

ANALYSIS AND IDENTIFICATION OF DNA SEQUENCE VARIATIONS IN CYPRINUS CARPIO IN LAKE KERINCI

Tomi Apra Santosa^{1*)}, Abdul Razak²⁾, Eria Marina Septiyani³⁾

Biology-Department, Mathematics and Natural Sciences Faculty, Padang State University
email: santosatomiapra@gmail.com

Abstract

This study aims to find out the analysis and identification of variations in DNA sequences in Cyprinus carpio in Lake Kerinci. 7. Research using qualitative research type with a literature study method. Data sources come from national and international journals. The results of the study can be concluded that Cyprinus carpio Cyprinus carpio has a varied gene that the number of DNA chromosomes 48 pairs or $2n = 96$ who have DNA sequence analysis 5' GCCTTCGTGGCCCTTCCCAC-3' and 5'-GGTTGCTCCTGTCCGCCACCCC-3' and has three microsatellite eloquence, MHF6, MFW7, and MFW9.

Keywords: Genetic, DNA, Cyprinus carpio

1. INTRODUCTION

I Goldfish or *Cyprinus carpio* is a species of the family Cyprinidae that has accounted for over 30% of the world's aquaculture (Wang et al., 2017; Xu et al., 2011; Tea Tomljanović, et.al., 2013). This fish is widely researched since 1758 is widely used in goldfish has a long history and has been cultivated by the ancestors of Europeans and Asians (Hu et al., 2016; Kohlmann et al., 2003; Street et al., 2008) Goldfish is an important commodity for the cultivation of both calm water ponds (KAT), heavy water ponds (KAD), floating nets (KJA) (Himawan et al., 2017). This species has a very high economic value. In addition, it has a high selling value of gold fish also has a protein content, high fat and has a very fast growth (Ye et al., 2018).

Goldfish (*Cyprinus carpio*) have a wide variety and are developed through geographic isolation, mutation accumulation, and very long selection pressures (Lin et al., 2015). To see the intraspecific relationship and genetic variability it is necessary to conduct a comprehensive study on the goldfish population (Zhao et al., 2020). By looking for kinship between species. This technique can be done by looking at the genetic variation of the goldfish (*Cyprinus carpio*) (Zhao et al., 2020). Mitochondria DNA is a way for variation regions to be criminalized between subspecies in goldfish (*Cyprinus carpio*) (Zhou et al., 2003). To reveal the development of taxonomy evolution and the

physical position of goldfish (*Cyprinus carpio*) can be seen by analyzing the mitochondrial genome (Ma et al., 2019).

The genome in *Cyprinus carpio* has undergone development including several large genetic markers (Xu et al., 2014). The genetics of *Cyprinus carpio* must be adapted to their properties (Marie et al., 2010). EDNA technology is used to monitor fish in waters and other aquatic species about eDNA in the natural environment (Eichmiller et al., 2014).

Previous research by Peng Xu, et al (2014) that goldfish (*Cyprinus carpio*) contain 52,610 genes in protein - coding and 93.2% contain paleotetraploid genomes ($2n = 100$). X. W.Chen research, (2012) that complete compiler DNA fragments in fabp2 in *Cyprinus carpio* cloned using reverse-transcription polymerase chain reaction (RT-PCR) enzyme consists of two genes namely putative intestinal type fabp gene, named fabp2a and fabp2b. Y. Wan's research (2007) that gtH-a357 subunits can be transmitted with HeLa cells and while GtH-a291 cannot be predicted and that gtH-a291 subunits can interact with FSH-b and LH-b.

Based on the background above researchers aim to describe the analysis and identification of genome variations dna *Cyprinus carpio*.

2. RESEARCH METHOD

This type of research is qualitative researchers using literature studies by finding reputable sources of literature derived from a trusted database, namely Sciencedirect, NCBI, Taylor of Francis, Sinta, Google Scholar, Sage Jurnal, Emerald Jurnal, Springer, Oxford journal, IEEE, and Cambridge (Mulkiyah et al., 2020).

3. RESULT AND DISCUSSION

Gen *Cyprinus carpio*

Genes are the part that has a function for controlling hereditary properties in organisms. Goldfish (*Cyprinus carpio*) has gene variations from two previous species namely *Cyprinus carpio* from Europe and *Cyprinus haematopterus* from Asia (Vandeputte, 2003). Currently, *Cyprinus carpio* has 24 species spread around the world (Ma et al., 2019). Of the 24 species have a variety of genetic diversity. Such genetic variations can be calculated by calculating haplotype diversity (Hd) and nucleotide diversity (Zhao et al., 2020). DNA sequences start from codon star AGC and TAA (Cao et al., 2015).

Many fish species undergo cold adaptations including *Cyprinus carpio* which has been involved in the fields of physiology, biochemistry, and molecular biology are included in the fluidity of cell membranes, lipid cells, nerves, and metabolism, but the genetic basis of cold adaptation is not yet apparent (Liang et al., 2009). The *Cyprinus carpio* gene has a variety of phenotypes that can be seen from skin color, body shape, body size, and also its growth (Bianka et al., 2020). The *C. carpio* gene has a number of chromosomes consisting of 48 pairs ($2n = 96$) (Wang et al., 2017). However, variations in *C. carpio* DNA chromosome between 48 and 200 depending on the species (Wang et al., 2017; Moens et al., 2020).

DNA Genome

Cyprinus carpio DNA identification consists of 454 sequences of transcriptome and DNA genotype (Zhang et al., 2013). Polypeptides are similar to the famous *C. Auratus* TLR3 (CcTLR3) where ccTLR3 signals consist of peptide signals (Yang &

Su, 2010). DNA in *Cyprinus carpio* has been denominated in different frequency of alleles where genetic varieties can be seen from the natural and artificial population structure of *Cyprinus carpio* (Nedoluzhko et al., 2020). However, this can be influenced by the genetic distance from the distance of its population (Haynes, et.al., 2009). DNA Sequence *Cyprinus carpio* using mega 7 application namely 5' GCCTTCGTGGCCCTTCCCCAC-3' and 5'-GGTTGCTCCTGTCCGCCACCCC-3' which has a display amplification of 480 bp (Syahputra et al., 2016; Saselah et al., 2012; Chen et al., 2015).

Cyprinus carpio has GH that serves as a growth hormone. GH works in influencing *Cyprinus carpio* genotype variation. In this analysis, genotypes used mega 7 and Bioedit applications that use three microsatellite levels in DNA namely MHF6, MFW7, and MFW9 (Syahputra, et al., 2016; Novita et al., 2020). Of the three microsatellites only taken fin parts (Didik Ariyanto, et.al., 2019). Observation parameters can be seen by using Genbank on the target organ through the NCBI website (Nuryati, 2013; Alvarez et al., 2006).

Identification of *Cyprinus carpio* DNA sequences can be seen from the genome. The DNA sequence is the process of sequencing nucleotide base sequences in DNA molecules (Gen et al., 2019). In performing DNA sequences also involves DNA extraction (Han & Sun, 2018). DNA extraction is a method that uses hot temperatures in the cell breakdown process (Mulyani & Purwanto, 2011)

4. CONCLUSION

From the explanation above can be concluded that *Cyprinus carpio* has a varied gene that the number of DNA chromosomes 48 pairs or $2n = 96$ that have DNA sequence analysis 5' GCCTTCGTGGCCCTTCCCCAC-3' and 5'-GGTTGCTCCTGTCCGCCACCCC-3' and has three microcephaly satellite, namely MHF6, MFW7, and MFW9.

5. REFERENCES

- Cao, X. L., Chen, J. J., Cao, Y., Nie, G. X., Wan, Q. Y., & Wang, L. F. (2015). Identification and expression of the laboratory of genetics and physiology 2 gene in common carp *Cyprinus carpio*. *Journal Of Fish Biolog*, 86(3), 74–91. <https://doi.org/10.1111/jfb.12541>
- Eichmiller, J. J., Bajer, P. G., & Sorensen, P. W. (2014). The Relationship between the Distribution of Common Carp and Their Environmental DNA in a Small Lake. *PLOS ONE*, 9(11), 1–8. <https://doi.org/10.1371/journal.pone.0112611>
- Gen, P., Pada, G. H., & Donggala, D. (2019). Available online at <http://jurnal.untad.ac.id/jurnal/index.php/AGRISAINS>. Amirudin Dg. Malewa 1, Lukman Hakim2, Dan Sucik Maylinda2 1Peternakan, 1(20), 46–56.
- Han, Z., & Sun, J. (2018). Biases from different DNA extraction methods in intestine microbiome research based on 16S rDNA sequencing : a case in the koi carp , *Cyprinus carpio* var . Koi. *Microbiology*, 34(2), 1–9. <https://doi.org/10.1002/mbo3.626>
- Himawan, Y., Syahputra, K., & Ariyanto, D. (2017). PERFORMA PEMBESARAN IKAN MAS RAJADANU (*Cyprinus carpio*) GENERASI KETIGA HASIL SELEKSI “ WALKBACK .” *Jurnal Riset Akuakultur*, 12(2), 121–129.
- Kohlmann, K., Gross, R., Murakaeva, A., & Kersten, P. (2003). Genetic variability and structure of common carp (*Cyprinus carpio*) populations throughout the distribution range inferred from allozyme , microsatellite and mitochondrial DNA markers. *Aquatic Living Resources*, 16(5), 421–431. [https://doi.org/10.1016/S0990-7440\(03\)00082-2](https://doi.org/10.1016/S0990-7440(03)00082-2)
- Lin, M., Zou, J., Wang, C., *Cyprinus*, L., Lin, M., Zou, J., & Wang, C. (2015). Complete mitochondrial genomes of domesticated and wild common carp (*Cyprinus carpio* L .) Complete mitochondrial genomes of domesticated and wild common. *Mitochondria DNA*, 1736(November), 20–22. <https://doi.org/10.3109/19401736.2013.869690>
- Ma, D., Fan, J., Zhu, H., & Huang, Z. (2019). The complete mitochondrial genome of *Cyprinus Carpio* Var . Guilin rice flower carp and its phylogeny in Cyprinidae. *Mitochondrial DNA Part B*, 4(1), 1253–1254. <https://doi.org/10.1080/23802359.2019.1591177>
- Mulkiyah, A., Armin, F., & Rivai, H. (2020). CANDESARTAN ANALYSIS METHODS DURING 2000-2020. *WORLD JOURNAL OF PHARMACY AND PHARMACEUTICAL SCIENCES*, 9(6), 1854–1884. <https://doi.org/10.20959/wjpps20206-16426>
- Mulyani, Y., & Purwanto, A. (2011). PERBANDINGAN BEBERAPA METODE ISOLASI DNA UNTUK DETEKSI DINI KOI HERPES VIRUS (KHV) PADA IKAN MAS (*Cyprinus carpio* L .). *Jurnal Akuatika*, 5(2), 1–16.
- Nedoluzhko, A. V, Slobodova, N. V, Sharko, F., Shalgimbayeva, G. M., Tsygankova, S. V, Boulygina, E. S., Nguyen, Z. J. V. Q., Pham, T. T., Nguyen, Đ. T., Volkov, A. A., Fernandes, J. M. O., & Rastorguev, S. M. (2020). ORIGINAL RESEARCH A new strain group of common carp : The genetic differences and admixture events between *Cyprinus carpio* breeds. *Ecology and Evolution*, 10(12), 1–9. <https://doi.org/10.1002/ece3.6286>
- Nuryati, S. (2013). Frekuensi dan persistensi vaksin DNA penyandi GP25 yang diberikan melalui pakan pada ikan mas Frequency and persistency of DNA vaccine encoding GP25 by oral on common carp. *Jurnal Akuakultur Indonesia*, 12(2), 150–157.
- Syahputra, K., Himawan, Y., Ariyanto, D., Palimirmo, S., Penelitian, B., & Ikan, P. (2016). PEWARISAN MARKA Cyca-DAB1 * 05 DAN KERAGAMAN GENETIK IKAN MAS (*Cyprinus carpio*) STRAIN RAJADANU TAHAN INFEKSI KOI HERPESVIRUS DAN TUMBUH

- CEPAT. *Ker*, 11(2), 115–123.
- Syahputra, K., Palimirmo, F. S., Himawan, Y., Penelitian, B., & Ikan, P. (2016). TRANSMISI GEN krt-GP11 DAN PERFORMA KETAHANAN IKAN MAS (*Cyprinus carpio*) TRANSGENIK F-2 TERHADAP INFEKSI KHV. *Jurnal Riset Akuakultur*, 11, 11(4), 297–305.
- Vandeputte, M. (2003). Selective breeding of quantitative traits in the common carp (*Cyprinus carpio*): a review. *Aquatic Living Resources*, 16(4), 399–407. [https://doi.org/10.1016/S0990-7440\(03\)00056-1](https://doi.org/10.1016/S0990-7440(03)00056-1)
- Xu, P., Li, J., Li, Y., Cui, R., Wang, J., Wang, J., Zhang, Y., & Zhao, Z. (2011). Genomic insight into the common carp (*Cyprinus carpio*) genome by sequencing analysis of BAC-end sequences. *BMC Genomics*, 12(188), 1–7. <https://doi.org/10.1186/1471-2164-12-188>
- Xu, P., Zhang, X., Wang, X., Li, J., Liu, G., Kuang, Y., Xu, J., Zheng, X., Ren, L., Wang, G., Zhang, Y., Huo, L., Zhao, Z., Cao, D., Lu, C., Li, C., Zhou, Y., Liu, Z., Fan, Z., ... Sun, X. (2014). Genome sequence and genetic diversity of the common carp , *Cyprinus carpio*. *Nature Publishing Group*, 46(11), 1212–1219. <https://doi.org/10.1038/ng.3098>
- Yang, C., & Su, J. (2010). Molecular identification and expression analysis of Toll-like receptor 3 in common carp *Cyprinus carpio*. *Journal Fish Biologi*, 76(34), 1926–1939. <https://doi.org/10.1111/j.1095-8649.2010.02624.x>
- Ye, X., Lv, Y., Wei, L., Huang, J., & Wen, Y. (2018). The complete mitochondrial genome of Jinbian carp *Cyprinus carpio* (*Cypriniformes* : *Cyprinidae*) The complete mitochondrial genome of Jinbian carp *Cyprinus carpio*. *Mitochondrial DNA Part B*, 3(2), 1096–1097. <https://doi.org/10.1080/23802359.2018.1495126>
- Zhang, Y., Wang, S., Li, J., Zhang, X., Jiang, L., Xu, P., Lu, C., Wan, Y., & Sun, X. (2013). Primary genome scan for complex body shape-related traits in the common carp *Cyprinus carpio*. *Journal Fish Biologi*, 82(3), 125–140. <https://doi.org/10.1111/j.1095-8649.2012.03469.x>
- Zhao, Y., Zheng, X., Zhu, X., Kuang, Y., & Sun, X. (2020). Genetic variation of common carp *Cyprinus carpio* L . in China based on mitochondrial COII gene. *Aquaculture Reports*, 18, 100462. <https://doi.org/10.1016/j.aqrep.2020.100462>
- Zhou, J. F., Wu, Q. J., Ye, Y. Z., & Tong, J. G. (2003). Genetic divergence between *Cyprinus carpio carpio* and *Cyprinus carpio haematopterus* as assessed by mitochondrial DNA analysis , with emphasis on origin of European domestic carp. In *Genetica 119*: (pp. 93–97).