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Viral sovereignty in aquatic world as a major consequence of climate change and environmental pollution

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Mini Review

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For many decades, bacterial pathogens have posed major threat to mostly the entire aquatic world. Bacterial threats could represent a major direct jeopardy to aquatic animals by causing clinical diseases with consequent mass mortalities or indirectly take the form of secondary infection with opportunistic organisms motivated by environmental stress and suppression of both cellular and acquired immune barriers of fish (Austin and Austin 2012, Eissa et al. 2013).

Controversially, during the past few years the above epidemiological variable has noticeably changed. Intense episodes of extreme climatic changes caused by voluminous emissions of carbon dioxide and green gases have resulted in sharp / unprecedented surge of global warming with concomitant melting of Antarctic glaciers. Further, sharp increase in oceans / seas levels with subsequent increase in water acidity to unprecedented degree that caused gradual depletion of calcium from scales of shellfish/fish. The eminent decalcification of aquatic species will trigger a chain of extinctions if the acidity rates continued to steadily increase (Callaway et al. 2012, Cochrane et al. 2009, Eissa and Zaki 2011, Marcogliese 2008).

On the other hand, and in view of the continuous decrease in the production of terrestrial animal protein, the world began to turn its eyes to the so-called blue revolution or fish farming. Fish farming has sometimes considered the sole source of finance supporting the economies of some south Asian and Latin American countries. Due to the continuous shortage of fish stocks in natural fisheries as a result of pollution,

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E-mail address: aeissa2012@cu.edu.eg DOI: <u>10.21608/EJAH.2021.131696</u> climate change and overfishing it has become very logical to devote efforts to developing fish farming technologies continuously reach maximum to productivity (Callaway et al. 2012, Cochrane et al 2009; Eissa and Zaki, 2012, Rosa et al. 2012). However, in the midst of all this, many negative aspects emerged that strongly affected the growth and sustainability of fish farming, most of which were related to the quality of aquaculture water, the quality of food, the sharp changes in climate, environmental pollution and Its consequences. This comes from an unprecedented breakdown of water properties, including low levels of oxygen, high levels of ammonia and organic matter, and a sharp increase in microbial load, severe suppression of the skin and systemic immune barriers, and the subsequent microbial invasion. Such microbial invasion will swiftly result in frequent episodes of clinical diseases and mass mortalities that abort all attempts to develop aquaculture procedures and drastically impact the sustainability of the entire aquaculture process (Eissa et al. 2013, 2015, 2016).

As a reflex action to the unprecedented sharp heat rises witnessed by the whole world, the concomitant low levels of dissolved oxygen and the change of other chemical water properties, and in the middle of uncountable erratic farm managements such as unsafe use of antibiotics, chemicals, hormones, wrong nutrition, wrong water treatments, water scarcity, primary dependence on agricultural drainage water, several reverse biological processes have arisen. Such reverse dynamic processes have inhibited the immune systems of fish, making them highly sus-

ceptible to microbial infection, even with those ubiquitous organisms permanently existing in pond's water (Eissa and Zaki 2011, Eissa et al. 2013, Eissa et al. 2016, Gubbins 2006). Moreover, these sharp changes have led to the emergence and development of the smallest and most dangerous organisms, precisely the viruses. These tiny nasty invaders will represent the era of microbial sovereignty across the globe for centuries. The unstoppable viral emergence will irreversibly change the genetic map of many organisms, whether terrestrial or aquatic with possible cascades of extinction among vulnerable creatures (Eissa et al. 2011, Eissa et al. 2012, Marcos-López et al. 2010, Walker and Winton 2010).

The steady increase in rates of viral emergences, development and mutations has made them a death tool that threatens the whole world with annihilation. Historically, the Hispanic influenza virus (H1N1) that appeared at the beginning of the twentieth century had exterminated 40 million people in 1918, and then forty years later (1958), another global epidemic of the same virus appeared in Asia, killing more than 5 million people. A decade later, the rate of viral mutations has terribly increased to cause a new epidemic in Hong Kong, killing thousands of people. In 1979, an epidemic of the same virus had killed tens of people together with hundreds of marine mammals across the coast of Mexican gulf. In 1999, mutation among the previously erupted viral strains has occurred to create novel influenza viruses (H5N1 and H3N7). Avian Influenza (H5N1) reappeared in 2004 / 2005 with consequent eradication of millions of poultry flocks worldwide (Hannoun et al. 2004; Hannoun, 2013, Knobler et al. 2005). This wave of avian influenza has resulted in severe recession in poultry industry and great economic losses to the top regional and global producers. The wave was mainly attributed to the erratic control strategies together with incompetent vaccination regimes used at that time. Since then, the avian flu virus has become endemic in some countries such as Indonesia, Vietnam and Egypt (Kayali et al. 2016).

Epidemiologically, the puzzling dogma behind pathogenic mechanism of these viruses was unlocked. Virologists have figured out that sea gull and ducks are the genetic reservoirs which have been incriminated in developing and mutating the virus to produce new deadly strains. The two birds were responsible for emergence of more than 20 strains of influenza virus, all of which have the ability to infect most terrestrial and aquatic animals, including marine mammals such as dolphins, whales, otters and seals (Eissa and Hosni 2015). These marine mammals were reported to contract clinical infections and die from invasion with strains of the influenza virus (H1- H7 and H13) (Knobler et al. 2005). Upon dissecting moribund and mortal animals, meningitis and bronchopneumonia were revealed. Molecular epidemiological studies have revealed that the isolated virus of sea gull origin, and it was also surprising that there are more than 15 influenza viral strains starting from H1 and ending with H 15 can infect migratory ducks and geese without showing any symptoms. Further, clinical studies have proven their ability to transmit infection to marine and terrestrial creatures, which precisely confirms the role of waterfowl and migratory birds in transmission and spread of viruses through global bird migration flyways (Eissa and Hosni 2015, Knobler et al. 2005).

In a three-year research study run between the period from 2009 to 2012 at the Department of Fish Diseases and Management, Faculty of Veterinary Medicine (Aquatic Animal Medicine & Management) Cairo University, a research team led by Prof. Dr. Alaa Eldin Eissa have detected H5N1 virus in the blood of some fish, such as catfish randomly fed on large meals of dead chickens that were illegally dumped in the waterways of some Egyptian provinces, as well as in the kidneys of puffer fish from the Gulf of Abu Qir, and in the haemolymph of some crustaceans such freshwater crayfish (Procambrus as clarkii) (Eissa et al. 2012). In 2012, while discussing these results in an internationally published paper, the research team has warned of possible mutations among the detected influenza virus that might render them capable of infecting fish and other aquatic organism in one way or another. Another eminent possibility is that humans could contract infection through handling and cleaning operations of these fish if god forbid unexpectedly reached the conjunctiva or the nasal or oral cavities. In conclusion, the research team was capable of emphasizing the epidemiological role of aquatic organisms in the transmission and spread of bird flu in the Egyptian environment (Eissa et al. 2012).

In 2014, Israel has announced the emergence of Tilapia Lake Virus (TiLv), a novel viral epidemic belonging to the Orthomyxovirus family. On genetic analysis, the virus was surprisingly found to have genetic linkage with Influenza A and B viruses (Eygnor et al. 2014). Over time, cases of mass kills of tilapias were recorded in different countries across the world such as Ecuador, Thailand, Indonesia, China and finally Lake Victoria, where three countries, Tanzania, Kenya and Uganda, have suffered mass kills in both cultured and wild tilapias. Upon investigating the cause behind mass mortalities, it was affirmed that Tilapia lake virus (TiLv) was behind such kills. Interestingly, the novel virus has shown variant signs from the originally reported one. The Lake Victoria viral strain appeared to have digestive and immune signs completely different from the nervous and ocular signs of Israeli and other Non-African countries (Mugimba et al. 2018). Recently, the virus has become one of the seasonal infectious diseases posing an eminent threat to the global Nile tilapia farming industry. It is not surprising that the epidemic spread of the virus is also linked to waterfowl migration pathways across the world (Jansen et al. 2019).

During the period from 2016-2019, a new virus epidemic belonging to the family iridoviridae called ISKNV (Infectious Skin & Kidney Necrosis Virus) caused mass kills among Nile tilapia cultured earthen ponds in Brazil, Thailand, USA and Ghana (Figueiredo et al. 2020, Suebsing, et al. 2016). It is worth to mention that this virus was known for many years to only infect marine fishes such as seabream, seabass, grouper and corals. This unexpected increase in the spectrum of Nonsusceptible hosts to include freshwater fish such as tilapia has raised questions about possible viral mutation, adaptability changes, changes in immune system together with stressful aquatic environments triggering swift emergence of a new epidemic disease in Nile tilapia fish to be added to the list of viruses threatening the sustainability of Nile tilapia farming regionally and globally.

It is also surprising that the spread of dozens of viruses that were confined to specific fish species have evolved to infect variant fish species in variant aquatic habitats. Viral Nervous Necrosis (VNN) virus, which was known to infect grouper and other marine fish have crossed the barrier of only infecting salty species to also infect Nile tilapia fish in Southeast Asia and South America (Bigarré et al. 2009). Also, the emergence of viral strains that were infecting frogs and freshwater amphibians to suddenly infect large-mouthed bass (LMB) such as the Large Mouth Bass Virus (LMBV), which almost could have caused extinction of this fish species through the Lake of Michigan, United States (Boonthai et al. 2018). Furthermore, the emergence and development of dozens of viruses that have moved from crustaceans vectors living in open water to cultured crustaceans such as shrimp, lobsters and crabs with consequent clinical diseases and acute episodes of mass kills. The horrific spread of these viruses from one country to another has posed real threats to the global shrimp industry (Chen et al. 2013, Lo et al. 1996, Walker and Winton 2010). A contagious virus, such as the white spot syndrome Virus (WSSV) has been officially recorded in many countries in the Southeast Asia, and from there to the Middle East through import and international trade movement with consequent colossal economic losses.

From the above mentioned epidemiological data about viral emergences worldwide, I might almost hypothesize that viruses will be the major determinant of survival among living organisms on planet earth. The developing countries and Underdeveloped countries are the most affected by severe climate change and aquatic environmental pollution and its linkages to continuous eruptions of novel killer viruses. These stressing circumstances have triggered governments to widely invest in developing diagnostic tools (probes, kits and rapid tests) for rapid detection of viruses, vaccine manufacture and adopting strict biosecurity as well as biosafety strategies.

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