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Cairo University Faculty of Veterinary Medicine

Department of Aquatic Animal Medicine and Management

Insights into the possible microbial challenges facing cultured tilapias in Egypt

A Thesis submitted by

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Abstract

In the last few years there were episodes of colossal mortalities in tilapia fish farms during summer season. This study was intended to investigate the possible microbial causes of such mortalities. A total of 250 moribund fish samples were collected from Kafr El-Sheikh, Sharqia and El Fayoum governorate. The most apparent clinical signs were hemorrhagic patches and darkness on skin, protruded vent, exophthalmia, and abdominal distension. The postmortem findings were enlarged, friable spleen and liver, abscesses, serosanguinous ascitic fluid and enlarged gallbladder. The molecular identification of Tilapia Lake Virus by PCR confirmed the absences of the virus in all examined samples collected from Kafr El-Sheikh governorate. A total of 48 pathogenic bacterial isolates were retrieved from the infected fish. Namely, *Streptococcus agalactiae* (14), *Enterococcus faecalis* (10),

Lactococcus garvieae (10), Streptococcus dysgalactiae (9), Aeromonas hydrophila (3), and Vibrio cholera (2). The predominance of Streptococci infections points to its intense involvement in such mortalities. All isolates were confirmed by 16s rRNA gene sequencing and phylogenetic analysis. The molecular screening confirmed the existence of Hyl, cylE, scpB and camp genes in all S. agalactiae strains. E. faecalis isolates possessed Hyl (50%), Asal (40%), CylA (70%), GelE (60%), Esp (50%), EF3314 (50%) and Ace (60%). L. garvieae isolates possessed Hlyl (40%), Hly2 (60%), Hly3 (60%), NADH oxidase (70%) and Eno (50%). The isolates of S. dysgalactiae possessed Mig (33%), brpA (55%), Lmb (77%), scpB (33%) and Rip (44%). The histopathological examination revealed that S. agalactiae and L. garvieae cause meningitis in tilapia. Ultimately, isolates showed variable antibiotic resistance profile against the majority of tested antibiotics.

Key words

Farmed tilapia, Pathogenicity, Summer mortality, Virulence profiles.

Dedication

I dedicate this study
to WHOM I LOVE My 4
Ms, My husband,
FATHER, MOTHER,
AND ALL MY FAMILLY

for their
understanding, support and
help to succeed.
Thank you for every
unconditional
love and guidance.

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Chapter

1

Introduction

INTRODUCTION

Aquaculture produces 52% of fish production used for human consumption (**Abdel-Latif** *et al.*, 2020). There is a significant increase in the total fish production in Africa compared to other continents (**FAO**, 2020). Tilapia is one of the most important farmed fish in the world and comes in the second place after carp (**Naylor** *et al.*, 2021). Egypt is the third country on the list of tilapia production after China and Indonesia (**Jansen** *et al.*, 2019). Tilapia production is expected to achieve 25 billion USD by 2028 (**FAO**, 2018). It is an important source of animal protein especially in developing countries and an income to many penurious families (**Mugwanya** *et al.*, 2022). There are many characters in tilapia making it appropriate for farming as it can tolerate a wide range of environmental conditions, its resistance to stress and diseases, and short production cycle. It accepts the artificial feed, as well as it can reproduce in captivity (**Ansah** *et al.*, 2014). Recently, diseases incidence has been increased in tilapia farms (**Dawood**, 2021).

During the last seven years in Egypt there were many episodes of colossal mortalities in tilapia farms relevant to microbial agents. The main causative agents were not clearly identified. Many factors affect these mortalities as deterioration of water quality parameters (**Abu-Elala** et al., 2020). Previous studies reported tilapia lake virus, which is a single stranded RNA virus belongs to Amnoonviridae family Tilapinevirus genus, in Egypt (Bacharach et al., 2016; Fathi et al.,