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

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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 saveral 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' GCCTTCGTGGCCCTTCCCAC-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' GCCTTCGTGGCCCTTCCCAC-3'and5'-GGTTGCTCCTGTCCGCCACCCC-3' and has three microcephaly satellite, namely MHF6, MFW7, and MFW9**.**

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