folkerts, O., Delcher, A. L., Jaiswal, P., Mockaitis, K., Liston, A., Mane, S. P., Burns, P., Davis, T. M., Slovin, J. P., Bassil, N., Hellens, R. P., Evans, C., Harkins, T., Kodira, C., Desany, B., Crasta, O. R., Jensen, R. V., Allan, A. C., Michael, T. P., Setubal, J. C., Celton, J.-M., Rees, D. J. G., Williams, K. P., Holt, S. H., Ruiz, J. J. R., Chatterjee, M., Liu, B., Silva, H., Meisel, L., Adato, A., Filichkin, S. A., Troggio, M., Viola, R., Ashman, T.-L., Wang, H., Dharmawardhana, P., Elser, J., Raja, R., Priest, H. D., Bryant Jr., D. W., Fox, S. E., Givan, S. A., Wilhelm, L. J., Naithani, S., Christoffels, A., Salama, D. Y., Carter, J., Girona, E. L., Zdepski, A., Wang, W., Kerstetter, R. A., Schwab, W., Korban, S. S., Davik, J., Monfort, A., Denoyes-Rothan, B., Arus, P., Mittler, R., Flinn, B., Aharoni, A., Bennetzen, J. L., Salzberg, S. L., Dickerman, A. W., Velasco, R., Borodovsky, M., Veilleux, R. E., & Folta, K. M. (2011). The genome of woodland strawberry (*Fragaria vesca*). *Nature Genetics*, *43*(2), 109–116. https://doi.org/10.1038/ng.740

Simbolo, M., Gottardi, M., Corbo, V., Fassan, M., Mafficini, A., Malpeli, G., Lawlor, R. T., & Scarpa, A. (2013). DNA qualification workflow for next generation sequencing of histopathological samples. *PLoS ONE*, *8*(6), 1–8. https://doi.org/10.1371/journal.pone.0062692

Song, Y., Li, C., Liu, L., Hu, P., Li, G., Zhao, X., & Zhou, H. (2023). The population genomic analyses of chloroplast genomes shed new insights on the complicated ploidy and evolutionary history in Fragaria. *Frontiers in Plant Science*, *13*, 1–11. https://doi.org/10.3389/fpls.2022.1065218

Staudt, G. (1989). The Species of *Fragaria*, Their Taxonomy and Geographical Distribution. *Acta Horticulturae*, *265*, 23–34. https://doi.org/10.17660/actahortic.1989.265.1

Staudt, G. (2009). Strawberry Biogeography, Genetics and Systematic. *Acta Horticulturae*, *842*, 71–84. https://doi.org/10.17660/actahortic.2009.842.1

Staudt, G., & Olbricht, K. (2008). Notes on Asiatic *Fragaria* species V: *F. nipponica* and *F. iturupensis*. *Botanische Jahrbücher*, *127*(3), 317–341. https://doi.org/10.1127/0006-8152/2008/0127-0317

Sun, S., Yi, J., Gu, P., Huang, Y., Huang, X., Li, H., Li, H., Fan, T., Zhao, J.,

UNIVERSITAS
GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Wang, R., Gaballah, M. M., Xiao, L., Li, H., & Li, H. (2025). Comprehensive characterization and functional analysis of the lateral organ boundaries domain gene family in Rice: evolution, expression, and stress response. *International Journal of Molecular Sciences*, *26*(9), 1–22. https://doi.org/10.3390/ijms26093948

Supek, F. (2016). The code of silence: widespread associations between synonymous Codon biases and gene function. *Journal of Molecular Evolution*, *82*(1), 65–73. https://doi.org/10.1007/s00239-015-9714-8

Surya, W., Goh, J., Ponniah, C., & Torres, J. (2025). AlphaFold prediction of Protein–Protein interactions in the flaviviridae proteomes. *International Journal of Molecular Sciences*, *26*(20), 1–19. https://doi.org/10.3390/ijms262010159

Takahashi, A., Yasutake, D., Hidaka, K., Ono, S., Kitano, M., Hirota, T., Yokoyama, G., Nakamura, T., & Toro, M. (2024). Yield and Photosynthesis Related to Growth Forms of Two Strawberry Cultivars in a Plant Factory with Artificial Lighting. *HortScience*, *59*(3), 394–399. https://doi.org/10.21273/hortsci17587-23

Tamura, K., Stecher, G., & Kumar, S. (2021). MEGA11: Molecular Evolutionary Genetics Analysis Version 11. *Molecular Biology and Evolution*, *38*(7), 3022–3027. https://doi.org/10.1093/molbev/msab120

Thudi, M., Li, Y., Jackson, S. A., May, G. D., & Varshney, R. K. (2012). Current state-of-art of sequencing technologies for plant genomics research. *Briefings in Functional Genomics*, *11*(1), 3–11. https://doi.org/10.1093/bfgp/elr045

Tillich, M., Lehwark, P., Pellizzer, T., Ulbricht-Jones, E. S., Fischer, A., Bock, R., & Greiner, S. (2017). GeSeq – versatile and accurate annotation of organelle genomes. *Nucleic Acids Research*, *45*(W1), W6–W11. https://doi.org/10.1093/nar/gkx391

Trisolini, L., Gambacorta, N., Gorgoglione, R., Montaruli, M., Laera, L., Colella, F., Volpicella, M., De Grassi, A., & Pierri, C. L. (2019). FAD/NADH dependent oxidoreductases: from different amino acid sequences to similar protein shapes for playing an ancient function. *Journal of Clinical Medicine*, *8*(12), 1–29. https://doi.org/10.3390/jcm8122117

Vaser, R., & Šikić, M. (2021). Time- and memory-efficient genome assembly with Raven. *Nature Computational Science*, *1*(5), 332–336. https://doi.org/10.1038/s43588-021-00073-4

Vaser, R., Sović, I., Nagarajan, N., & Šikić, M. (2017). Fast and accurate de novo genome assembly from long uncorrected reads. *Genome Research*, *27*(5), 737–746. https://doi.org/10.1101/gr.214270.116

Voet, D., Voet, J. G., & Charlotte, W. P. (2014). *Fundamental of biochemistry: Life at the molecular level* (4th ed.). John Wiley & Sons, Inc.

Von Loetzen, C. S., Schweimer, K., Schwab, W., Rösch, P., & Hartl-Spiegelhauer, O. (2012). Solution structure of the strawberry allergen Fra a 1. *Bioscience Reports*, *32*(6), 567–575. https://doi.org/10.1042/bsr20120058

Wang, C., Yamamoto, H., & Shikanai, T. (2015). Role of cyclic electron transport around photosystem I in regulating proton motive force. *Biochimica Et Biophysica Acta (BBA) - Bioenergetics*, *1847*(9), 931–938. https://doi.org/10.1016/j.bbabio.2014.11.013

UNIVERSITAS GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Wang, J., Yang, C., & Tseng, C. (2010). Reconstruction of Protein Backbone with the α-Carbon Coordinates. *Journal of Information Science and Engineering*, *26*(3), 1107–1119. https://doi.org/10.6688/jise.2010.26.3.23

Wang, P., Duan, W., Takabayashi, A., Endo, T., Shikanai, T., Ye, J., & Mi, H. (2006). Chloroplastic NAD(P)H dehydrogenase in tobacco leaves functions in alleviation of oxidative damage caused by temperature stress. *PLANT PHYSIOLOGY*, *141*(2), 465–474. https://doi.org/10.1104/pp.105.070490

Wang, W., Liang, L., Dai, Z., Zuo, P., Yu, S., Lu, Y., Ding, D., Chen, H., Shan, H., Jin, Y., Mao, Y., & Yin, Y. (2024). A conserved N-terminal motif of CUL3 contributes to assembly and E3 ligase activity of CRL3KLHL22. *Nature Communications*, *15*(1), 1–14. https://doi.org/10.1038/s41467-024-48045-2

Wang, Y., Zhao, Y., Bollas, A., Wang, Y., & Au, K. F. (2021). Nanopore sequencing technology, bioinformatics and applications. *Nature Biotechnology*, *39*(11), 1348–1365. https://doi.org/10.1038/s41587-021-01108-x

Wang, Z., Cai, Q., Wang, Y., Li, M., Wang, C., Wang, Z., Jiao, C., Xu, C., Wang, H., & Zhang, Z. (2022). Comparative analysis of Codon bias in the chloroplast genomes of Theaceae species. *Frontiers in Genetics*, *13*, 1–20. https://doi.org/10.3389/fgene.2022.824610

Wankhede, D. P., Aravind, J., & Mishra, S. P. (2019). Identification of Genic SNPs from ESTs and Effect of Non-synonymous SNP on Proteins in Pigeonpea. *Proceedings of the National Academy of Sciences India Section B Biological Sciences*, *89*(2), 595–603. https://doi.org/10.1007/s40011-018-0973-1

Waswa, E. N., Mkala, E. M., Odago, W. O., Amenu, S. G., Mutinda, E. S., Muthui, S. W., Ding, S., Hu, G., & Wang, Q. (2023). Comparative chloroplast genome analysis of *Sambucus* L. (Viburnaceae): inference for phylogenetic relationships among the closely related *Sambucus adnata* Wall. ex DC *Sambucus javanica* Blume. *Frontiers in Plant Science*, *14*, 1–18. https://doi.org/10.3389/fpls.2023.1179510

Wee, J., & Wei, G. (2024). Evaluation of AlphaFold 3's Protein–Protein Complexes for Predicting Binding Free Energy Changes upon Mutation. *Journal of Chemical Information and Modeling*, *64*(16), 6676–6683. https://doi.org/10.1021/acs.jcim.4c00976

Wen, H., Wang, L., Gong, Y., Zhang, Y., Zhao, T., Feng, C., Wang, J., & Lin, J. (2024). Genome-Wide Identification and Characterization of GRAS Transcription Factor Family in Cultivated Hybrid Sugarcane ZZ1 (*Saccharum officinarum*) and Their Role in Development and Stress. *International Journal of Molecular Sciences*, *25*(24), 1–17. https://doi.org/10.3390/ijms252413470

Wennmann, J. T. (2024). Nanopore reads spanning the whole genome of arthropod-infecting large dsDNA viruses of the class Naldaviricetes enable assembly-free sequence analysis. *Journal of Invertebrate Pathology*, *209*, 1–10. https://doi.org/10.1016/j.jip.2025.108277

Whitaker, V. M., Knapp, S. J., Hardigan, M. A., Edger, P. P., Slovin, J. P., Bassil, N. V., Hytönen, T., Mackenzie, K. K., Lee, S., Jung, S., Main, D., Barbey,

UNIVERSITAS GADJAH MADA
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Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

C. R., & Verma, S. (2020). A roadmap for research in octoploid strawberry. *Horticulture Research*, *7*(1), 1–17. https://doi.org/10.1038/s41438-020-0252-1

Wijayanti, I. K. E., Jamhari, J., Dwidjono, H. D., & Suryantini, A. (2020). Stochastic Frontier Analysis on Technical Efficiency of strawberry farming in Purbalingga Regency Indonesia. *Jurnal Teknosains*, *9*(2), 105–115. https://doi.org/10.22146/teknosains.40944

Yamamoto, H., Peng, L., Fukao, Y., & Shikanai, T. (2011). An SRC homology 3 Domain-Like fold protein forms a ferredoxin binding site for the chloroplast NADH Dehydrogenase-Like complex in Arabidopsis. *The Plant Cell*, *23*(4), 1480–1493. https://doi.org/10.1105/tpc.110.080291

Yamori, W., Shikanai, T., & Makino, A. (2015). Correction: Corrigendum: Photosystem I cyclic electron flow via chloroplast NADH dehydrogenase-like complex performs a physiological role for photosynthesis at low light. *Scientific Reports*, *5*(1), 15593. https://doi.org/10.1038/srep15593

Yan, M., Dong, S., Gong, Q., Xu, Q., & Ge, Y. (2023). Comparative chloroplast genome analysis of four *Polygonatum* species insights into DNA barcoding, evolution, and phylogeny. *Scientific Reports*, *13*(1), 1–23. https://doi.org/10.1038/s41598-023-43638-1

Yang, J., Wei, S., Su, D., Chen, S., Luo, Z., Xue-Mei, S., Arslan, J., JiangYun, T., & Cui, X. (2020). Molecular identification and evolutionary characteristics of *Fragaria nilgerrensis* in Yunnan based on nrDNA ITS and cpDNA *psbA-trnH* sequence analysis. *Nanfang Nongye Xuebao*, *51*(4), 748–757. https://www.cabdirect.org/cabdirect/abstract/20203238507

Yang, S., Gill, R. A., Zaman, Q. U., Ulhassan, Z., & Zhou, W. (2020). Insights on SNP types, detection methods and their utilization in *Brassica* species: Recent progress and future perspectives. *Journal of Biotechnology*, *324*, 11–20. https://doi.org/10.1016/j.jbiotec.2020.09.018

Ye, J., Cui, C., Fan, R., & Cui, Q. (2024). Estimating the selection pressure and evolutionary rate of proteins on the non-neutral hypothesis of synonymous mutations. *bioRxiv (Cold Spring Harbor Laboratory)*. https://doi.org/10.1101/2024.04.14.589335

Zerpa-Catanho, D., Zhang, X., Song, J., Hernandez, A. G., & Ming, R. (2021). Ultra-long DNA molecule isolation from plant nuclei for ultra-long read genome sequencing. *STAR Protocols*, *2*(1), 1–17. https://doi.org/10.1016/j.xpro.2021.100343

Zhang, B., Gao, Y., Zhang, L., & Zhou, Y. (2021). The plant cell wall: Biosynthesis, construction, and functions. *Journal of Integrative Plant Biology*, *63*(1), 251–272. https://doi.org/10.1111/jipb.13055

Zhang, C., Li, W., Wu, Y., Li, S., Hua, B., & Sun, H. (2025). Chloroplast Functionality at the Interface of Growth, Defense, and Genetic Innovation: A Multi-Omics and Technological Perspective. *Plants*, *14*(6), 1–35. https://doi.org/10.3390/plants14060978

Zhang, Y., Ma, Y., Gao, J., & Yu, T. (2025). Deciphering codon usage patterns in six *Quercus* genome. *Discover Applied Sciences*, *8*(1), 1–13. https://doi.org/10.1007/s42452-025-07917-y

Zhang, Z. (2022). KAKS_Calculator 3.0: Calculating Selective Pressure on

UNIVERSITAS
GADJAH MADA
Karakterisasi Gen ndh Penyandi Kompleks NADH Dehydrogenase-like pada Stroberi (Fragaria Ã— ananassa (Weston) Duchesne â€˜Mencirâ€™) Berdasarkan Complete Chloroplast Genome
Tan Rendy, Ganies Riza Aristya, S.Si., M.Sc., Ph.D.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

Coding and Non-Coding sequences. *Genomics Proteomics & Bioinformatics*, *20*(3), 536–540. https://doi.org/10.1016/j.gpb.2021.12.002

Zheng, H., Peng, G., Zhao, L., Dai, W., Xu, M., Xu, X., & Tang, M. (2025). Comparative and evolutionary analysis of chloroplast genomes from five rare *Styrax* species. *BMC Genomics*, *26*(1), 1–15. https://doi.org/10.1186/s12864-025-11629-3