

## Daftar Pustaka

- Abbas, G., Nadeem, A., Babar, M.E., Hussain, T., Tahir, M.S., Shehzad, W., Aslam, N., Tayyab, M., & Javed, M. 2016. Sequence diversity and phylogenetic analysis in Pakistani spotted deer (*Axis axis*). *Pakistan Journal of Agricultural Sciences*, 53(4): 16.5365. DOI: 10.21162/PAKJAS/16.5365.
- Adji, D. & Astuti, D. 2020. Profil Darah Rusa totol (*Axis axis*) betina sehat Pusat Inovasi Agroteknologi (PIAT), Universitas Gadjah Mada. *Jurnal Sain Veteriner*, 38(1): 7-11.
- Aghazadeh, L., Nikbin, S., Mirzaei, F., & Hedayat, N. 2020. Using *D-loop* region to study the genetic structure and phylogenetic analysis of Iranian red deer. *Animal Science Researches (Faculty of Agriculture, University of Tabriz)*, 29(4): 17-33.
- Arisuryanti, T., Firdaus, N.U.N., & Hakim, L. 2020. Genetic characterization of striped snakehead (*Channa striata* Bloch, 1793) from Arut River, Central Kalimantan inferred from COI mitochondrial gene. *AIP Conference Proceedings*, 2260, 020001.
- Bagchi, S., Goyal, S.P., & Sankar, K. 2004. Herbivore density and biomass in a semi-arid tropical dry deciduous forest of western India. *Journal of Tropical Ecology*, 20: 475-478.
- Barrette, C. 1991. The size of *Axis* deer fluid groups in Wilpattu National Park, Sri Lanka. *Mammalia*, 55: 207-220.
- Bayarlkhagva, D., Bayarlkhagva, M., Gun-Aajav, B., & Batsuuri, S. 2013. Genetic diversity of mitochondrial *D-loop* sequence of siberian roe deer (*Capreolus pygargus*) inhabiting Mongolia. *International Journal of Sciences*, 2(3): 105-108.
- Brown, W.M., George Jr., M., & Wilson, A.C. 1979. Rapid evolution of animal mitochondrial DNA. *Proc Natl Acad Sci U S A*, 76(4): 1967-1971.

- Catibog-Sinha, C. 2008. Zoo tourism: Biodiversity conservation through tourism. *Journal of Ecotourism*, 7(2&3): 160-178.
- Darriba, D., Taboada, G.L., Doallo, R., D., P. 2012. jModelTest 2: more models, new heuristics and parallel computing. *Nature Methods* 9(8), 772.
- Duckworth, J.W., Kumar, N.S., Anwarul Islam, M., Sagar Baral, H., & Timmins, R. 2015. *Axis axis*. *The IUCN Red List of Threatened Species* 2015: e.T41783A22158006. <https://dx.doi.org/10.2305/IUCN.UK.2015-4.RLTS.T41783A22158006.en>.
- Farquharson, K.A., Hogg, C.J., & Grueber, C.E. 2021. Offspring survival changes over generations of captive breeding. *Nature Communications*, 12, 3045.
- Fernandez-Garcia, J.L., Carranza, J., Martinez, J.G., & Randi, E. 2014. Mitochondrial *D-loop* phylogeny signals two native Iberian red deer (*Cervus elaphus*) lineages genetically different to Western and Eastern European red deer and infers human-mediated translocations. *Biodiversity and Conservation*, 23: 537-554.
- Fumagalli, L., Taberlet, P., Favre, L., & Hausser, J. 1996. Origin and evolution of homologous repeated sequences in the mitochondrial DNA control region of shrews. *Mol Biol Evol.* 13(1): 31-46.
- Garsetiasih, R. & Herlina, N. 2005. Evaluasi plasma nutfah Rusa totol (*Axis axis*) di halaman Istana Bogor. *Buletin Plasma Nutfah*, 11(1): 34-40
- GLZoo. 2021. Gembira Loka Zoo. <https://gembiralokazoo.com/>. Diakses terakhir pada 4 Juni 2021, pukul 10.52 WIB.
- Grehenson, G. 2015. UGM Siap Jadi Pusat Budidaya Ternak Rusa. <https://www.ugm.ac.id/id/berita/10570-ugm-siap-jadi-pusat-budidaya-ternak-rusa>. Diakses terakhir pada 26 Juni 2021, pukul 07.13 WIB.
- Gupta, S.K., Kumar, A., Angom, S., Singh, B., Ghazi, M.G.U., Tuboi, C., & Hussain, S.A. 2018. Genetic analysis of endangered hog deer (*Axis porcinus*) reveals two

- distinct lineages from the Indian subcontinent. *Scientific Reports*, 8: 16308.  
<https://doi.org/10.1038/s41598-018-34482-9>
- Hill, E., Linacre, A., Toop, S., Murphy, N., & Strugnell, J. 2019. Widespread hybridization in the introduced hog deer population of Victoria, Australia, and its implications for conservation. *Ecology and Evolution*: 1-15.  
<https://doi.org/10.1002/ece3.5603>.
- Jiang, P., Lang, Q., Fang, S., Ding, P., & Chen, L. 2005. A genetic diversity comparison between captive individuals and wild individuals of Elliot's Pheasant (*Syrnaticus ellioti*) using mitochondrial DNA. *Journal of Zhejiang University SCIENCE*, 6B(5): 413-417.
- Kasamatsu, H., Robberson, D.L., & Vinograd, J. 1971. A novel closed-circular mitochondrial DNA with properties of a replicating intermediate. *Proc. Natl. Acad. Sci. U S A*, 68(9): 2252-2257.
- Kompas. 2020. Asal-usul Istana Bogor, dari Buitenzorg hingga jadi tempat kediaman presiden. <https://www.kompas.com/tren/read/2020/03/14/094500665/asal-usul-istana-bogor-dari-buitenzorg-hingga-jadi-tempat-kediaman-presiden?page=all>.  
Diakses terakhir pada 4 Juni 2021, pukul 11.35 WIB.
- Kumar, S., Stecher, G., & Tamura, K. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. *Molecular Biology and Evolution*, 35(6):1547–1549.
- Larizza, A., Pesole, G., Reyes, A., Sbisa, E., & Saccone, C. 2002. Lineage specificity of the evolutionary dynamics of the mtDNA *D-Loop* region in rodents. *Journal of Molecular Evolution*, 54:145-155.
- Madden, T. 2013. *The BLAST Sequence Analysis Tool dalam The NCBI Handbook 2<sup>nd</sup> edition*. USA: National Center for Biotechnology Information, U.S. National Library of Medicine.
- Maddison, W. P. & D.R. Maddison. 2019. Mesquite: a Modular System for

Evolutionary Analysis. Version 3.61. <http://mesquiteproject.org>.

- Nagata, J., Masuda, R., Kaji, K., Kaneko, M., & Yoshida, M.C. 1998. Genetic variation and population structure of the Japanese sika deer (*Cervus nippon*) in Hokkaido Island, based on mitochondrial *D-loop* sequences. *Molecular Ecology*, 7(7): 871-877.
- Nowak, C., Büntjen, M., Steyer, K., & Frosch, C. 2014. Testing mitochondrial markers for noninvasive genetic species identification in European Mammals. Conservation Genetic Resources. DOI: 10.11/s12686-013-0068-5.
- Parkanyi, V., Ondruska, L., Vasicek, D., & Slamecka, J. 2014. Multilevel *D-loop* PCR identification of hunting game. *Applied Translational Genomics*, 3(1): 1-7.
- Peakall, R & Smouse, P.E. 2012. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. *Bioinformatics*, 28: 2537-2539.
- PIAT UGM. 2021. Tentang Kami. <https://piat.ugm.ac.id/sejarah/>. Diakses terakhir pada 5 Juni 2021, pukul 16.01 WIB.
- Pun, K., Albrecht, C., Castella, V., & Fumagalli, L. 2009. Species identification in mammals from mixed biological samples based on mitochondrial DNA control region length polymorphism. *Electrophoresis*, 30: 1008-1014.
- Purohit, D., Manu, S., Ram, M.S., Sharma, S., Patnaik, H.C., Deka, P.J., Narayan, G., & Umapathy, G., 2021. Genetic effects of long-term captive breeding on the endangered pygmy hog. *PeerJ*, 9.
- Rozas, J., Rerrer-Matta, A., Sanchez-DelBarrio, J.C., Guirao-Rico, S., Librado, P., Ramos-Onsins, S.E., & Sanchez-Gracia, A. 2017. DnaSP 6: DNA sequence polymorphism analysis of large data sets. *Molecular Biology and Evolution*, 13(12): 3299-3302.

- Sankar, K. & Acharya, B, Spotted Deer, in Sankar, K. & Goyal, S.P. (eds.), *Ungulates of India*. ENVIS Bulletin: Wildlife Protected Areas, vol. 07, no. 1. Wildlife Institute of India. Deheradun. 2004, pp. 171-180.
- Schaller, G.B. 1967. *The Deer and Tiger: A study of wildlife in India*. The University of Chicago Press. Chicago, p.370.
- Šprem, N., Stipoljev, S., Ugarković, D., & Buzan, E. 2021. First genetic analysis of introduced axis deer from Croatia. *Mammalian Biology*, 101: 1121–1125. <https://doi.org/10.1007/s42991-021-00164-9>.
- Su, Q., Yao, Y., Zhao, Q., Li, D., Xie, M., Wu, J., Wen, A., Wang, Q., Zhu, G., Ni, Q., Zhang, M., & Xu, H. 2019. Genetic diversity and phylogenetic analyses of 11 cohorts of captive rhesus macaques from Chinese zoos. *PeerJ*, 7:e6957, DOI 10.7717/peerj.6957.
- Suchard, M.A., Lemey, P., Baele, G., Ayres, D.L., Drummond, A.J., & Rambaut, A. 2018. Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. *Virus Evolution* 4(1), vey016
- Suryanto, D. 2013. Penangkaran Rusa Prambanan. <https://www.solopos.com/penangkaran-rusa-prambanan-435004>. Diakses terakhir pada 5 Juni, pukul 16.21 WIB.
- Taberlet, P. & Bouvet, J. 1994. Mitochondrial DNA polymorphism, phylogeography, and conservation genetics of the brown bear *Ursus arctos* in Europe. *Proceedings of the Royal Society B: Biological Sciences*, 255: 195-200.
- West, P. 2018. *Guide to Introduced Pest Animals of Australia*. CSIRO Publishing. Clayton South, p. 16.
- Wheeler, T.J. & Kececioglu, J.D. 2007. Multiple alignments by aligning alignments. *Bioinformatics*, 23: i559-i568.

- Whitford, H.L., & Young, R. 2004. Trends in the captive breeding of threatened and endangered birds in British Zoos. *Zoo Biology*, 23: 85-89.
- Wirdateti, Brahmantyo, B., Semiadi, G., & Reksodihardjo, A. 2010. Variasi genetik pada rusa sambar (*Rusa unicolor*) di penangkaran, Kabupaten Penajam, Kalimantan Timur. *Biota*, 15(3): 441-447.
- Xiu, Y., Liu, C., Xu, S., Lin, C., & Chou, C. 2020. The genetic diversity and population genetic structure of the Red Panda, *Ailurus fulgens*, in zoos in China. *Animals*, 10(6). <https://doi.org/10.3390/ani10061008>.
- Yudha, D.S., Pratama, M.Z.M., & Eprilurahman, R. 2019. Antlers characterization for identification of deer species (family Cervidae) in Indonesia. *Journal of Tropical Biodiversity and Biotechnology*, 4(3): 97-106.