

MITOCHONDRIAL D-LOOP VARIANTS AS GENETIC MARKERS FOR DISTINGUISHING MORPHOLOGICAL GROUPS IN COMMON CARP *CYPRINUS CARPIO*

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ABSTRACT

In the rivers of Iraq, two morphologically distinct groups of common carp, *Cyprinus carpio*, have emerged without human intervention, exhibiting remarkable differences across a wide range of characteristics. Given the significance of the mitochondrial D-loop in regulating mitochondrial functions and subsequent species evolution, this study aimed to investigate whether D-loop variations could serve as genetic markers to distinguish between these two groups, designated as Group I and Group II. Mitochondrial variations were analyzed in 70 samples using Sanger sequencing of D-loop PCR fragments, followed by the construction of a median-joining network and neighbor-joining tree. The morphological differences between the two groups were corroborated by genetic variations, as 17 variants were detected, with 3 variants being exclusive to Group-I and 2 variants exclusive to Group II. Linkage disequilibrium (LD) analysis showed that these exclusive variants showed entire co-inheritance in each group. This distribution, combined with network and phylogenetic analyses, revealed that the variations formed two distinct phylogenetic groups with clearly differentiated ancestral origins. Group I exhibited higher mitochondrial diversity and broader haplotyping capacity, suggesting greater biological adaptability. The distinct maternal lineage distributions further support a genetic basis for the observed phenotypic differences. These findings underscore the role of the mitochondrial D-loop in shaping the adaptation of *C. carpio* to diverse ecological conditions.

Keywords: Common carps, diversity, D-loop, mitochondria, phylogenetic tree.

INTRODUCTION

Aquatic organisms are an important component of the world's biological wealth. in the complex mosaic of biodiversity. Genetic diversity among these species not only sustains ecological stability and the

resilience of populations to changing environments, but also serves as a critical predictor of their survival and evolutionary paths (Grummer et al., 2019). As the pressures of climate change, habitat destruction, and increased overfishing, there is an urgent need for creative and efficient technologies for monitoring and conserving aquatic biodiversity. One of these technologies is concerned with the utilization of mitochondrial DNA (mtDNA) as an

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