

## DAFTAR PUSTAKA

- Abdurakhmonov, I. Y., & Abdulkarimov, A. 2008. Application of association mapping to understanding the genetic diversity of plant germplasm resources. *International journal of plant genomics*, 2008(1), 574927.
- Abebe, A. T., Kolawole, A. O., Unachukwu, N., Chigeza, G., Tefera, H., & Gedil, M. 2021. Assessment of diversity in tropical soybean (*Glycine max* (L.) Merr.) varieties and elite breeding lines using single nucleotide polymorphism markers. *Plant Genetic Resources*, 19(1), 20-28.
- Athanasopoulou, K., Boti, M. A., Adamopoulos, P. G., Skourou, P. C., & Scorilas, A. 2021. Third-generation sequencing: the spearhead towards the radical transformation of modern genomics. *Life*, 12(1), 30.
- Baziad, A. 2007. Polimorfisme sebagai suatu uji genetik: Sebuah tinjauan kritis. *Indonesian Journal of Obstetrics and Gynecology*.
- Behjati, S., & Tarpey, P. S. 2013. What is next generation sequencing. *Archives of Disease in Childhood-Education and Practice*, 98(6), 236-238.
- Bhat, J. A., Adeboye, K. A., Ganie, S. A., Barmukh, R., Hu, D., Varshney, R. K., & Yu, D. 2022. Genome-wide association study, haplotype analysis, and genomic prediction reveal the genetic basis of yield-related traits in soybean (*Glycine max* L.). *Frontiers in genetics*, 13, 953833.
- Bourrat, P. 2020. Causation and single nucleotide polymorphism heritability. *Philosophy of Science*, 87(5), 1073-1083.
- Carpentieri-Pipolo, V., Almeida, L. A. D., Kiihl, R. A. D. S., & Pagliosa, E. S. 2014. Inheritance of late flowering in natural variants of soybean cultivars under short-day conditions. *Pesquisa Agropecuária Brasileira*, 49(10), 796-803.
- Casci, T. 2010. SNPs that come in threes. *Nature Reviews Genetics*, 11(1), 8-8.
- Contreras-Soto, R. I., de Oliveira, M. B., Costenaro-da-Silva, D., Scapim, C. A., & Schuster, I. 2017. Population structure, genetic relatedness and linkage disequilibrium blocks in cultivars of tropical soybean (*Glycine max*). *Euphytica*, 213(8), 173.
- Doo, M., & Kim, Y. 2015. Obesity: interactions of genome and nutrients intake. *Preventive Nutrition and Food Science*, 20(1), 1.

- Astuti, K., Ramdhani, D. M., Khasanah, N. I. 2023. *Analisis Produktivitas Jagung dan Kedelai di Indonesia 2022 (Hasil Survei Ubinan)*. Jakarta: Badan Pusat Statistik.
- Elhaik, E. 2022. Principal Component Analyses (PCA)-based findings in population genetic studies are highly biased and must be reevaluated. *Scientific Reports*, 12(1), 14683.
- Endo, T., Fujii, H., & Shimada, T. 2022. Development of cultivar identification system using 12 InDel markers for widely distributed citrus cultivars in Japan. *Japan Agricultural Research Quarterly: JARQ*, 56(4), 329-340.
- Enyew, M., Feyissa, T., Carlsson, A. S., Tesfaye, K., Hammenhag, C., Seyoum, A., & Geleta, M. 2022. Genome-wide analyses using multi-locus models revealed marker-trait associations for major agronomic traits in Sorghum bicolor. *Frontiers in Plant Science*, 13, 999692.
- Fietri, W. A., Rasak, A., & Ahda, Y. 2021. Analisis Filogenetik Ikan Tuna (*Thunnus spp*) di Perairan Maluku Utara Menggunakan COI (Cytocrome Oxydase I). *BIOMA: Jurnal Biologi Makassar*, 6(2), 31-39.
- Flint-Garcia, S. A., Thornsberry, J. M., & Buckler IV, E. S. 2003. Structure of linkage disequilibrium in plants. *Annual review of plant biology*, 54(1), 357-374.
- Fujii, H., Ogata, T., Shimada, T., Endo, T., Iketani, H., Shimizu, T., ... & Omura, M. 2013. Minimal marker: an algorithm and computer program for the identification of minimal sets of discriminating DNA markers for efficient variety identification. *Journal of bioinformatics and computational biology*, 11(02), 1250022.
- Galeano, C. H., Cortés, A. J., Fernández, A. C., Soler, Á., Franco-Herrera, N., Makunde, G., ... & Blair, M. W. 2012. Gene-based single nucleotide polymorphism markers for genetic and association mapping in common bean. *BMC genetics*, 13, 1-11.
- Ganal, M. W., Altmann, T., & Röder, M. S. 2009. SNP identification in crop plants. *Current opinion in plant biology*, 12(2), 211-217.
- Gaitán-Solís, E., Choi, I. Y., Quigley, C., Cregan, P., & Tohme, J. 2008. Single nucleotide polymorphisms in common bean: their discovery and genotyping using a multiplex detection system. *The Plant Genome*, 1(2).
- Gouda, G., Gupta, M. K., Donde, R., Kumar, J., Parida, M., Mohapatra, T., ... & Behera, L. (2020). Characterization of haplotypes and single nucleotide

- polymorphisms associated with Gn1a for high grain number formation in rice plant. *Genomics*, 112(3), 2647-2657.
- Gupta, S., Kumawat, G., Yadav, S., Tripathi, R., Agrawal, N., Maranna, S., ... & Mohan, Y. 2021. Identification and characterization of a novel long juvenile resource AGS 25. *Genetic Resources and Crop Evolution*, 68, 1149-1163.
- Gur, A., Tzuri, G., Meir, A., Sa'ar, U., Portnoy, V., Katzir, N., ... & Tadmor, Y. 2017. Genome-wide linkage-disequilibrium mapping to the candidate gene level in melon (*Cucumis melo*). *Scientific reports*, 7(1), 9770.
- Gusmiaty, G., Sari, N. A., Safira, T. N., Budiman, A., & Larekeng, S. H. 2021. Polimorfisme Penanda Rapd Untuk Analisis Keragaman Genetik Kemiri (Aleurites Mollucana) Di Kabupaten Maros. *Bioma: Jurnal Biologi Makassar*, 6(1), 22-30.
- Jaekel, A., Lill, P., Whitelam, S., & Saccà, B. 2020. Insights into the Structure and Energy of DNA Nanoassemblies. *Molecules*, 25(23), 5466.
- Jaiswal, V., Gupta, S., Gahlaut, V., Muthamilarasan, M., Bandyopadhyay, T., Ramchiary, N., & Prasad, M. 2019. Genome-wide association study of major agronomic traits in foxtail millet (*Setaria italica* L.) using ddRAD sequencing. *Scientific reports*, 9(1), 5020.
- Kuang, M., Wei, S. J., Wang, Y. Q., Zhou, D. Y., Lei, M. A., Dan, F. A. N. G., & Yang, W. H. 2016. Development of a core set of SNP markers for the identification of upland cotton cultivars in China. *Journal of integrative agriculture*, 15(5), 954-962.
- Kumar, S., Banks, T. W., & Cloutier, S. 2012. SNP discovery through next-generation sequencing and its applications. *International journal of plant genomics*, 2012.
- LaFramboise, T. 2009. Single nucleotide polymorphism arrays: a decade of biological, computational and technological advances. *Nucleic acids research*, 37(13), 4181-4193.
- Lestari, P., Risliawati, A., Utami, D. W., Hidayatun, N., Santoso, T. J., & Chaerani, C. 2017. Pengembangan identitas spesifik berbasis marka SSR pada 29 varietas kedelai lokal Indonesia. *Jurnal Biologi Indonesia*, 12(2).
- Lestari, P., Putri, R. E., Rineksane, I. A., Handayani, E., Nugroho, K., & Terryana, R. T. 2021. Keragaman genetik 27 aksesori Kedelai (*Glycine max* l. Merr.) introduksi subtropis berdasarkan marka SSR. *Vegetalika*, 10(1), 1-17.

- Li, S., Cao, Y., Wang, C., Yan, C., Sun, X., Zhang, L., ... & Song, S. 2023. Genome-wide association mapping for yield-related traits in soybean (*Glycine max*) under well-watered and drought-stressed conditions. *Frontiers in Plant Science*, 14, 1265574.
- Mammadov, J., Aggarwal, R., Buyyarapu, R., & Kumpatla, S. 2012. SNP markers and their impact on plant breeding. *International journal of plant genomics*, 2012.
- McVean, G. 2009. A genealogical interpretation of principal components analysis. *PLoS genetics*, 5(10), e1000686.
- Mederos-Ramirez, A., Ortiz-Perez, R., & Postal, G. 2021. Analysis of the genotype environment interaction in the of soybean crop (*Glycine max* (L) Merrill). *Cultivos Tropicales*, 42(1), 1-10.
- Munjal, G., Hanmandlu, M., & Srivastava, S. 2019. Phylogenetics algorithms and applications. In *Ambient Communications and Computer Systems: RACCCS-2018* (pp. 187-194). Springer Singapore.
- Mursyidin, D. H., & Hernanda, M. A. 2021. Phylogenetic positions of three *Amorphophallus* species natively growing in the Meratus Mountains, South Kalimantan, Indonesia. *Biodiversitas Journal of Biological Diversity*, 22(5).
- Noble, T. J., Tao, Y., Mace, E. S., Williams, B., Jordan, D. R., Douglas, C. A., & Mundree, S. G. 2018. Characterization of linkage disequilibrium and population structure in a mungbean diversity panel. *Frontiers in plant science*, 8, 306490.
- Nofitahesti, I., & Daryono, B. S. 2016. Karakter fenotip kedelai (*Glycine Max* (L.) Merr.) hasil poliploidisasi dengan kolkisin. *Scientiae Educatia: Jurnal Pendidikan Sains*, 5(2), 90-98.
- Nugroho, K., Terryana, R. T., & Lestari, P. 2017. Analisis keragaman genetik kedelai introduksi menggunakan marka mikrosatelit. *Informatika Pertanian*, 26(2), 121-132.
- Oliver, G. R., Hart, S. N., & Klee, E. W. 2015. Bioinformatics for clinical next generation sequencing. *Clinical chemistry*, 61(1), 124-135.
- Pacey-Miller, T., & Henry, R. 2003. Single-nucleotide polymorphism detection in plants using a single-stranded pyrosequencing protocol with a universal biotinylated primer. *Analytical Biochemistry*, 317(2), 166-170.

- Palupi, D., Aryani, R. D., Sukarsa, S., & Lestari, S. 2023. Hubungan Kekerbatan Fenetik 6 Spesies Anggota Genus Hibiscus Berdasarkan Karakter Morfologi. *Bioscientist: Jurnal Ilmiah Biologi*, 11(1), 98-109.
- Pangestika, Y., Budiharjo, A., & Kusumaningrum, H. P. 2015. Analisis filogenetik Curcuma zedoaria (temu putih) berdasarkan gen Internal Transcribed Spacer (ITS). *Jurnal Akademika Biologi*, 4(4), 8-13.
- Poland, J. A., & Rife, T. W. 2012. Genotyping-by-sequencing for plant breeding and genetics. *The plant genome*, 5(3).
- Pujar, M., Gangaprasad, S., Govindaraj, M., Gangurde, S. S., Kanatti, A., & Kudapa, H. 2020. Genome-wide association study uncovers genomic regions associated with grain iron, zinc and protein content in pearl millet. *Scientific Reports*, 10(1), 19473.
- Radji M. 2012. Pendekatan Farmakogenomik dalam Pengembangan Obat Baru. *Pharmaceutical Sciences and Research (PSR)*, 2(1), 1-11.
- Rani, R., Raza, G., Ashfaq, H., Rizwan, M., Razzaq, M. K., Waheed, M. Q., ... & Arif, M. 2023. Genome-wide association study of soybean (*Glycine max* [L.] Merr.) germplasm for dissecting the quantitative trait nucleotides and candidate genes underlying yield-related traits. *Frontiers in Plant Science*, 14, 1229495.
- Rathan, N. D., Krishna, H., Ellur, R. K., Sehgal, D., Govindan, V., Ahlawat, A. K., ... & Mahendru-Singh, A. 2022. Genome-wide association study identifies loci and candidate genes for grain micronutrients and quality traits in wheat (*Triticum aestivum* L.). *Scientific Reports*, 12(1), 7037.
- Rohilla, M., Singh, N., Singh, J., Chowdhury, D., & Mondal, T. K. 2023. Exploration of eQTLs regulating transcript for internode elongation under deep water treatment employing haplotype network in diverse deep water rice landraces of Assam, India. *Journal of Plant Biochemistry and Biotechnology*, 32(3), 525-535.
- Rohmah, E. A., & Saputro, T. B. 2016. Analisis Pertumbuhan Tanaman Kedelai (*Glycine max* L.) Varietas Grobogan Pada Perlakuan Cekaman Genangan. *Jurnal Sains dan Seni ITS*, 5(2).
- Rossi, M., Bitocchi, E., Bellucci, E., Nanni, L., Rau, D., Attene, G., & Papa, R. 2009. Linkage disequilibrium and population structure in wild and domesticated populations of *Phaseolus vulgaris* L. *Evolutionary Applications*, 2(4), 504-522.

- Sales, E., García-Romeral, J., & Domingo, C. 2023. Bioinformatics approach for developing a minimum set of SNP markers for identification of temperate japonica rice varieties cultivated in Spain. *Plos one*, 18(6), e0286839.
- Salgotra, R. K., & Chauhan, B. S. 2023. Genetic diversity, conservation, and utilization of plant genetic resources. *Genes*, 14(1), 174.
- Satam, H., Joshi, K., Mangrolia, U., Waghoo, S., Zaidi, G., Rawool, S., ... & Malonia, S. K. 2023. Next-generation sequencing technology: Current trends and advancements. *Biology*, 12(7), 997.
- Satyawan, D., Tasma, I. M. 2021. Pengembangan Sistem Seleksi Kandidat Tetua Pemuliaan Kedelai dari Koleksi Sumber Daya Genetik Berbasis Genotip dan Fenotip. *Prosiding Seminar Nasional Komisi Nasional Sumber Daya Genetik*. Bogor: 15 September 2021. Hal 28
- Sedivy, E. J., Wu, F., & Hanzawa, Y. 2017. Soybean domestication: the origin, genetic architecture and molecular bases. *New Phytologist*, 214(2), 539-553.
- Setyawan, G., & Huda, S. 2022. Analisis pengaruh produksi kedelai, konsumsi kedelai, pendapatan per kapita, dan kurs terhadap impor kedelai di Indonesia. *KINERJA*, 19(2), 215-225.
- Sjafaraenan, S., Lolodatu, H., Johannes, E., Agus, R., & Sabran, A. 2018. Profil Dna Gen Follicle Stimulating Hormone Reseptor (Fshr) pada Wanita Akne dengan Teknik Pcr dan Sekuensing Dna. *BIOMA: Jurnal Biologi Makassar*, 3(1), 1-11.
- Singh, I., Singh, K. K., & Gautam, U. S. 2012. Constraints in adoption of soybean production technology. *Indian Research Journal of Extension Education*, 2, 169-171.
- Slatkin, M. (2008). Linkage disequilibrium—understanding the evolutionary past and mapping the medical future. *Nature Reviews Genetics*, 9(6), 477-485.
- Souza, T. L. P., de Barros, E. G., Bellato, C. M., Hwang, E. Y., Cregan, P. B., & Pastor-Corrales, M. A. 2012. Single nucleotide polymorphism discovery in common bean. *Molecular breeding*, 30, 419-428.
- Susanto, G. W. A., Mangoendidjojo, W., Yudono, P., & Kasno, A. 2014. Mode of inheritance of genes control maturity in soybean. *ARPJ J. Agric. Biol. Sci*, 9(5), 178-182.
- Tasma, I. M., Satyawan, D., & Rijzaani, H. 2015. Pembentukan pustaka genom, resekuensing, dan identifikasi SNP berdasarkan sekuen genom total genotipe kedelai Indonesia J. *Jurnal AgroBiogen*, 11(1), 7-16.

- Tasma, I. M., Yani, N. M. G., Purwaningdyah, R., Satyawan, D., Nugroho, K., Lestari, P., ... & Mastur, M. 2018. Genetic diversity analysis and F2 population development for breeding of long juvenile trait in soybean. *Jurnal AgroBiogen*, 14(1), 11-22.
- Terryana, R. T., Ningrum, N. D. S. A., Nugroho, K., Saptadi, D., Kurniawan, H., & Lestari, P. 2020. Analisis keragaman genetik dan pengembangan profil sidik jari DNA 20 varietas cabai lokal Indonesia berdasarkan marka SSR. *Jurnal AgroBiogen*, 16(2), 45-58.
- Trent, R. J. 2012. *Molecular Medicine: Genomics to Personalized Healthcare*. New York: Academic Press.
- Tsindi, A., Eleblu, J. S. Y., Gasura, E., Mushoriwa, H., Tongoona, P., Danquah, E. Y., ... & Derera, J. 2023. Analysis of population structure and genetic diversity in a Southern African soybean collection based on single nucleotide polymorphism markers. *CABI Agriculture and Bioscience*, 4(1), 15.
- Utami, D. W., Rosdianti, I., Yuriah, S., Ambarwati, A. D., Hanarida, I., Suwarno, S., & Miftahudin, M. 2017. IDENTIFIKASI GEN/QTL (Quantitative Trait Loci) SIFAT TOLERAN CEKAMAN ALUMINIUM PADA GALUR-GALUR PADI GOGO. *Berita Biologi*, 15(2), 113-124.
- Utami, D. W. 2014. Teknologi Genome Scanning Menggunakan 1536-dan 384-SNP Chip untuk Mendukung Program Pemuliaan Padi Rice Genome Scanning using 1536-and 384-SNP Chip Technology for Supporting Rice Breeding Programs.
- Van Berloo, R. 2008. GGT 2.0: versatile software for visualization and analysis of genetic data. *Journal of Heredity*, 99(2), 232-236.
- Walling, J. G., Shoemaker, R., Young, N., Mudge, J., & Jackson, S. 2006. Chromosome-level homeology in paleopolyploid soybean (*Glycine max*) revealed through integration of genetic and chromosome maps. *Genetics*, 172(3), 1893-1900.
- Wang, Y., Lv, H., Xiang, X., Yang, A., Feng, Q., Dai, P., ... & Zhang, X. 2021. Construction of a SNP fingerprinting database and population genetic analysis of cigar tobacco germplasm resources in China. *Frontiers in plant science*, 12, 618133.
- Yang, J., Lv, Y., Zhang, X., Xia, C., Zhao, H., & Wen, C. 2023. Genetic diversity analysis and variety identification using SSR and SNP markers in melon. *BMC Plant Biology*, 23(1), 39.

- Yue, Y., Liu, N., Jiang, B., Li, M., Wang, H., Jiang, Z., ... & Nian, H. 2017. A single nucleotide deletion in J encoding GmELF3 confers long juvenility and is associated with adaption of tropic soybean. *Molecular Plant*, 10(4), 656-658.
- Zatybekov, A., Yermagambetova, M., Genievskaya, Y., Didorenko, S., & Abugalieva, S. 2023. Genetic Diversity Analysis of Soybean Collection Using Simple Sequence Repeat Markers. *Plants*, 12(19), 3445.
- Zhang, J., Yang, J., Zhang, L., Luo, J., Zhao, H., Zhang, J., & Wen, C. 2020. A new SNP genotyping technology Target SNP-seq and its application in genetic analysis of cucumber varieties. *Scientific reports*, 10(1), 5623.
- Zhu, Y. L., Song, Q. J., Hyten, D. L., Van Tassell, C. P., Matukumalli, L. K., Grimm, D. R., ... & Cregan, P. B. 2003. Single-nucleotide polymorphisms in soybean. *Genetics*, 163(3), 1123-113